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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

## NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

#### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

#### 2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

#### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1350. The polypeptides sequences are designated SEQ ID NO: 1351-2700. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1350 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1350. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1350 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

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The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1350.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1 - 1350; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-1350. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 1351-2700); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1350; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and form a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

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The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypcptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases o disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

## 10 4. DETAILED DESCRIPTION OF THE INVENTION

#### **4.1 DEFINITIONS**

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It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

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As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-1350.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

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The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1350. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4<sup>20</sup> possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match  $(1 \div 4^{25})$  times the increased probability for mismatch at each nucleotide position  $(3 \times 25)$ . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

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The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

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The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. ct. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader scquence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

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## 4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1350; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1351-2700; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1351-2700. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1350; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1351-2700. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1350 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1350 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1350 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1350, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

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The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1350, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1350 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1350, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

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In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1350, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early. HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM I (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

## 25 **4.3 ANTISENSE**

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1350, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO:1351-2700 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1350 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

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Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1350), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

## 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region.

Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988)

Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1350). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

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Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

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#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1351-2700 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1350 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1350 or (b)

polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:1351-2700 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1351-2700 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1351-2700.

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Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1351-2700.

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The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat<sup>TM</sup> kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl<sup>TM</sup> or Cibacrom blue 3GA Sepharose<sup>TM</sup>; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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# 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

## 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

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In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction in vivo. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, e.g., cancer as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of 10 the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively 25 regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

# 4.10 USES AND BIOLOGICAL ACTIVITY

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The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

### 4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

# 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan

eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells

include, without limitation, those described in: Measurement of Human and Murine Interleukin 2
and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in
Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991;
deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988;
Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse
and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol
1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci.

Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

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U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J.,

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in

PCT/US01/03800 WO 01/57188

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

# 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce 15 large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

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Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

# 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) . as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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#### 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.

15 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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### 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

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Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β<sub>2</sub> microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

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Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

# 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

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Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

# 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:
Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

# 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide). Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen'mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

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In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

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In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

# 30 4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

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# 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

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Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282:*63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

#### 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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# 4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### 4.10.16 **LEUKEMIAS**

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Leukemias and related disorders may be treated or prevented by administration of a

therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see

Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

# 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

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- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
  - (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
  - (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
  - (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
  - (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular
   neurotoxins; and
  - (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo:
- increased production of a neuron-associated molecule in culture or in vivo, e.g., (iii) choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
  - decreased symptoms of neuron dysfunction in vivo. (iv)

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

#### 4.10.18 OTHER ACTIVITIES

30 A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

# 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

# 10 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally introdermally, of a

Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 4.11 THERAPEUTIC METHODS

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The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

# 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

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The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

#### 4.12.1 ROUTES OF ADMINISTRATION

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Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

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When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

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For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, tale, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

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Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

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The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

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The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

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## 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC<sub>50</sub> as determined in cell culture (i.e., the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01  $\mu$ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1  $\mu$ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

#### 4.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

## 4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab, Fab and F(ab)2 fragments, and an Fab expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG1, IgG2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

#### 5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

## 10 5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol.</u>, <u>133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

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The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

#### 5.13.2 Humanized Antibodies

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10 The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-15 binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the 20 corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable 25 domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 30 2:593-596 (1992)).

#### 5.13.3 Human Antibodies

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Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

## 5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_{v}$  fragments.

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., <u>J. Exp. Med.</u> 175:217-225 (1992) describe the production of a fully humanized bispecific antibody  $F(ab')_2$  molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

#### 5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

#### 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include <sup>212</sup>Bi, <sup>131</sup>I, <sup>131</sup>In, <sup>90</sup>Y, and <sup>186</sup>Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

# 4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1350 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1350 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

#### 4.15 TRIPLE HELIX FORMATION

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In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

## 4.16 DIAGNOSTIC ASSAYS AND KITS

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The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that annual to a polynucleotide of the invention under such conditions, and amplifying annualed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

#### 35 4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide in vivo at the target site.

## 4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1350, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
  - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

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For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspezak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

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In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

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Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

#### 10 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1350. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1350 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

# 10 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

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Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

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More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

## 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI\*\*), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

#### 4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

# 20 5.0 EXAMPLES

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## 5.1 EXAMPLE 1

# Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

#### 5.2 EXAMPLE 2

# **Novel Contigs**

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-1350 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO:189-282) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 189-282. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-1350 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and Geneseq database October 12, 2000, update 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the

closest homologue for SEQ ID NO:1-1350. The nearest neighbor results for SEQ ID NO: 1-1350 are shown in Table 2 below.

Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-1350. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/496,914.

# TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	111 151 188 215 662-665 877 910 927
	l·		976 1233 1319 41 49 74 101 111 120 132 141-142 151
adult brain	GIBCO	ABD003	217 225 238 271 317 404 446 469 503
	1		513-514 535 550 564 573 666-669 798
	Ì		898 910 927 976 1067 1083 1085 1178
			1254
		ABR001	39 216 238 327 356 535 927 1056 1121
adult brain	Clontech	ABROOT	1178-1180 1199 1251
	Clontech	ABR006	74 611 949 1034 1136
adult brain	Clontech	ABR008	14 32 41 61 81 86 89 120 132 138 145
adult brain	Cionieca	ADROOG	147 188 197 208 225 227-239 250 300-
			303 312 316 328-331 340 357-362 374
			380 384-391 408 414 446 448 464-467
			483 488 495-496 505 512 521 535 550
	}	}	566 571 577 585 590 594 598 634 641
			658 666 683 725 742 764 767 786 801
			805 810 823 826 829 831 836 841 887-
			923 927 934 943 950-951 963 976 995
	1		1000-1001 1006 1026 1034 1048 1057- 1067 1086 1088 1090 1118 1120 1122-
		,	1128 1142 1162 1181-1192 1199 1204
			1218-1219 1225 1232 1253 1267 1271-
			1306 1342 1347 1349-1350
		100011	49 238 1219
adult brain	Clontech	ABR011	74 238
adult brain	BioChain	ABR012 ABR013	868 1268
adult brain	Invitrogen	ABT004	49 117 138 191 217 252 291 305 535
adult brain	Invitrogen	AB1004	566 596 663 670 746 798 816-819 876
	<b>[</b>		892 898 922 943 963 1034-1036 1121
	Strategene	ADP001	41 74 101 138 211 238 304 537 582
cultured	Surregene	ADI OUI	740 798 883 943 976 1067
preadipocytes	Clontech	ADR002	49 74 101 111 120 127 151 215 238
adrenal gland	Cionicon	1101000	240-247 316 330 363-364 404 414 534-
İ			535 833 924-940 950 963 976 1001
			1003 1067-1070 1118 1156 1193-1200
			1325
adult heart	GIBCO	AHR001	38 49 71-72 74-77 79 92 99 101 111
			118 129 132 138 151 158-163 182 195-
			203 215 217 238 264 269 353 384 398 408 434-439 446 504 512-513 519 537
	İ		562-573 577 611-614 616-619 658 661
	į		671-672 722 734 757-773 815 828-835
	į		874 891 898 919 926-927 976 988
			1021 1037 1041 1062 1067 1071 1080
	•	,	1083 1093 1122 1131 1185 1201 1254
			1308 1331 1335
		AKD001	41 49 51 71-74 78-85 94 100-101 103-
adult kidney	GIBCO	AKIDOOL	107 111 119-120 138 151 157 215 217-
-			218 238 250 264 294 304 384 404 440
	Ì		446 454 477 504-505 509 514 518-519
1		{	535 537 564 574-583 620-627 639 653
			673-675 705 753 789 831 844 851 859
			877 909 918 927 956 963 976 1067
			1074 1083 1095 1178 1302 1331 1335
adult kidney	Invitrogen	AKT002	11-12 41 49 111-112 215-217 294 316
addit Midiloj	1	,	446 487 564 575 844 868 910 927 976
1		1	1116
		ALG001	8 101 111 151 187 402 446 490 514

# PCT/US01/03800

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
	2247004100	Alysed Library Name	518 537 545 549 580 582 592 594 634
1			640 651-652 676-678 725 851 873 918
			952 976 1042 1067 1076 1083 1152
lymph node	Clontech	ALN001	8 111 121 151 180-182 188 215 537
,,		7111001	545 549 651 679-682 789 804-810 868
			873 927 952 976 1042 1059 1335
young liver	GIBCO	ALV001	8 64 79 111 186 215-216 238 446 514
,	GIB00	ALVOOL	510 527 564 652 692 684 698 752 708
	1	-	519 537 564 653 683-684 698 753 798
i	1	i	813 833 840 858 927 976 1038-1039
adult liver	Invitrogen	ALV002	1051 1085 1224 1245 1256
	MIVIMO GOII	ALV002	40 71 292-293 305 384 468-469 496
			505 657 675 714 753 832 844 941-942
adult liver	Clontech	ALV003	976 1040 1076 1256 1293
adult ovary	Invitrogen		976
addit oval y	invidogen	AOV001	8 32 36 38 41 49 51 71 74 79-80 101
			104 111 120 122-125 138 140 143-149
			151 188-190 207-212 215-217 238 264
	•		316 384 409 440 445-446 496 504 512
			514 518-519 535 537 549-550 564 566
			571 580 582 600 618 638 657 667 681
			685-697 699 705 722 735-744 761 771
			815 833 842-865 868 875-876 918 926-
			927 950 952 963 976 1023 1042 1048
			1051 1059 1072 1076 1083 1117 1120
			1124 1131 1144 1174 1224 1268 1331
<u> </u>			1335
adult placenta	Clontech	APL001	102 217 238 537 641 700
placenta	Invitrogen	APL002	663 851 1048
adult spleen	GIBCO	ASP001	8 45 74 111 132 140 151 185 217 238
	İ		294 414 446 477 504 514 534 545 549
	į		592 722 873 883 952 976 1041-1042
		_i	1083 1093-1094 1152 1224
testis	GIBCO	ATS001	72 107 111 113 126 140 151 183 215
	1	1	238 446 497 537 642 701-706 811 877
		· ·	927 962 976 1083 1117 1131
adult bladder	Invitrogen	BLD001	41 151 191 402-405 409 414 496 545
			592 607 706 873 952 1178 1329-1335
bone marrow	Clontech	BMD001	8 58-62 65-68 74 79 108 111 116 137
	ĺ		147 151 164-174 213-215 238 305-307
			374 404 446 460 466 516 519 534 538-
	.]		541 544-546 549-554 566 584 586 592
			596 607 610 628-629 643-645 652 707-
			708 774-789 844 866-871 873 919 927
			952 963 976 998 1034 1042 1064 1083
	)		1085 1120 1132 1152 1225 1229 1268
			1307 1310
bone marrow	Clontech	BMD002	6 8 37-38 52 74 77 105 111 129 132
			210 317 510-511 545 549 581 598 628
	1		638 724 766 789 844 860 868 873 919
		.	927 952 963 968 976 1042 1111 1141
		1	1160-1161 1229 1266 1346
bone marrow	Clontech	BMD004	111 238 282 549 1083
adult colon	Invitrogen	CLN001	
		CLITOUI	52 260 264 299 494 536 545 564 592
		j	844 873 877 952 976 1042 1152 1268
adult cervix	BioChain	CVV001	1336-1337
II OOI VIA	DIOCUAIN	CVX001	49 51-129 132 151 205 207 238 332-
•	1.	] !	335 365-367 392-401 440 466 470-471
			518 537 597 629 832 877 927 976 1006
		j l	1085 1117 1129-1134 1192 1202-1205
diaphragm	BioChain	DIA002	1219 1309-1328 74 976 1083

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS: 32 40-41 49 74 79 101 111 120 132
endothelial cells	Strategene	EDT001	138 151 204-206 215-217 238 269 316
			138 151 204-206 215-217 236 209 510
. :			414 433 505 510 513 550 555 580 582
			596 675 722 745 798 814 836-841 851
			918 976 1041 1043 1073 1083 1131
to the state of th			1331
Genomic clones	Genomic DNA	EPM001	525-532 927
from the short arm	from Genetic		
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM003	47 525
	from Genetic	221.2005	
from the short arm	Research		
of chromosome 8		EPM004	525 927
Genomic clones	Genomic DNA	EPMI004	323 727
from the short arm	from Genetic	Ì	
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM005	531
from the short arm	from Genetic		
of chromosome 8	Research		
esophagus	BioChain	ESO002	74 138 238
fetal brain	Clontech	FBR001	441-442 927
fetal brain	Clontech	FBR004	215 893 927 1001
	Clontech	FBR006	48 61 101 120 132 138 140 147 208
fetal brain	Cioniecii	Throw	225 271 317 319 336 359 368 405-414
			519 550 571 594 686 715 722 764 824
			829 836 859 909 927 943 947 963 105
			1067-1068 1104 1135-1140 1162 1206
			1207 1235 1268 1288 1307-1308 1319
	.   .		1338-1350
fetal brain	Clontech	FBRs03	111 446
fetal brain	Invitrogen	FBT002	41 51 120 151 192-194 264 504 512
iciai viam	22		535 683 761 798 820-827 844 876 909
		,	963 976 1026 1048 1083 1144 1302
67.11	Invitrogen	FHR001	446 566 761
fetal heart	Clontech	FKD001	51 74 111 127 140 151 184 294 537
fetal kidney	Ciontech	INDOOL	550 630-631 1319
		FKD002	111 976 1083
fetal kidney	Clontech	FKD002	238 974
fetal kidney	Invitrogen		463 566 976 1074 1083 1093
fetal lung	Clontech	FLG001	41 238 330 407 415-416 537 573 844
fetal lung	Invitrogen	FLG003	41 238 330 407 413-410 337 373 044
•			859 1048 1083 1116 1192
fetal liver-spleen	Columbia	FLS001	8 14 34-35 37 41 43 49 51 54-56 63-6
TOTAL MACE SPACES	University		69-71 74 77 79 87-90 101 107 110-11
	0.11. 0.11.	• •	114 120 128-131 138 140 147 150-15
			197 210 215 217 225 238 312 367 38
			414 440 446 460 468 483 496 504-50
	i		511-515 518-519 523 533-535 537 54
	{		544-545 547-550 555-560 564 566 57
	1	1	577 582 585-586 598 636 646-647 64
		\	652 664 698 709-710 714 722-723 73
		[	004 004 070 107-110 114 144-145 15
	Į.		735-736 746-753 761 784 798 823 82
		1	832 844 851 858-859 868 873 876 89
	}	1	927 943 949 952 963 976 984 1002
			1021 1023 1040 1042 1044 1050 108
	}	}	1093 1116 1120 1129 1131 1144 117
{			1217 1251 1254 1256 1302 1308 131
	}		1319
		TET 5000	8 36-37 41-46 49 54 64 71 74 79 101
fetal liver-spleen	Columbia	FLS002	111 120 129 147 207 210 215-216 23
	University	İ	250 330 353 359 366 383-384 414 47
1	1		505 508-509 511 515-524 534-535 5
1	1	1	1 505 508-509 511 515-524 554-555 5.
1		1	544-545 564 566 571 577 591 598 63

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			663 671 698 714 722 725 727 751 798 851 859 873 876 909 927 949 952 983- 984 1002 1023 1042-1044 1085 1095 1131 1144 1178 1199 1233 1240-1270 1331 1340
fetal liver-spleen	Columbia University	FLS003	64 535 976 1256
fetal liver	Invitrogen	FLV001	8 101 120 138 217 446 468 535 566 580 722 730 749 844 918 943 976 1051 1256 1331
fetal liver	Clontech	FLV004	537 926 1256
fetal muscle	Invitrogen	FMS001	51 111 264 312 369-370 404 417-421 425 535 537 577 598 614 836 857 1141 1208 1268
fetal muscle	Invitrogen	FMS002	537
fetal skin	Invitrogen	FSK001	13-26 32 41 51 89 107 111 147 151 225 264 316 405 422-429 488-494 496 519 534-535 537 566 675 732 859 876- 877 898 947 949-950 963 976 1001 1062 1076 1083 1117 1144 1165 1268 1281
fetal skin	Invitrogen	FSK002	537 812
fetal spleen	BioChain	FSP001	87 549
umbilical cord	BioChain	FUC001	27-33 41 49 151 215 238 248-249 301 316 446 495-503 519 521 534-535 537 582 634 691 877 883 927 944-950 963 976 1001 1075 1142-1143 1171 1218 1243 1308
fetal brain	GIBCO	HFB001	41 49 57 79 87 103 111 120 132-135 138 145 151 188 197 207 215 238 264 271 294 316 367 414 440 446 466 504 513-514 535 542-543 550 564 571 596 635 648-654 675 711-715 722-723 798 832 872 876 883 927 976 1095 1144 1168 1171 1178 1211 1335
macrophage	Invitrogen	HMP001	238
infant brain	Columbia University	IB2002	49-50 77 81 89 105 111 136-138 140 151 161 175-179 185 216-217 264 295 299 308-310 371-373 462 476 504 511- 513 533 537 564 566 571 655-657 662 683 716-720 723 752 790-803 829 832 858-859 876 898 909 949 976 1045- 1047 1076-1087 1090 1093 1116 1122 1144 1209-1213 1225 1233 1256 1319 1341
infant brain	Columbia University	IB2003	41 50 77 104 132 215 238 508 512-513 519 566 655 714 794 918 943 976 1067 1092-1093 1233
infant brain	Columbia University	IBM002	311 472-473 753 1214
infant brain	Columbia University	IBS001	51 111 376 474 790 876 949 1144 1204 1221
lung , fibroblast lung tumor	Strategene Invitrogen	LFB001 LGT002	151 316 462 514 534 582 675 939 1131 1-7 41 74 79 94 115 120 138-139 156 215 217 269 280 296 337 374-375 384 404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705 721-724 754-756 779 859 868 872-874 876-877 919 927 949 951-952 959 976 1002 1042 1048-1053 1076 1083 1088- 1089 1131 1144-1147 1216-1218 1229

Fissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS: 1293 1311
	+ mag	T PC001	41 74 111 132 151 253 316 446 550
ymphocytes	ATCC	LPC001	634 844 927 976 1085 1268
		7770001	8 11 41 74 86 91-98 101 109 111 120
eukocyte	GIBCO	LUC001	147 151 212 215 218 238 252 288 312-
		1	314.316 338 359 408 427 443-447 505
			510 512 514 518 534 545 549-550 561
			564 566 571 577 580 582 587-609 615
	•		632-638 658-659 698 714 725-728 832
			836 841 859 866 873-874 882-883 918-
			919 927 943 952 963 976 1042 1076
	•		1083 1090 1148 1152 1168 1195 1219-
			1220 1224
			74 100 215 232 238 339-341 446 545
leukocyte	Clontech	LUC003	657 660 729 873 883 927 952 963 1008
•			657 660 729 873 883 927 932 903 1000
			1042 1116 1120 1149-1150 1215 1222
Melanoma from cell	Clontech	MEL004	210 215 238 342 534 545 592 722 873
line ATCC #CRL	İ		919 929 939 952 976 1071 1118 1218
1424	1		1235 1245
mammary gland	Invitrogen	MMG001	8-10 40-41 49 73 80 114 138-140 147
Bronze			217 250-256 264 297-299 305 377-378
		,	398 446 481-486 505 512 537 545 549
		'	571 592 725 730-733 816 829 836 844
•	ļ	ł	868 873 876-877 898 926 943 951-960
			963 976 995 1034 1042 1048 1054-
	}		1055 1076 1083 1091 1093 1116-1117
			1124 1152 1302
induced neuron cells	Strategene	NTD001	39 101 111 138 238 361 1225 1251
mancea neuron cens	Sualegene	11,200.	1319
retinoid acid induced	Strategene	NTR001	74 225 976
	Strategene	1412001	· ·
neuronal cells	Ctrotograpo	NTU001	129 225 238 304 313 361 657 976
neuronal cells	Strategene	PITO04	976
pituitary gland	Clontech	PLA003	38 976
placenta	Clontech		111 188 238 257-258 564 724 961-966
prostate	Clontech	PRT001	1067 1095
		7777001	238 430-431 841 859 868 963 1001
rectum	Invitrogen	REC001	1116
			8 151 402 432-433 446 496 868 952
salivary gland	Clontech	SAL001	976 1083 1120 1151 1184
			8 101 147 215 259-266 446 462 505
small intestine	Clontech	SIN001	545 592 660 789 836 866 873 927 952
	1	]	545 592 660 789 856 800 875 927 952
,			963 967-978 1042 1120 1152 1223-
			1224
skeletal muscle	Clontech	SKM001	238 302 927 943 992 1031
spinal cord	Clontech	SPC001	74 111 132 151 215-216 238 264 267-
Spring Cold			270 343-344 353 379 516 537 566 740
			828 927 976 979-994 1092 1153-1159
	ŀ	,	1225 1250
adult enlage	Clontech	SPLc01	698 859 1042
adult spleen stomach	Clontech	STO001	210 238 271-272 537 580 705 918 952
Stomach	Cionicon	1	995 1171
41-1	Clontech	THA002	61 219-220 273-276 312 315 330 596
thalamus	Ciontecn	11175002	963 996-1007 1059 1093 1160-1162
	Clamatash	THIM001	8 120 151 208 221 316-317 353 639
thymus	Clonetech	THIMOUT	750 867 874 878-881 927 963 1023
			1083 1094-1096 1124
		77716.00	8 61 114 129 132 210 225 231 306
thymus	Clontech	THMc02	317-319 336 340 359 380 398 446 448
· .	*		463 512 519 545 554 587 598 698 724
}	1	ì	725 789 812 836 868 873 927 947 952
1 .	· ·		MYE 400 010 634 688 814 611 641 4 11

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			976 1007 1042 1083 1085 1097-1116
	1	•	1122 1147 1177 1226-1229 1234 1311
<u> </u>			1313
thyroid gland	Clontech	THR001	14 41 49 76 94 111 144 151 183 188
]			210 217 222 253 264 271 277-286 294
1	1		320-326 345-352 361 381-382 446 467
		1	483 514 534 549-550 564 578 602 649
			844 882-883 927 950 956 976 1008-
!	-		1028 1076 1083 1117-1120 1142 1163-
trachea	Clarate 1	777 0001	1175 1230-1238 1308
uachea	Clontech	TRC001	223-225 238 287 353-354 514
	Ì		545 592 611 873 883-884 927
			952 1029-1031 1042 1151-1152
			1170 1176-1177 1239
uterus	Clontech	UTR001	151 226 288-290 355 537 877
			885-886 976 1001 1032-1033
			1232

# TABLE 2

SEQ ID	Accession	Species	Description	Smith-	1%
NO:	No.			Waterman	Identity
NO:	Doggo	<del></del>		Score	1
•	B02829	Homo sapiens	Human G protein coupled receptor hRUP5 protein SEQ ID NO:10.	460	100
2	G03564	Homo sapiens	Human secreted protein, SEO ID NO: 7645.	111	151
3	R26173	Homo sapiens	Part of Major Yo paraneoplastic antigen (CDR62) encoded by clone pY2.	293	76
4	L29536	Homo sapiens	calcium channel (type alpha I subunit	191	65
5	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	251	50
6	M11507	Homo sapiens	transferrin receptor	120	95
7	AF099100	Homo sapiens	WD-repeat protein 6	1941	93
8	Y92338	Homo sapiens	Human cancer associated antigen precursor from clone NY-REN-45.	245	82
9	G01343	Homo sapiens	Human secreted protein, SEQ ID NO: 5424.	226	91
10	AJ133798	Homo sapiens	copine VII protein	1127	68
11	G02449	Homo sapiens	Human secreted protein, SEQ ID NO: 6530.	584	99
12	X98330	Homo sapiens	ryanodine receptor 2	282	78
13	AL024498	Homo sapiens	dJ417M14.2 (novel serine/threomine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase))	293	100
14	AF045577	Pan troglodytes	olfactory receptor OR93Ch	191	36
15	G03131	Homo sapiens	Human secreted protein, SEQ ID NO: 7212.	93	39
16	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein precursor	569	89
17	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75,	99	44
18	Y36203	Homo sapiens	Human secreted protein #75.	165	75
19	U15647	Mus musculus	reverse transcriptase	106	40
20	G02701	Homo sapiens	Human secreted protein, SEQ ID NO: 6782.	544	100
21	Y35923	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 172.	1691	100
22	G04030	Homo sapiens	Human secreted protein, SEQ ID NO: 8111.	380	96
23	G02455	Homo sapiens	Human secreted protein, SEO ID NO: 6536.	123	50
24	AF036329	Homo sapiens	gonadotropin-releasing hormone precursor, second form	284	90
25	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	96	32
26	S80119	Rattus sp.	reverse transcriptase homolog	100	34
27	U83303	Homo sapiens	line-1 reverse transcriptase	101	35
28	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	135	45

SEQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:		· .		83	42
9	G04067		Human secreted protein, SEQ ID NO: 8148.	116	72
0	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	96	67
1	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	58	32
32	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.		98
13	Y66688	Homo sapiens	Membrane-bound protein PRO1152.	2457	95
34	Y87071	Homo sapiens	Human secreted protein sequence SEQ ID NO:110.	348	
35	U15131	Homo sapiens	p126	182	48
36	Y73464	Homo sapiens	Human secreted protein clone yl4_1 protein sequence SEO ID NO:150.	982	90
37	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	687	99
38	AC067969	amino acids 3338-4088	Homo sapiens ryanodine receptor 1 (skeletal)	386	66
39	AL031588	Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN, FGENES and GENEWISE)	493	76
40.	002/09	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	110	51
40	G03628		CGI-35 protein	228	68
41	AF132969	Homo sapiens	Human secreted protein encoded by gene 45.	220	88
42	Y36268	Homo sapiens	mini collagen	105	35
43	X61048	Hydra sp.	mini-collagen	110	31
44	M76546	Helianthus annuus	hydroxyproline-rich protein	139	70
45	U82288	Caenorhabditi s elegans	Rac-like GTPase	118	58
46	G03477	Homo sapiens	Human secreted protein, SEQ ID NO: 7558.	113	63
47	AF090942	Homo sapiens	PRO0657	90	59
48	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	72	56
49	AJ005560	Mus musculus	SPR2B protein		98
50	G02450	Homo sapiens	Human secreted protein, SEQ ID NO: 6531.	385	94
51	Y91649	Homo sapiens	Human secreted protein sequence encoded by gene 60 SEQ ID NO:322.	973	
52	U93563	Homo sapiens	putative p150	105	38
53	Y55927	Homo sapiens	Human STLK2 protein.	699	85
	G02607	Homo sapiens	Human secreted protein, SEO ID NO: 6688.	145	56
54 55	AB008175	Mus musculus	hepatic nuclear factor 1-beta short form	356	74
	1460041	Homo sapiens	protein-tyrosine phophatase	165	41
56	M68941	Homo sapiens	c390E6.1 (chloride channel 7)	338	76
57 58	AL031600 AF011417	Mus musculus	putative pheromone receptor	143	55
59	AF 167320	Mus	zinc finger protein ZFP113	558	68
		musculus	interferon regultory factor 7	263	96
60 61	X07984	Mus	protein-tyrosine kinase	297	69
		musculus	Human secreted protein clone cb98_4.	791	98
62	Y29861	Homo sapiens		485	65
63 64	U35376 AF265555	Homo sapiens Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	785	74
L		<del></del>	APOLLON  Human secreted protein, SEQ ID NO: 7964.	88	95
65 66	G03883 AF177390	Homo sapiens Manduca	antennal specific membrane protein AMP	274	54
		sexta	CDTD2	614	100
67 68	AB040800 AF030027	Homo sapiens Equine	24	213	26
		herpesvirus 4		261	95
69	G02965	Homo sapien		1144	98
70	W75770	Homo sapien		239	76
71	AB011135	Homo sapien	KIAA0563 protein		78
72	AB014885	Halocynthia roretzi	HrPOPK-1	813	
73	AF045454	Cavia porcellus	phospholipase B	955	73
74	J02870	Mus	laminin receptor	308	61

SEQ	Accession	Species	Description	Smith-	%
NO:	No.			Waterman	Identity
110.	<del>-                                    </del>	musculus		Score	
75	Y00826	Rattus	gp210 (AA 1-1886)	<del>                                     </del>	10.
	100020	norvegicus	gp210 (AA 1-1886)	413	84
76	AF117754	Homo sapiens	thyroid hormone receptor-associated protein	351	54
	_		complex component TRAP240	) 331	J.4
77	Y38422	Homo sapiens	Human secreted protein.	468	76
78	Y14596	Homo sapiens	Human T-type voltage-gated Ca channel alpha-	1357	99
P 5			1-I (hCavT3).	ļ .	1
79	Y14591	Human	APM-1 protein	767	100
		papillomaviru s type 68	·	1	· ·
80	AL137802	Homo sapiens	dJ798A10.2 (KIAA0445 protein)	1	<u> </u>
81	AP000383	Arabidopsis	protein arginine N-methyltransferase-like protein	71 359	34 65
		thaliana	proton argume is meany in ansterase-like protein	339	60
82	L46815	Mus	DNA binding protein Rc	895	75
		musculus		5,5	/"
83	G01600	Homo sapiens	Human secreted protein, SEQ ID NO: 5681.	315	96
84	Y53886	Homo sapiens	A suppressor of cytokine signalling protein	538	71
85	AB029002	+	designated HSCOP-6.		
86	Y28678	Homo sapiens Homo sapiens	KJAA1079 protein	134	42
87	Y99368	Homo sapiens	Human cw272_7 secreted protein. Human PRO1326 (UNQ686) amino acid	325	62
	1,,,,,,	Tromo sapions	sequence SEQ ID NO:100.	156 · · ·	48
88	AJ225124	Mus	hyperpolarization-activated cation channel,	487	95
		musculus	HAC3	10%	33
89	AF177203	Homo sapiens	cerebral cell adhesion molecule	290	56
90	Y28280	Homo sapiens	Human G-protein coupled receptor GRIR-2.	326	79
91 92	L39891	Homo sapiens	polycystic kidney disease-associated protein	1751	95
93	AF064876 AF170723	Homo sapiens	ion channel BCNG-1	953	99
94	X13292	Homo sapiens	protein kinase STK10	401	53
•	X13292	Trypanosoma brucei	GPI-phospholipase C (AA 1 - 358)	151	37
95	Y34127	Homo sapiens	Human potassium channel K+Hnov11.	661	00
96	X03638	Rattus	sodium channel protein I (aa 1-2009)	1775	99
		norvegicus	(m 1 2003)	1773	72
97	AF134213	Homo sapiens	ubiquitin-specific protease	1995	99
98	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	213	38
99	AF021935	Rattus	mytonic dystrophy kinase-related Cdc42-binding	675	48
100	AF279265	norvegicus Homo sapiens	kinase		
101	AC007878	Homo sapiens	putative anion transporter 1 match to nuclear protein, NP220; note: sequence	867	98
	11000,070	Tionio sapions	difference at residue 58	160	60
102	U22829	Mus	P2Y purinoceptor	264	42
		musculus		207	42
103	Y45023	Homo sapiens	Human sensory transduction G-protein coupled	516	99
104	V04000	<del>  ,                                   </del>	receptor-B3.		
105	Y94990 Y87342	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	787	98
103	16/342	Homo sapiens	Human signal peptide containing protein HSPP-	343	57
106	AF169312	Homo sapiens	119 SEQ ID NO:119. hepatic angiopoietin-related protein	010	
107	AF116657	Homo sapiens	PRO1310	212	67
108	AE000401	Escherichia	sialic acid transporter	74 587	52 96
		coli	· •	<b>7</b> 01	30
109	Y38395	Homo sapiens	Human secreted protein encoded by gene No. 10.	693	100
110	Y78801	Homo sapiens	Hydrophobic domain containing protein clone	182	94
111	775575		HP00631 amino acid sequence.	ŀ	• [
12	Z25535 Y94939	Homo sapiens	nuclear pore complex protein hnup153	464	85
	177737	Homo sapiens	Human secreted protein clone ye90_1 protein	274	51
113	AF016365	Homo sapiens	sequence SEQ ID NO:84. hexokinase 1 isoform td	201	
14	AC007956	Homo sapiens	unknown	301	71
15	M83738	Homo sapiens	protein-tyrosine phosphatase	520 251	75 92
16	AL157952	Homo sapiens	dJ875K15.1.1 (ets homologous factor (ets-	484	92
.17			domain transcription factor ESE-3A, isoform 1))		-1
	W18084	Homo sapiens	Human Aurora-2.		

D NO: 118 119 120 121 122 123	L41816 AJ006710 AF026954	Rathus	cam kinase I	Score 407	62
118 119 120 121 122	AJ006710	Rathus	cam kinase i		
19 20 21 22	AJ006710	nominarimis		607	93
21 22	AF026954		phosphatidy imostor 5-kmase	627	94
22	l	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDPr	1646	
	S39392	Homo sapiens	protein tyrosine phosphatase, PTPase {EC	373	68
	U60805	Homo sapiens	oncostatin-M specific receptor beta subunit	262	88
	Y44403	Homo sapiens	Human truncated tankyrase-1.	111	35
24	U88167	Caenorhabditi s elegans	contains similarity to C2 domains	219	29
25	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit	693	90
126	AB021861	Mus musculus	apoptosis signal-regulating kinase 2	153	65
127	AF305210	Homo sapiens	concentrative Na+-nucleoside cotransporter hCNT3	807	97
		17	protein kinase	220	73
128	M90360	Homo sapiens	alpha 1C adrenergic receptor isoform 2	574	86
129	D32202	Homo sapiens		496	67
130 131	AF208043 AF201734	Homo sapiens Mus	IFI16b testis specific serine kinase-3	800	87
		musculus	differentiation enhancing factor 1	159	74
132	AF112886	Bos taurus	phospholipase C-beta-1b	554	85
133 134	AJ278314 W74802	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 73	1157	87
	t	<u> </u>	clone HSQEL25.  Pancreas-specific gene	668	96
135	AB020335	Homo sapiens	A secreted protein encoded by clone dt674_2.	866	98
136 137	W80408 AC002563	Homo sapiens Homo sapiens	putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860)	5041	99
	l		PRO3434, a novel secreted protein.	891	100
138 139	Y96736 AB024034	Homo sapiens Arabidopsis	DNA-damage inducible protein DDI1-like	147	55
	l	thaliana	Human GTPase regulator GRAF.	248	56
140	W97809	Homo sapiens	Human G Pase regulator Grows.	125	46
141	Y51557 AF090113	Homo sapiens Rattus	Human PLA2 protein.  AMPA receptor binding protein	623	93
	l	norvegicus	Human RECK cancer-inhibiting protein.	641	82
143	W26642 U87306	Homo sapiens Rattus	transmembrane receptor UNC5H2	578	84
145	AF264014	norvegicus Homo sapiens	scavenger receptor cysteine-rich type I protein	727	92
			M160 precursor	140	40
146	W63683	Homo sapiens	Human secreted protein 3.	513	81
147	M96264 D64014	Homo sapiens Escherichia	galactose-1-phosphate uridyl transferase HrsA	818	90
149	M83316	Escherichia	pppGpp phosphohydrolase	915	95
150	AL163279	Homo sapiens	homolog to cAMP response element binding and beta transducin family proteins	1261	99
	1	1 11 1 1 1 1 1		940	99
151 152	AF179867 R95332	Homo sapiens Homo sapiens	1 1 4 1	392	61
		<del>-  </del>		370	92
153	AF151859	Homo sapiens		489	81
154	X66957	Homo sapiens		432	92
155	Y16355	Homo sapiens		349	78
156 157	G00857 AF159455	Homo sapien: Mus	zinc finger protein	352	74
1		musculus	- Lated Irings	537	76
158	L76191 AP001743	Homo sapien	s I nutative gene, ankirin like, possible dual	670	98
160	AJ250425	Rattus	specifity Ser/Thr/Tyr kinase domain Collybistin I	556	74
1		norvegicus		370	100
161	G02885	Homo sapien	s Human secreted protein, SEQ ID NO: 6966.	13,0	1.00

- <del></del>	<del></del>	1.0	·		,
SEQ	Accession	Species	Description	Smith-	%
ID	No.	1	}	Waterman	Identity
NO:		- <del>  </del>		Score	
162	Z22968	Homo sapiens	M130 antigen	610	100
163	AF181121	Homo sapiens	ATP-dependent Ca2+ pump PMR1	336	92
164	AF055636	Homo sapiens	leucine-rich glioma-inactivated protein precursor	455	94
165	AF160798	Rattus norvegicus	calcium transporter CaT1	700	96
166	Y76332	Homo sapiens	Fragment of human secreted protein encoded by	327	45
100	1,0332	Tromo saprous	gene 38.	327	45
167	Y48607	Homo sapiens	Human breast tumour-associated protein 68.	1072	22
168	AB020741	Mus	NIK-related kinase	197	43
100	110020141	musculus	TVIN-Telated Killase	197	43
169	AF252293	Homo sapiens	PAR3	596	44
170	U59429	Cricetinae	diacylglycerol kinase eta	481	82
	1 000	gen. sp.	diacyigiyeder kindse em	401	02
171	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	386	42
172	AF127085	Mus	semaphorin cytoplasmic domain-associated	507	82
		musculus	protein 3B	1 307	02
173	Y27918	Homo sapiens	Human secreted protein encoded by gene No.	653	99
			123.	1 033	,,,
174	G02979	Homo sapiens	Human secreted protein, SEQ ID NO: 7060.	538	97
175	U36488	Mus	embryonic stem cell phosphatase	168	55
	1	musculus	, same years on preoppression	1.00	1 33
176	W95629	Homo sapiens	Homo sapiens secreted protein gene clone	1022	100
	1		gm196 4.	1022	100
177	AF289023	Homo sapiens	formiminotransferase cyclodeaminase form D	255	93
178	X04936	Homo sapiens	T-cell receptor alpha-chain (413 is 2nd base in	710	99
	Ī	1	codon)	1	1
179	AF127481	Homo sapiens	non-ocogenic Rho GTPase-specific GTP	175	80
			exchange factor	1	
180	G00978	Homo sapiens	Human secreted protein, SEQ ID NO: 5059.	517	94
181	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	671	96
182	AF110640	Homo sapiens	orphan seven-transmembrane receptor	862	100
183	AB020854	Bos taurus	orphan transporter short splicing variant	766	84
184	AF169691	Homo sapiens	cadherin-like protein VR8	375	38
185	AF126372	Homo sapiens	thyrotropin-releasing hormone degrading	985	99
	<u> </u>	<u> </u>	ectoenzyme	·	
186	L20966	Homo sapiens	phosphodiesterase	541	76
187	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	254	93
188	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein	301	98
100	111111111111111111111111111111111111111		sequence SEQ ID NO:42.		
189	Y66713	Homo sapiens	Membrane-bound protein PRO1309.	694	100
190	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	331	73
191	U36771	Rattus	sn-glycerol 3-phosphate acyltransferase	707	92
160		norvegicus			
192	R05935	Homo sapiens	Secreted GPIIb subunit of multiple subunit	157	72
193	M92084	I	polypeptide (MSP)GPIIb-IIIa.		
173	M192U84	Theileria	casein kinase II alpha subunit	364	50
194	Y66645	parva	Visit and the second		
195	W95631	Homo sapiens	Membrane-bound protein PRO1310.	448	90
193	W 23031	Homo sapiens	Homo sapiens secreted protein gene clone	382	49
196	AF255614	Rattus	hj968_2.		
170	AL 255014	norvegicus	scaffolding protein SLIPR	680	99
197	AC021640	Arabidopsis	putative phosphatidate phosphohydrolase	300	ļ.,
.,,	110021040	thaliana	putative phosphaddate phosphonydrorase	300	41
198	AF073967	Mus	olfactory receptor	316	43
	120,550	musculus	onactory receptor		43
		domesticus			
199	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	617	98
200	AF117948	Homo sapiens	pancreas-enriched phospholipase C	625	
201	AF128625	Homo sapiens	CDC42-binding protein kinase beta	636	89
202	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	1303	94
203	Y53021	Homo sapiens	Human secreted protein clone qc646 1 protein	701	100 99
	]	Tronto papiens	sequence SEQ ID NO:48.	/01	ענ
204	AF227968	Homo sapiens	SH2-B beta signaling protein	182	79
205	S81752	Homo sapiens	DPH2L=candidate tumor suppressor gene	375	100
	1 30:132	Tromo sapions	21 1127 curarrate transit subblessor Rene	31J	100

	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			{ovarian cancer critical region of deletion}		
06	U18315	Sus scrofa	parathyroid recentor	122	60
	AF255342	Homo sapiens	putative pheromone receptor V1RL1 long form	170	96
<del>``</del>		Rattus sp.	neurotransmitter transporter	715	94
08	S52051		Thuman georated protein 3	840	99
09	W63683	Homo sapiens	similar to Drosophila photoreceptor cell-specific	541	82
10	D79992	Homo sapiens	protein, calphotin.		ł
			pancreas-enriched phospholipase C	1348	99
11	AF117948	Homo sapiens	pancreas-enricheu phospholipase e	471	69
12	U81035	Rattus	ankyrin hinding cell adhesion molecule	7/1	1 .
.		norvegicus	neurofascin	798	56
13	AF154846	Homo sapiens	zinc finger protein	933	93
14	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	933	1 /3
		musculus		503	89
115	AL163303	Homo sapiens	putative gene containing transmembrane domain	523	
16	U26595	Rattus	prostaglandin F2a receptor regulatory protein	563	78
.10	020373	norvegicus	precursor		
	G04005	Homo sapiens	Human secreted protein, SEQ ID NO: 8176.	644	98
17	G04095	Homo sapiens	protein kinase C mu	314	81
18	X75756		Membrane-bound protein PRO1100.	770	98
19	Y66723	Homo sapiens	Westfor cell recentor	567	40
220	D88577	Mus	Kupffer cell receptor	1	1
		musculus		853	100
221	AF258465	Homo sapiens	OTRPC4	636	96
222	AF021935	Rattus	mytonic dystrophy kinase-related Cdc42-binding	0.0	<b>*</b> .
		norvegicus	kinase	1	100
223	AL136527	Homo sapiens	bA215B13.1 (A kinase (PRKA) anchor protein	693	100
LLJ	11515052		11)		
224	AB032417	Homo sapiens	WNT receptor Frizzled-4	690	99
225	AF030430	Mus	semaphorin VIa	703	68
225	VI 020420	musculus		·	
	4 5000010	Escherichia	putative dihydroxyacetone kinase (EC 2.7.1.2)	297	39
226	AE000218		putative unitarion and and a control of the control	1	l
		coli	phosphoinositol 3-phosphate-binding protein-2	2080	100
227	AF302150	Homo sapiens	GTP-binding like protein 2	265	88
228	AB024573	Mus	GIP-binding like protein 2		
		musculus		316	40
229	AF122924	Xenopus	Wnt inhibitory factor-1	13.0	"
	1	laevis		229	100
230	G03205	Homo sapiens	Human secreted protein, SEQ ID NO: 7286.		92
231	X98260	Homo sapiens	M-phase phosphoprotein 11	265	95
232	R92754	Homo sapiens	Human growth differentiation factor-12.	682	
233	R75111	Homo sapiens	Glycosyl-phosphatidylinositol-specific	290	100
233	17,5111	120	phospholipase-D.	1	
534	W69431	Homo sapiens	Human secreted protein cw1233 3.	235	97
234		Homo sapiens		859	81
235	Y08686			117	37
236	AF118275	Homo sapiens	Embryo Brain Kinase	460	62
237	X81466	Mus	Emplyo Brain Kinase		-
	<b></b>	musculus	TOTAL TOTAL TO S	284	33
238	U64857	Caenorhabditi	similar to the BPTI/Kunitz family of inhibitors;	20-7	1
	1	s elegans	most similar to tissue factor pathway inhibitor		1
	1	1	precursor (TFPI)	1220	63
239	AJ250840	Mus	serine/threonine protein kinase	739	03
237		musculus	· · · · · · · · · · · · · · · · · · ·		
240	AJ223472	Mus	transcription elongation factor TFIIS.h	222	38
240	F.344.3712	musculus	.1		
04:	¥94906	Homo sapiens	Human secreted protein clone rb649_3 protein	353	52
241	194900	TOMO Sabiens	sequence SEQ ID NO:18.		1.
	1	VV	. 07770 1	591	99
242	AF169301	Homo sapiens	NAT/SUITAGE COLIGISPOTOT GO 1-1	667	93
243	L22022	Rattus	orphan transporter v7-3	1	\ ·-
1	<u> </u>	norvegicus		1043	98
244	AF016191	Rattus	potassium channel	1043	1 /3
I		norvegicus		100	100
245	AF097366	Homo sapien	s cone sodium-calcium potassium exchanger	645	98
246	Y29868	Homo sapien		497	98
247		Homo sapien	s Not4-Np	188	83
. /4/	AF180475			690	99
248	Y17227	Homo sapien			

SEO	- 1 A		·		
ID ID	Accession No.	Species	Description	Smith-	1%
NO:	No.	l'		Waterman	Identity
NO.				Score	1
250	AT102266	sexta	protein SCLP		- <del> </del>
230	AF192756	Kaposi's	Orf73	134	34
1	ŀ	sarcoma-	1		1
j		associated			1
100		herpesvirus		1	1
251	AB022694	Homo sapiens		209	83
252	W55045	Homo sapiens		. 469	100
253	L46815	Mus	DNA binding protein Rc	251	57
		musculus			1 "'
254	W68505	Homo sapiens	Human acid sensing ionic channel.	173	82
255	AF070066	Mus	Citron-K kinase	1201	98
	_1	musculus		1201	98
256	G02491	Homo sapiens	Human secreted protein, SEQ ID NO: 6572.	460	1,00
257	Z12841	Oryctolagus	Phospholipase	368	100
L	_ ] .	cuniculus	- morphism page	308	80
258	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	1055	<del> </del>
259	AJ222968	Mus	L-periaxin	1857	99
1		musculus	2 portural	430	72
260	AJ250839	Homo sapiens	serine/threonine protein kinase	<del>-</del>	
261	AJ249977	Homo sapiens	AMP-activated protein kinase gamma 3 subunit	861	100
262	AF141386	Rattus	SLIT-2	758	98
	12,111000	norvegicus	3L11-2	198	40
263	AF022859	Homo sapiens			.1
264	AF160477	Homo sapiens	neuropilin-2(a0)	335	62
265	Y44662		Ig superfamily receptor LNIR precursor	387	91
1 203	144002	Homo sapiens	Human 14273 G-protein coupled receptor	636	99
266	U27269	Mus	(GPCR).	1	·
200	02/209	1	sodium glucose cotransporter	204	56
267	AF124491	musculus			1
268	AF127389	Homo sapiens	ARF GTPase-activating protein GIT2	159	75
200	AF 12/369	Rattus	putative taste receptor TR1	209	39
269	X98296	norvegicus		j	1
270	X78482	Homo sapiens	ubiquitin hydrolase	215	95
270	1/0462	Streptococcus	Fc-gamma receptor	129	26
271	AB009883	pyogenes		1	
2/1	AB009883	Nicotiana	KED	109	26
272	AF137367	tabacum			
212	AF13/36/	Mus	VPS10 domain receptor protein SORCS	899	97
273	7 24000	musculus			-
2/3	L34938	Rattus	ionotropic glutamate receptor	460	86
274	AT 00000	norvegicus		1	"
214	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent	188	74
	}	j	Expressed Protein LIKE PUTATIVE protein)	1	'
275	1706055		(isoform 1)	1	1
275	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	173	94
200	-		APOLLON		- '
276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	56
277	L40380	Homo sapiens	thyroid receptor interactor	430	61
278	AB046851	Homo sapiens	KIAA1631 protein	283	96
279	AC008075	Arabidopsis	Contains PF 00069 Eukaryotic protein kinase	157	43
		thaliana	domain.	137	43
280	M83738	Homo sapiens	protein-tyrosine phosphatase	181	72
281	AK024397	Homo sapiens	unnamed protein product		73
282	AF141326	Homo sapiens	RNA helicase HDB/DICEI	439	91
283	AF156530	Mus	ETS-domain transcriptional repressor PE1	197	84
	L	musculus		605	76
284	Y29336	Homo sapiens	Human secreted protein clone cs756_2 alternate		لا
			reading frame protein.	647	100
285	Y73402	Homo sapiens	Human secreted protein clone yc25_1 protein	1	
İ			sequence SEQ ID NO:26.	300	90
286	AF016411	Homo sapiens	KCNA3:1B		
287	W89253	Homo sapiens		137	100
288	AF112886		Human ALP.		97
289	AF113131	Bos taurus	differentiation enhancing factor 1	750	96
290	U52111	Homo sapiens	host cell factor homolog LCP	367	44
291	AF026504	Homo sapiens	plexin-related protein	698	100
	43L-0403U4	Rattus	SPA-1 like protein p1294	603	89

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
ю:					T
	AF102854	norvegicus Rattus	membrane-associated guanylate kinase-	124	53
92	AF102854	norvegicus	interacting protein 2 Maguin-2		
93	X99211	Drosophila	ubiquitin-specific protease	143	38
"	,XJ211	melanogaster			
94	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	185	94
~ I	1,1,1,1	•	sequence SEQ ID NO:92.	100	59
95	Y94890	Homo sapiens	Human protein clone HP02798.	108	96
96	AF019767	Homo sapiens	zinc finger protein	154 568	84
97	Y28568	Homo sapiens	Secreted peptide clone bd577_1.	182	97
98	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	182	
-	B08906	Homo sapiens	Human secreted protein sequence encoded by	605	69
99	B08909	Motino asbicara	gene 16 SEO ID NO:63.		
00	R58890	Homo sapiens	Human-32 cadhcrin-related molecule.	212	97
00	AF022859	Homo sapiens	neuropilin-2(a0)	277	100
01	Y71124	Homo sapiens	Human mitogenic regulator duox2.	716	97
02		Homo sapiens	Human receptor tyrosine kinase.	228	97
303	Y44297 D32050	Homo sapiens	alanyl-tRNA synthetase	192	80
304		Homo sapiens	protein kinase related to Raf protein kinases;	428	72
305	U43586	Homo sapicus	Method: conceptual translation supplied by		
		<del> </del>	author Human H13 viral receptor mutant 4.	280	95
306	R54872	Homo sapiens	Human H13 viral receptor mutain 4.	199	41
307	D78572	Mus	membrane glycoprotess		
		musculus	scaffolding protein SLIPR	639	88
308	AF255614	Rattus	scariolding protein SLM K		· ·
		norvegicus	semaphorin homolog-M-Sema F	162	89
309	S79463	Mus sp.	ATP-binding cassette sub-family A member 2	736	100
310	AF178941	Homo sapiens	calcium binding protein	151	36
311	U03413	Dictyostelium discoideum			
212	Y87347	Homo sapiens	Human signal peptide containing protein HSPP-	744	100
312	18/34/	Homo sapicus	124 SEQ ID NO:124.	·	
313	Z97055	Homo sapiens	4r388M5 4 (putative GS2 like protein)	789	99
314	AC004010	Homo sapiens	similar to Leucine-rich transmembrane proteins;	197	38
314	AC004010	110mo sapions	44% similarity to U42767 (PID:g1736918)		
315	AL021392	Homo sapiens	dJ439F8.2 (supported by GENSCAN and	278	38
313	111021372		GENEWISE)	<del> </del>	<del></del>
316	U70209	Mus	polycystic kidney disease 1 protein	165	38
510	1	musculus		1000	38
317	AF109643	Rattus	coxsackie-adenovirus-receptor homolog	223	36
		norvegicus		138	84
318	AF104923	Homo sapiens	putative transcription factor	141	38
319	AF100287	Trypanosoma	activated protein kinase C receptor homolog	141	1 36
		vivax	SPO TO NO. 4660	125	51
320	G00588	Homo sapiens		459	97
321	Y21591	Homo sapiens		232	97
322	D26070	Homo sapiens		232	1
			receptor	306	88
323	Y27918	Homo sapiens	Human secreted protein encoded by gene No.	1 300	
			123.	209	70
324	AF010144	Homo sapiens		214	97
325	M19650	Homo sapiens		~	1
		<del></del> _	3.1.4.37)  A secreted protein encoded by clone bp646_10.	140	70
326	W80396	Homo sapiens		540	78
327	X75756	Homo sapiens		721	99
328	G02292	Homo sapiens		877	99
329	AF168990	Homo sapien:	putative GTP-binding protein s anti-HIV gp120 antibody heavy chain variable	581	80
330	S67984	Homo sapien:		1	
			region s LDL-receptor related precursor (AA -19 to 4525)	2823	98
331	X13916	Homo sapien		1127	100
332	Y87330	Homo sapien	107 SEQ ID NO:107.	1	
L			- I D A T T T T T T T T T T T T T T T T T T	320	98
333	Y28503	Homo sapien	s putative RHO/RAC effector protein; 95%	327	93

SEO	Accession	Species	Description	Smith-	10
ID.	No.	- DP00103	Description		%
NO:	1			Waterman	Identity
<del>-110.</del> -		<del></del>	similarity to P49205 (PID:g1345860)	Score	
335	Y87347	Homo sapiens			
333	10/34/	Homo sapiens	Human signal peptide containing protein HSPP-	1111	67
336	AF006466		124 SEQ ID NO:124.		1
330	Ar000400	Mus	lymphocyte specific formin related protein	193	75
	150755	musculus		1	
337	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	632	97
			APOLLON	1	1
338	Y13443	Homo sapiens	Amino acid sequence of hSlo3-2,	516	100
339	Y07637	Homo sapiens	putative GABA-gated chloride channel	189	100
340	Y05734	Homo sapiens	Human Grb7 effector 2.2412 protein.	2156	99
341	AE000497	Escherichia	L-idonate transcriptional regulator	928	
1	]	coli	D-idonate danscriptional regulator	928	98
342	D90855	Escherichia	glycerol-3-phosphate dehydrogenase (EC	<del> </del>	<u> </u>
	250055	coli	gryceroi-3-phosphate denydrogenase (EC	769	99
343	D85613		1.1.99.5) chain A, anaerobic		
343	D92013	Escherichia	membrane component	399	100
	-	coli		1	
344	M93239	Escherichia	transmembrane protein	232	100
		coli	<u>l</u>	1	
345	M60177	Escherichia	enterobactin	759	99
		coli		1	1
346	D90699	Escherichia	Sensor protein copS (EC 2.7.3).	638	97
	1.	coli		1 030	31
347	D90843	Escherichia	CapB protein.	552	100
- 1	1 - 7 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5	coli	Caps proteit.	332	100
348	M13422	Escherichia	49 kd protein		
3,0	11115722	coli	49 ku protem	1193	96
349	L10328				
347	L10328	Escherichia	similar to drug resistance translocases	340	90
250	+	coli		1	
350	X69942	Mus	enhancer-trap-locus-1	560	82
	<del></del>	musculus		1	1
351	AF239613	Homo sapiens	apamin-sensitive small-conductance Ca2+-	463	80
			activated potassium channel	1	1
352	D90777	Escherichia	3-hydroxybutyryl-CoA dehydrogenase (EC	577	100
		coli	1.1.1.157) (b- hydroxybutyryl-CoA	1	•••
		,	dehydrogenase) (BhbD).	-	1
353	D90863	Escherichia	similar to	311	98
	1	coli			1 20
354	Y52386	Homo sapiens	Human transmembrane protein HP02000.	133	58
355	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-	482	
		ZZOMO Bupidila	7).	402	55
356	Y58637	Homo sapiens			
357	AF119226		Protein regulating gene expression PRGE-30.	119	51
358	Y87219	Homo sapiens	dual-specificity tyrosine phosphatase YVHI	1788	100
٥٥٦	18/219	Homo sapiens	Human secreted protein sequence SEQ ID	165	100
360	10000		NO:258.		
359	J00132	Homo sapiens	beta-fibrinogen	233	93
360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	70
361	R28916	Homo sapiens	Type III procollagen (prior art).	108	40
362	U16655	Rattus	phospholipase C delta-4	649	65
	1	norvegicus			
363	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	95	42
364	U47276	Gallus gallus	chicken brain factor-2	104	
365	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.		34
366	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	183	65
367	X98258		Human secreted protein, SEQ ID NO: 8172.	118	46
		Homo sapiens	M-phase phosphoprotein 9	564	75
368	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3387	99
369	U70932	Peromyscus	reverse transcriptase	92	59
	1	leucopus			
370	X86400	Homo sapiens	gamma subunit of sodium potassium ATPase	242	73
		1 1	like		
371	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	56
372	U49974	Homo sapiens	mariner transposase	257	
373	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)		55
374	AF234765	Rattus	sering projects sick miles	21193	99
	24204103	norvegicus	serine-arginine-rich splicing regulatory protein	1182	78
375	U49974		SRRP86		
J1J	U437/4	Homo sapiens	mariner transposase	172	55

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	Accession No.	Species	Description	Smith- Waterman Score	% Identity
O:	1		50 TO NO. 5065	221	67
			Human secreted protein, SEQ ID NO: 6065.	600	100
17		Homo sapiens	Human secreted protein, SEQ ID NO: 4750.	1456	91
78	X52574	Mus musculus	GTP binding protein		37
79	R69095	Homo sapiens	Anti-HIV Fab tat31 light chain.	68	
	J04974	Homo sapiens	alpha-2 type XI collagen	125	37
	AB002405	Homo sapiens	LAK-4p	530	43
82	U64830	Dictyostelium discoideum	protein tyrosine kinase	115	44
	G02916	Homo sapiens	Human secreted protein, SEQ ID NO: 6997.	618	98
83		Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	617	93
84	G01194	Homo sapiens	type I transmembrane receptor	4560	100
85	AJ245822		KIAA0220	2148	98
86	D86974	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	142	50
87	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	99	59
88	G04072	Homo sapiens	numan secreted protein, SEQ 1D NO. 0133.	197	51
389	M12140	Homo sapiens	envelope protein	461	77
390	AJ293309	Homo sapiens	NHP2 protein	181	94
391	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	241	66
392	W48351	Homo sapiens	Human breast cancer related protein BCRB2.		54
393	Y14442	Homo sapiens	olfactory receptor protein	339	100
394	W85607	Homo sapiens	Secreted protein clone da228_6.	957	
395	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	171	34
206	G03930	Homo sapiens	Human secreted protein, SEQ ID NO: 8011.	250	100
396 397	AB032904	Hylobates syndactylus	dopamine receptor D4	105	35
	4 7000000	Homo sapiens	stromal antigen 3, (STAG3)	861	.85
398 399	AJ007798 Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	1047	92
		**	Human secreted protein clone cb98_4.	162	37
400	Y29861	Homo sapiens Homo sapiens	similar to rat integral membrane glycoprotein;	527	78
401	D87002	Homo Sapiens	accession number 721513.	<u> </u>	
402	AF100754	Homo sapiens	ancient ubiquitous protein AUP1 isoform	853	95
403	X74904	Gallus gallus	alpha-2-macroglobulin receptor	258	60
404	AF075462	Mus musculus	ADP-ribosylation factor-directed GTPase activating protein isoform b	545	89
405	X92887	Human endogenous retrovirus K	pol/env	162	30
	3700160		Human dorsal root receptor 4 hDRR4.	325	72
406	Y30162	Homo sapiens	unnamed protein product	2833	99
407	AK022626	Homo sapiens		264	92
408 409	L13802 Y91600	Homo sapiens Homo sapiens		1788	89
410	W88745	Homo sapiens		2004	99
411	AB043953	Mus	Chat-H	2628	82
412	Y86233	Homo sapiens	Human secreted protein HNTMX29, SEQ ID NO:148.	1014	92
413	U10542	Pan troglodytes	MHC class I A	265	71
<del> </del>	10155005	Homo sapiens	NY-REN-7 antigen	850	95
414	AF155097		1000 YO 310 5004	88	48
415	G03203	Homo sapiens		266	89
416	Y57911	Homo sapiens		481	60
417	W27651	Homo sapiens		3077	87
418	Y76884	Homo sapien:	Retinoblastoma binding protein-7sequence.	289	68
419	AF255559	Notothenia coriiceps	alpha tubulin		74
420	G01984	Homo sapien	s Human secreted protein, SEQ ID NO: 6065.	209	
421	AL109827	Homo sapien	A ODES / similar		96
422	AC008075	Arabidopsis thaliana	F24J5.4	112	35

SEQ	Accession	Species	Description	Smith-	1%
D	No.			Waterman	Identity
NO:				Score	
423	AF231705	Homo sapiens	Alu co-repressor 1	1090	100
424	AF234887	Homo sapiens	FLAMINGO 1	6268	97
425	Y35942	Homo sapiens	Extended human secreted protein sequence, SEQ	1961	99
426	AB009288	- IVama sanisas	ID NO. 191.		
427	L12392	Homo sapiens	N-copine	635	98
428	Y94990	Homo sapiens Homo sapiens	Huntington's Disease protein	16080	99
429	AJ293573	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	768	98
430	Y84441	Homo sapiens	zinc finger protein Cezenne Amino acid sequence of a human RNA-	542	87
130	1	Homo sapiens	associated protein.	2074	100
431	G02850	Homo sapiens	Human secreted protein, SEQ ID NO: 6931.	723	95
432	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	73	42
433	AF159296	Lycopersicon	extensin-like protein	613	48
	1	esculentum	The state of the s	0.3	40
434	W48351	Ilomo sapiens	Human breast cancer related protein BCRB2.	135	44
435	X73874	Homo sapiens	phosphorylase kinase	3442	97
436	AF161426	Homo sapiens	HSPC308	268	74
437	Y30812	Homo sapiens	Human secreted protein encoded from gene 2.	1055	52
438	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	168	56
439	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2294	96
440	X02344	Homo sapiens	beta-tubulin	311	95
441	AF168418	Homo sapiens	activating signal cointegrator !	1882	100
442	L11672	Homo sapiens	zinc finger protein	795	54
443	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	93	26
444	A52140	unidentified	HUMAN NDR	2451	100
445	X98330	Homo sapiens	ryanodine receptor 2	9356	99
446	AF116712	Homo sapiens	PRO2738	227	49
447	AF245447	Homo sapiens	sphingosine kinase type 2 isoform	576	99
448	AF133086	Homo sapiens	membrane-type serine protease 1	2630	94
449	U87305	Rattus	transmembrane receptor UNC5H1	817	93
450	AF081249	norvegicus	7		
451	AC005498	Homo sapiens Homo sapiens	JAW1-related protein MRVIIA long isoform	4568	99
452	M60235	Homo sapiens	R31665_1	316	62
453	AB036706	Homo sapiens	granule membrane protein-140 intelectin	464	73
454	G00918	Homo sapiens	Human secreted protein, SEQ ID NO: 4999.	730 263	88
455	Y22634	Homo sapiens	Human cytokine inducible regulatory protein-1	192	81
	1	Tromo supicias	(CIRP-1).	192	67
456	Y36705	Homo sapiens	Fragment of human secreted protein encoded by	106	40
	1		gene 62.	100	10
457	N91325	Homo sapiens	DNA encoding human growth hormone receptor.	3282	96
458	M19155	Plasmodium	S-antigen precursor	110	36
		falciparum			
459	Y13377	Homo sapiens	Amino acid sequence of protein PRO257.	509	98
460	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	149	43
	-		clone HTDAD22.		
461	Y14482	Homo sapiens	Fragment of human secreted protein encoded by	184	54
160	1/82005	I	gene 17.		
162	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein	135	47
162	V940C0		sequence SEQ ID NO:16.		
463	X84960	Triticum	low molecular weight glutenin	109	33
164	W19919	aestivum	YI		
165	AF189764	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	1781	85
	AF 109/04	Mus musculus	alpha/beta hydrolase-1	502	59
166	U93569	Homo sapiens	p40	101	
67	Y41528	Homo sapiens		101	30
	141520	nomo sapiens	Fragment of human secreted protein encoded by gene 77.	1172	99
68	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	140	-
169	AJ000008	Homo sapiens	PI3-kinase	149	52
70	X70922	Mus Mus	neurotoxin homologue	5832	97
	11.0522	musculus	nonomain nonnongue	118	47
71	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	198	75

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
40:				30010	<del> </del>
		<u> </u>	gene 62. Human secreted protein, SEQ ID NO: 6394.	328	100
.73	G02313	Homo sapiens	Breast cancer associated antigen precursor	1013	97
74	Y07007	Homo sapiens		1015	1
			sequence.	943	80
75	W93254	Homo sapiens	Human ESRP1 protein.  Human breast cancer related protein BCRB2.	236	65
76	W48351	Homo sapiens	Human secreted protein encoded by gene 44	202	60
77	Y02693	Homo sapiens	clone HTDAD22.		
78	G01870	Homo sapiens	Human secreted protein, SEQ ID NO: 5951.	267	100
79	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	3427	92
		musculus		<u> </u>	<del></del>
80	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	123	53
81	W87701	Homo sapiens	A human membrane fusion protein designated	221	77
••	1		SYTAX1.		
82	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	131	39
83	AF210651	Homo sapiens	NAG18	124	59
84 84	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	343	50
85 85	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
86 <sup>.</sup>	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein	149	73
00	0151/4	Figure sapiens	3	1	l
05	V26162	Homo sapiens	Human secreted protein encoded by gene 44.	627	100
87	Y76167		stabilin-1	1244	91
88	AJ275213	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	313	65
89	G03798	Homo sapiens		16081	100
90	L12392	Homo sapiens	Huntington's Disease protein	197	66
91 _	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	228	70
92	J03799	Homo sapiens	laminin-binding protein	128	41
193	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3		
494	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	197	67
495	AC005175	Homo sapiens	R31449 3	889	94
<del>493</del> 496	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	229	61
490 497	AB030237	Canis	D4 dopamine receptor	90	48
49/	ABUSUZSI	familiaris	D4 dopamine receptor	1	<u> </u>
400	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	228	65
498		Peromyscus	reverse transcriptase	213	52
499	U70935	maniculatus	leverse transcriptase		l
	<del> </del>		skeletal muscle ryanodine receptor	26406	99
500	U48508	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	105	58
501	G03371	Homo sapicns		156	62
502	AF119851	Homo sapiens	PRO1722	116	50
503	AF113685	Homo sapiens	PRO0974	322	59
504	U79458	Homo sapiens	WW domain binding protein-2	608	55
505	W29651	Homo sapiens	Human secreted protein CD124_3.		70
506	W85459	Homo sapiens	Secreted protein encoded by clone dh1135 9.	986	33
507	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID NO:180.	115	
508	AL 160175	Homo sapiens	bA243J16.3 (similar to MYLK (myosin, light polypeptide kinase))	184	92
509	U43360	Peromyscus maniculatus	reverse transcriptase	97	62
545			Human secreted protein, SEQ ID NO: 7870.	117	63
510	G03789	Homo sapiens		1058	100
511	W79092	Homo sapiens		205	64
512	AF010144	Homo sapiens		2151	100
513	AJ133439	Homo sapiens	GRIP1 protein	259	42
514	AE003456	Drosophila melanogaster	CG6393 gene product		
515	Z17206	Xenopus laevis	p46XIEg22	128	40
<del>41</del> 2	AF104413	Homo sapions	large tumor suppressor 1	1766	94
516		Homo sapiens		92	40
517	G03797	Homo sapiens		444	98
518	AF151083			318	50
519 520	S80864	Homo sapiens Plasmodium		170	61
	X92485	i Piesmodium	pva1	1	1

SEQ	Accession	16			
ID OIL	No.	Species	Description	Smith-	%
NO:	140.	j		Waterman	Identity
521	G03790	Home conione		Score	
522	AF121857	Homo sapiens Homo sapiens		159	59
523	G02654	Homo sapiens		259	40
524	W88627	Homo sapiens		82	37
			HPMBQ32.	253	73
525	AF119851	Homo sapiens		162	57
526	Y27761	Homo sapiens	Human secreted protein encoded by gene No. 47.	154	57
527	G02707	Homo sapiens	Human secreted protein SEO ID NO- 6788	70	45
528	U47924	Homo sapiens	C8	1112	86
529	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	84	45
530	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	60
531	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	92	65
532	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	75	29
533	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	182	48
534	AF068286	Homo sapiens	HDCMD38P	861	100
535	U07707	Homo sapiens	epidermal growth factor receptor substrate	228	60
536	G01955	Homo sapiens	Human secreted protein, SEQ ID NO: 6036.	484	75
537	AF219232	Gallus gallus	qin-induced kinase	206	53
538	AF135022	Homo sapiens	mediator	128	100
539	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	141	59
540	AF016430	Caenorhabditi	contains similarity to a BR-C/TTK domain	853	39
541	4.0000000	s elegans		1	1
341	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45%	408	66
542	M29487	<del> </del>	similarity to P22059 (PID:g129308)	1	
543		Homo sapiens	integrin alpha subunit precursor	517	81
343	AF102530	Mus musculus	olfactory receptor F3	327	73
544	Y73431				Li
344	173431	Homo sapiens	Human secreted protein clone yb186_1 protein sequence SEQ ID NO:84.	386	100
545	AE004833	Pseudomonas	probable TonB-dependent receptor		
	1	aeruginosa	probable rolls-dependent receptor	279	42
546	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	264	<u> </u>
547	Y69192	Homo sapiens	A human monocyte-macrophage apolipoprotein	1772	53 67
	ļ		B receptor protein.	1772	0'
548	Y91493	Homo sapiens	Human secreted protein sequence encoded by	176	100
L			gene 43 SEQ ID NO:166.	170	100
549	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
550	AF044588	Homo sapiens	protein regulating cytokinesis 1; PRC1	1953	88
551	Y29332	Homo sapiens	Human secreted protein clone pe584 2 protein	1224	94
			sequence.	122-7	7
552	X98330	Homo sapiens	ryanodine receptor 2	24621	99
553	Y42782	Homo sapiens	Human UC Band #331 protein.	684	95
554	AB025258	Mus	granuphilin-a	501	41
400		musculus	<u>· · ·</u>		
555	AJ010346	Homo sapiens	RING-H2	1468	100
556	W92388	Homo sapiens	Human TR-interacting protein S239a.	538	92
557	AF119851	Homo sapiens	PRO1722	175	59
558	AF117756	Homo sapiens	thyroid hormone receptor-associated protein	183	32
559	G02872	<del>                                      </del>	complex component TRAP150		
560	D86214	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	319	68
200	200214	Mus	Ca2+ dependent activator protein for secretion	1010	93
561	AF187325	musculus Canis			
201	A 10/323	familiaris	melanoma antigen	287	55
562	АЈ001981	Homo sapiens	OXAIL		
563	Z17238	Rattus		2512	99
		norvegicus	glutamate receptor subtype delta-1	338	66
564	W30638	Homo sapiens	Portial human 7 transmers		
-		- Tomo Sapiens	Partial human 7-transmembrane receptor HAPO167 protein.	371	100
565	AC005620	Homo sapiens		1/7	-
566	Y99358	Homo sapiens	Human PRO1772 (UNQ834) amino acid	467	97
		Suprois	sequence SEQ ID NO:63.	1138	78
567	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1002	50
568	AF151043	Homo sapiens		798	58 100
	<del></del>			170	100

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
io:		4			100
59	AF097518	Homo sapiens	nver-specific transporter	231	
70	AB035698	Homo sapiens	MIRCHARMININ-ICIALCU MILUSO	1532	100
71	Y07096	Homo sapiens	Colon cancer associated antigen precursor sequence.	1064	100
72	AL031177	Homo sapiens	d1889M15 3 (novel protein)	735	55
	Y66639	Homo sapiens	Membrane-bound protein PRO290.	254	45
73	AB037108	Homo sapiens	seven transmembrane domain orphan receptor	1883	99
74		Homo sapiens	This gene is novel.	836	100
75	D43949	Homo sapiens	Human breast tumour-associated protein 57.	108	50
76	Y48596		Human secreted protein, SEQ ID NO: 4433.	141	75
77	G00352	Homo sapiens	Neural thread protein.	140	65
78	R95913	Homo sapiens	Neural inread protein.	201	70
79	AK025116	Homo sapiens	unnamed protein product	77	70
80	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.		100
81	AF196779	Homo sapiens	JM10 protein	450	98
82	AF188706	Homo sapiens	g20 protein	330	
83	AB030234	Canis femiliaris	D4 dopamine receptor	64	56
64	002621	Homo sapiens	Human secreted protein, SEQ ID NO: 6702.	345	90
84 85	G02621 AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	268	85
			Antigen) Human secreted protein encoded from gene 9.	235	35
86	Y30819	Homo sapiens	Human secreted protein encoded from gene 3.  Human secreted protein, SEQ ID NO: 4438.	132	56
587	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.  Human secreted protein, SEQ ID NO: 6953.	182	79
88	G02872	Homo sapiens	Human secreted protein, SEQ ID NO. 0933.	764	80
89	AF235017	Mus musculus	2PI protein		81
590	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	329	
591	Y30709	Homo sapiens	Amino acid sequence of a human secreted protein.	110	43
592	Y53875	Homo sapiens	A human seven transmembrane signal transducer	1369	92
593	Y53051	Homo sapiens	Human secreted protein clone dd119_4 protein sequence SEQ ID NO:108.	1112	
594	¥27658	Homo sapiens	Human secreted protein encoded by gene No. 92.	763	79
<del>594</del>	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	156	58
596	AF151110	Mus musculus	COP1 protein	2215	95
500	G0200C	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	157	65
597 598	G03786 AF192499	Mus	putative secreted protein ZSIG37	143	40
	<u> </u>	musculus	PRO1847	236	76
599	AF119855	Homo sapiens	PRO1847	212	73
600 <sup>.</sup>	G02872	Homo sapiens		567	88
601	Y00295	Homo sapiens		2015	74
602	AF184971	Homo sapiens		773	96
603	AF061936	Homo sapiens			93
604	AL096828	Homo sapiens			
605	AB033106	Homo sapiens	KIAA1280 protein	3915	100
606	X75756	Homo sapiens	nrotein kinase C mu	3916	99
607	D86983	Homo sapiens	similar to D.melanogaster peroxidasin(U11052)	5758	99
608	W69341	Homo sapiens	Secreted protein of clone CG279 1.	1377	99
608	W88627	Homo sapiens		339	82
610	Y27868	Homo sapiens		116	62
	1700000	Homo sapiens		2164	100
611	AF202636	1		218	82
612	AF090944	Homo sapiens		195	59
613	Y02693	Homo sapiens	clone HTDAD22.	1	84
614	M87053	Rattus norvegicus	lens membrane protein	450	
615	AC004232	Homo sapien	s FPM315	163	37
1010	G01984	Homo sapien		205	79

SEQ	Accession	Species	Description	1.65-51	
ID	No.	Species .	Description	Smith-	%
NO:	1	4		Waterman	Identity
617	Y91524	Homo sapiens	Human secreted protein sequence encoded by	Score	
• • •	77.524	110mo sapiens	gene 74 SEQ ID NO:197.	821	99
618	AJ245621	Homo sapiens	CTL2 protein		
619	Y76198	Homo sapiens	C1L2 protein	2258	99
620	AF067864	Homo sapiens		108	. 64
621	D90721		transferrin receptor 2 alpha	3922	94
021	D90/21	Escherichia coli	Transmembrane protein dppC	573	90
622	W75858		<del>                                  </del>		
623		Homo sapiens	Human secretory protein of clone CS752-3.	730	100
624	Y94982	Homo sapiens	Human secreted protein vb12_1, SEQ ID NO:4.	733	100
024	AF034745	Mus	LNXp80	637	83
-	111000	musculus		ŀ	
625	U42580	Paramecium	Pro-rich, IPPPNMSLPLS (3x)	94	46
	1	bursaria		ľ	
l	1	Chlorella	1		1
		virus 1	<u>L</u>	}	1
626	U79260	Homo sapiens	unknown	194	70
627	R95913	Homo sapiens	Neural thread protein.	99	50
628	G03450	Homo sapiens	Human secreted protein, SEQ ID NO: 7531.	427	100
629	Y36281	Homo sapiens	Human secreted protein encoded by gene 58.	590	100
630	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	165	76
ĺ	1		clone HTDAD22.	103	/0
631	G02139	Homo sapiens	Human secreted protein, SEQ ID NO: 6220.	1200	06
632	U16996	Homo sapiens	protein tyrosine posphatase	268	96
633	AF121857	Homo sapiens	sorting nexin 7	351	80
634	AF283772	Homo sapiens	Soruting nexts /	2019	100
00.	14 203112	monio sapiens	similar to Homo sapiens ribosomal protein L10	340	77
1 .		1.	encoded by GenBank Accession Number		
635	Y07090	Trans and	L25899		
033	10/090	Homo sapiens	Renal cancer associated antigen precursor	277	64
636	AD012200		sequence.	1	1
637	AB013382	Homo sapiens	DUSP6	414	76
638	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	315	71
038	M95762	Rattus	GABA transporter	924	89
639	000,500	norvegicus			
640	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	219	60
040	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone	137	79
-			HNHFO29.	Ĭ	
641	AC008075	Arabidopsis	F24J5.4	121	33
		thaliana		i	
642	W74824	Homo sapiens	Human secreted protein encoded by gene 96	615	62
		<u> </u>	clone HAQBK61.		
643	AB015982	Homo sapiens	serine/threonine kinase	485	98
644	Y25806	Homo sapiens	Human secreted protein fragment encoded from	162	46
	<u>L</u>		gene 23.	.02	10
645	AF122904	Homo sapiens	membrane protein DAP10	474	100
646	AF233323	Homo sapiens	Fas-associated phosphatase-1	200	38
647	W48804	Homo sapiens	Homo sapiens clone BK158_I protein.	1203	99
648	AF257330	Homo sapiens	COBW-like protein	1440	
649	Y36203	Homo sapiens	Human secreted protein #75.		98
650	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	233	73
651	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by	173	78
		-romo supività	Incyte clone 2022379.	1012	100
			THOSE CIONE 20223/9.		
652	AB032000	Wydobatas	dense in the St		
652	AB032909	Hylobates	dopamine receptor D4	122	32
		agilis			
653	AK021848	agilis Homo sapiens	unnamed protein product	186	69
		agilis	unnamed protein product Human secreted protein encoded by Gene No.		
653 654	AK021848 W73411	agilis Homo sapiens Homo sapiens	unnamed protein product Human secreted protein encoded by Gene No. 15.	186	69
653	AK021848	agilis Homo sapiens Homo sapiens Rattus	unnamed protein product Human secreted protein encoded by Gene No.	186	69
653 654 655	AK021848 W73411 L22455	agilis Homo sapiens Homo sapiens Rattus norvegicus	unnamed protein product  Human secreted protein encoded by Gene No.  15.  mu opioid receptor	186 57	69 37
653 654 655	AK021848 W73411 L22455 G03112	agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens	unnamed protein product  Human secreted protein encoded by Gene No. 15. mu opioid receptor  Human secreted protein, SEO ID NO: 7193.	186 57	69 37
653 654 655 656 657	AK021848 W73411 L22455 G03112 G02345	agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	unnamed protein product  Human secreted protein encoded by Gene No. 15. mu opioid receptor  Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426.	186 57	69 37 34 45
653 654 655	AK021848 W73411 L22455 G03112	agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens	unnamed protein product  Human secreted protein encoded by Gene No. 15. mu opioid receptor  Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426.	186 57 116 110 459	69 37 34 45 97
653 654 655 656 657 658	AK021848 W73411 L22455 G03112 G02345 W88627	agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426. Secreted protein encoded by gene 94 clone HPMBQ32.	186 57 116	69 37 34 45
653 654 655 656 657 658	AK021848 W73411 L22455 G03112 G02345	agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426. Secreted protein encoded by gene 94 clone HPMBQ32.	186 57 116 110 459 291	69 37 34 45 97 75
653 654 655 656 657 658	AK021848 W73411 L22455 G03112 G02345 W88627	agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426. Secreted protein encoded by gene 94 clone	186 57 116 110 459	69 37 34 45 97

D D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:		·		168	68 .
61	G03789	Homo sapiens	Himman secreted bioletic aco in 110.	375	43
62	Y53886	Homo sapiens	designated HSCOP-6.		
63	W75771	Homo sapiens	Philippin (11 F Dilluting Diownia 12 200).	629	100
	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor	480	55
64	ALU90770	Homo sapiens	(rhodopsin family) (olfactory receptor like) protein (hs6M1-21))		
	AT0027724	Homo sapiens	KIAA1313 protein	978	96
65	AB037734	Homo sapiens	Human cerebral protein-1.	192	84
66	W82841		Human cerebral protein-1.	182	87
67	W82841	Homo sapiens	contains transmembrane (TM) region and ATP	757	68
668	AB030184	Mus musculus	binding region	85	37
669	AB032919	Hylobates muelleri	dopamine receptor D4		1
670	AF107295	Rattus norvegicus	outer membrane protein	746	81
	722642	Homo sapiens	leukocyte surface protein	394	93
571	Z33642		Secreted protein clone du410_5.	261	91
72	W85608	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	106	48
573	G03203	Homo sapiens		2388	99
574	AL035587	Homo sapiens	dJ475N16.4 (KIAA0240)	1134	53
575	Y59668	Homo sapiens	Secreted protein 108-005-5-0-C1-FL.	174	74
576	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.		95
677	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDPr	1013	
678	L11625	Mus musculus	receptor protein-tyrosine kinase	545	96
200	AL031427	Homo sapiens	dJ167A19.3 (novel protein)	745	100
679 680	AJ133430	Mus	olfactory receptor	528	77
		musculus	Human secreted protein, SEQ ID NO: 6613.	179	70
681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	336	76
682	G03789	Homo sapiens	Human secreted protein, SEQ ID NO. 7676.	118	100
683	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.		37
684	U43360	Peromyscus maniculatus	reverse transcriptase	100	
685	G00885	Homo sapiens	Human secreted protein, SEQ ID NO: 4966.	162	60
	AK001518	Homo sapiens	unnamed protein product	590	100
686		Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
687 688	G01982 Y92241	Homo sapiens	Human cancer associated antigen precursor	2405	99
689	AC024792	Caenorhabditi	(MO-REN-46). contains similarity to TR:P78316	423	36
690	Y27868	s elegans Homo sapiens	Human secreted protein encoded by gene No.	183	81
		Homo sapiens	107.	180	88
691	Y56514		ORF protein sequence.	1539	99
692	Y27795	Homo sapiens		428	98
693	Y36268	Homo sapiens		308	89
694	U12465	Homo sapiens		1517	99
695	Y45272	Homo sapiens	Human secreted protein encoded from gene 16.	1242	98
696	AF191838	Homo sapiens	TANK binding kinase TBK1		
697	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	275	75
698	Y87280	Homo sapiens	Human signal peptide containing protein HSPP-	576	90
L	Y97999	Homo sapiens	Human SCAD family molecule HSFM-1, SEQ ID NO:1.	729	99
699		<del></del>		610	79
	A 1006701	Homo sanien:			100
700	AJ006701	Homo sapien		2357	
L	AJ006701 AF209198 AJ298841	Homo sapien: Mus		709	45
700 701 702	AF209198 AJ298841	Homo sapien: Mus musculus	s zinc finger protein 277 torsinA protein		
700 701	AF209198	Homo sapien: Mus	s zinc finger protein 277 torsinA protein s unnamed protein product	709	45

SEQ	Accession	Species	Description	10.5	<del></del>
ID `	No.	0,000	Description	Smith- Waterman	%
NO:		.		Score	Identity
706	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	125	58
707	R95326	Homo sapiens	Tumor necrosis factor receptor 1 death domain	121	95
	_		ligand (clone 2DD).	121	1 33
708	G03002	Homo sapiens		125	39
709	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	516	98
710	M63577	Saccharomyc	SFP1	131	159
711	1000001	es cerevisiae			1 "
1 /11	AB026291	Rattus	acetoacetyl-CoA synthetase	457	85
712	D21211	norvegicus		_  .	1
713	AF044033	Homo sapiens Marmota			44
1	74,044033	marmota	olfactory receptor	615	83
714	G03561	Homo sapiens	Human secreted protein, SEQ ID NO: 7642.		
715	AB033062	Homo sapiens	KIAA1236 protein  KIAA1236 protein	251	100
716	G00577	Homo sapiens		1380	100
717	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	80	73
718	AJ243396	Homo sapiens	voltage-gated sodium channel beta-3 subunit	835	99
719	U47334	Homo sapiens	similar to chicken gamma aminobutyric acid	234	100
L		· ·	receptor beta4 subunit	578	99
720	AB020598	Homo sapiens	peptide transporter 3	1096	100
721	Y53886	Homo sapiens	A suppressor of cytokine signalling protein	570	74
			designated HSCOP-6.	370	/*
722	J05046	Homo sapiens	insulin receptor-related receptor	6787	100
723	AF001958	Ambystoma	electrogenic Na+ bicarbonate cotransporter:	111	41
724	45100004	tigrinum	I NBC		"
124	AF127084	Mus	semaphorin cytoplasmic domain-associated	5253	94
725	X54673	musculus	protein 3A	_[	1
726	AF016191	Homo sapiens Rattus	GABA transporter	3114	99
1 .20	1010191	norvegicus	potassium channel	370	100
727	AB029559	Rattus	BATI		
ł		norvegicus	DATI .	139	35
728	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	2186	
729	AJ011415	Homo sapiens	plexin-B1/SEP receptor	729	97
730	Z93096	Homo sapiens	bK390B3.1 (manic fringe (Drosophila)	142	56 68
<u> </u>			homolog)	172	00
731	Z10062	Homo sapiens	cDNA encoding a human vanilloid receptor	675	99
732	AF161382	-	homologue Vanilrep1.		"
733	AB029033	Homo sapiens	HSPC264	192	94
734	AE000493	Homo sapiens	KIAA1110 protein	3826	99
754	13000493	Escherichia coli	putative transport protein	592	97
735	AL033379	Homo sapiens	dI/17022 0 /12		
		1101110 sapicits	dJ417O22.2 (novel 7 transmembrane receptor (rhodopsin family) protein similar to high-	2173	99
	1	1 1	affinity lysophosphatidic acid receptor homolog)		
736	AF132599	Homo sapiens	RANTES factor of late activated T lymphocytes-	245	
			1	243	56
737	X55019	Homo sapiens	acetylcholine receptor delta subunit	883	99.
738	X91906	Homo sapiens	voltage-gated chloride ion channel	1978	100
739	AB026116	Homo sapiens	organic anion transporter 4	1444	98
740	D00570	Mus	open reading frame (196 AA)	83	24
741	W03626	musculus		ļ	
742	U66059	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	118	40
743	AF119815	Homo sapiens	V_segment translation product	614	100
744	X16663	Homo sapiens	G-protein-coupled receptor	2751	99
745	W67838	Homo sapiens Homo sapiens	haematopoietic lineage cell protein (AA 1-486)	148	93
	1, 0,000	Troute sabiens	Human secreted protein encoded by gene 32 clone HLTCJ63.	448	95
746	W57260	Homo sapiens	Human semaphorin Y.		
747	W21578		Alzheimer's diseasa motels	2414	100
		Suprons	Alzheimer's disease protein encoded by DNA from plasmid pGCS2232.	968	65
748	Y94935	Homo sapiens	Human secreted protein clone yd218_1 protein	630	
		1	sequence SEQ ID NO:76.	622	100
749	AL022238	Homo sapiens	dJ1042K10.5 (novel protein)	314	06
750	G03889		Human secreted protein, SEQ ID NO: 7970.		85 87
			· · · · · · · · · · · · · · · · · · ·	· / L	U/

	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	AB025258	Mus	granuphilin-a	773	41
		musculus		000	99
752	Y52386	Homo sapiens	Human transmembrane protein HP02000.	900	99
753	Y48586	Homo sapiens	Human breast tumour-associated protein 47.	2527	100
754	AJ272207	Homo sapiens	putative G protein-coupled receptor 92	694	
755	M85183	Rattus norvegicus	vasopressin receptor	979	68
756	AP190501	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6	388	71
757	Y02692	Homo sapiens	Human secreted protein encoded by gene 43 clone HTADX17.	461	87
	Z22535	Homo sapiens	ALK-3	439	98
758		Homo sapiens	Interferon-gamma receptor segment from clone	564	97
759	R04932	Homo sapiens	30 responsible for hinding the target.	1217	99
760	W74902	Homo sapions	Human secreted protein encoded by gene 175 clone HE8BI92.		
761	G03706	Homo sapiens	Human secreted protein, SEQ ID NO: 7787.	223	88
762	AB020676	Homo sapiens	KIAA0869 protein	4433	99
	AK026992	Homo sapiens	unnamed protein product	2285	99
763	AF173358	Homo sapiens	glucocorticoid receptor AF-1 coactivator-1	573	100
764 765	AF268066	Mus	netrin 4	2019	89
		musculus	Human breast tumour-associated protein 46.	1169	89
766 767	Y48585 AF230378	Homo sapiens Mus	interleukin-1 delta	309	45
768	AF121975	musculus Mus	odorant receptor S18	268	62
	1	musculus		611	57
769	AB008515	Homo sapiens	RanBPM	458	50
770	Y09945	Rattus norvegicus	putative integral membrane transport protein		1
771	AF226731	Homo sapiens	AD026	688	99
772	Y27132	Homo sapiens	Human glioblastoma-derived polypeptide (clone OA004FG).	1384	100
		TTo a comiono	NOV/plexin-A1 protein	1821	98
773 774	X87832 AB025258	Homo sapiens Mus	granuphilin-a	500	41
		musculus		232	93
775	AF125101	Homo sapiens	HSPC040 protein	314	95
776	G02815	Homo sapiens	Human secreted protein, SEQ ID NO: 6896.	191	68
777	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.		45
778	R03301	Homo sapiens	Sequence of pre-human atrial natriuretic peptide.	213	100
779	AL357374	Homo sapiens	LA353C18 2 (novel protein)	232	89
780	AF100346	Homo sapiens	neuronal voltage gated calcium channel gamma-	1	
781	Y19566	Homo sapiens	Amino acid sequence of a human secreted	103	52
700	1726222	Homo sapiens		1098	93
782 783	Y36233 AF084464	Rattus	GTP-binding protein REM2	141	30
784	W49042	norvegicus Homo sapiens	Human low density lipoprotein binding protein LBP-3.	2693	99
-	AT22222	Homo sapiens		1904	91
785	AF238381	Homo sapiens	Human apoptosis related protein.	547	100
786	Y91870			1062	94
787 788	Y71062 AF117754	Homo sapiens	thyroid hormone receptor-associated protein	8684	98
l			complex component TRAP240	2848	96
789	AL049569	Homo sapien	s dJ37C10.3 (novel ATPase)	745	96
790	AF151848	Homo sapien	S CGI-90 protein	1421	95
791	Y08639	Homo sapien		644	99
792	Y41706	Homo sapien	Human PRO381 protein sequence.	1037	100
793	AF121228	Homo sapien	complex component TRAP95		
794	G04072	Homo sapien	s Human secreted protein, SEQ ID NO: 8153.	124	62
	Y69384	Homo sapien		119	100
795	109304	TAOLIO UPA	protein.		99

SEQ	Accession	Species	Description	Smith-	1%
ID T	No.	opecies	Description	Waterman	
NO:				Score	Identity
797	AF258340	Homo sapiens	hepatocellular carcinoma-associated antigen 112	1151	99
798	AF159615	Homo sapiens	FGP receptor activating protein 1	461	98
799	Y59863	Homo sapiens	Human normal uterus tissue derived protein 26.	797	99
800	W70459	Homo sapiens	Human T1-receptor ligand III splice variant 2.	572	92
801	L00073	Homo sapiens	renin	1913	93
802	P92219	Homo sapiens	CRI protein.	11963	97
	}	(human)	Care product	11703	3"
803	X15357	Homo sapiens	ANP-A recentor preprotein (AA -32 to 1029)	5100	98
804	W64473	Homo sapiens	Human secreted protein from clone EC172 1.	4018	95
805	AJ243874	Homo sapiens	oligophrenin-4	2067	100
806	G01731	Homo sapiens	Human secreted protein, SEQ ID NO: 5812.	284	100
807	Z24680	Homo sapiens	garp	1562	83
808	AF171669	Homo sapiens	glycoprotein-associated amino acid transporter	1364	90
		Tablic suprems	LAT2	1304	190
809	W70321	Homo sapiens	Secreted protein CC198_1.	1154	96
810	W74843	Homo sapiens	Human secreted protein encoded by gene 115	855	99
			clone HOVBA03.	. 833	) J
811	AF108831	Homo sapiens	K:Cl cotransporter 3	4561	100
812	AF092135	Homo sapiens	PTD014	862	100
813	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10	784	100
	1		encoded by GenBank Accession Number	/64	100
		1	L25899	Ī	[
814	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
815	AF051151	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	3850	99
816	W95630	Homo sapiens	Homo sapiens secreted protein gene clone	358	100
	ł		gni14 1.	1 330	100
817	G01082	Homo sapiens	Human secreted protein, SEQ ID NO: 5163.	549	100
818	AF151800	Homo sapiens	CGI-41 protein	1106	95
819	L00352	Homo sapiens	low density lipoprotein receptor	3980	100
820	X04434	Homo sapiens	IGF-I receptor	5832	99
821	G03844	Homo sapiens	Human secreted protein, SEQ ID NO: 7925.	572	100
822	AF212220	Homo sapiens	TERA	396	48
823	Y50125	Homo sapiens	Human glycophosphatidylinositol-anchored	4897	99
		1	protein GPI-122.		
824	AF156778	Homo sapiens	ASB-3 protein	2675	98
825	AF096322	Homo sapiens	neuronal voltage-gated calcium channel gamma-	1105	100
			2 subunit		
826	Y07972	Homo sapiens	Human secreted protein fragment #2 encoded	1540	100
	L	· .	from gene 28.		
827	AB032013	Homo sapiens	potassium channel Kv8.1	2435	95
828	Y13620	Homo sapiens	BCL9	5284	96
829	Y91474	Homo sapiens	Human secreted protein sequence encoded by	541	98
070	166,000	ļ.,	gene 24 SEQ ID NO:147.		,
830	X54232	Homo sapiens	glypican	1625	87
831	X14830	Homo sapiens	acetylcholine receptor beta-subunit preprotein	2540	100
832	Y71262 .	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1002	100
833	G03873	Homo sapiens	Human secreted protein, SEQ ID NO: 7954.	638	96
834	AC003030	Homo sapiens	R29828_1	1389	93
835	Y38422	Homo sapiens	Human secreted protein.	964	87
836	U41557	Caenorhabditi	glycine-rich	85	36
027	47 101000	s elegans			
837	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in	998	75
929	A 1011415	<del>                                     </del>	AL023803))		
838 839	AJ011415	Homo sapiens	plexin-B1/SEP receptor	1580	60
	W80398	Homo sapiens	A secreted protein encoded by clone cw1543_3.	1105	67
840	G00862	Homo sapiens	Human secreted protein, SEQ ID NO: 4943.	255	92
841	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
842	AF036717	Homo sapiens	FGFR signalling adaptor SNT-1	2629	99
843	Y73446	Homo sapiens	Human secreted protein clone yc27_1 protein	1089	100
844	C02972	177	sequence SEQ ID NO:114.		
845	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	357	69
846	AF151810	Homo sapiens	CGI-52 protein	1443	88
847	X83378 AC004883	Homo sapiens	putative chloride channel	1620	99
	へしいみおおろ	Homo sapiens	similar to general transcription factor 2I; similar	655	96

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
VO:				Score	
			to AF038969 (PID:g2827207)		-
348	X99886	Homo sapiens	monocyte chemotactic protein-2	160	76
349	AC005587	Homo sapiens	similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305)	963	98
350	AB038237	Homo sapiens	G protein-coupled receptor C5L2	1767	100
351	AF124490	Homo sapiens	ARF GTPase-activating protein GIT1	3415	98
352	Y86217	Homo sapiens	Human secreted protein HWHGU54, SEQ ID NO:132.	1189	99
353	AF224741	Homo sapiens	chloride channel protein 7	3748	99
354	X17094	Homo sapiens	furin (AA 1-794)	3550	99
855	W78245	Homo sapiens	Fragment of human secreted protein encoded by gene 19.	1245	99
856	R97569	Homo sapiens	Interleukin-2 receptor associated protein p43.	1926	100
857	Y41765	Homo sapiens	Human PRO1083 protein sequence.	3211	99
858	AF057306	Homo sapions	transmembrane proteolipid	481	84
859	AK025116	Homo sapiens	unnamed protein product	374	69
860	Y41312	Homo sapiens	Human secreted protein encoded by gene 5 clone HI.DRM43.	824	100
862	Y25776	Homo sapiens	Human secreted protein encoded from gene 66.	895	99
863	Y74188	Homo sapiens	Human prostate tumor EST fragment derived protein #375.	96	30
864	AF167473	Homo sapiens	heme-binding protein	870	99
865	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	211	67
866	X54870	Homo sapiens	Type II integral membrane protein	1201	100
867	G00700	Homo sapiens	Human secreted protein, SEQ ID NO: 4781.	640	99
868	Y07894	Homo sapiens	Human secreted protein fragment encoded from gene 43.	388	88
869	J00123	Homo sapiens	preproenkenhalin (	1349	95
870	Y91632	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEO ID NO:305.	1048	98
871	L04311	Homo sapiens	GABA-alpha receptor beta-3 subunit	237	93
872	Y29988	Homo sapiens	Human cytokine family member EF-7 protein.	960	94
873	AF161382	Homo sapiens	HSPC264	1124	99
874	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
875	Y27572	Homo sapiens	Human secreted protein encoded by gene No. 6.	573	96
876	M15530	Homo sapiens	B-cell growth factor	171	56
877	W63681	Homo sapiens	Human secreted protein 1.	1652	99
878	1.27867	Rattus norvegicus	neurexophilin	1448	98
879	Y10835	Homo sapiens	Amino acid sequence of a human secreted protein.	321	100
880	W88991	Homo sapiens	Polypeptide fragment encoded by gene 144.	936	100
881	AF118670	Homo sapiens	orphan G protein-coupled receptor	1971	100
882	AF208865	Homo sapiens	EDRF	528	100
883	Y18462	Homo sapiens	cathepsin L	209	72
884	Y94950	Homo sapiens	Human secreted protein clone dh1073_12 protein sequence SEQ ID NO:106.	348	100
885	AF070661	Homo sapiens	HSPC005	404	100
886	Y04315	Homo sapiens	Human secreted protein encoded by gene 23.	385	100
887	X92744	Homo sapiens	hBD-1	375	100
888	Y22496	Homo sapiens	Human secreted protein sequence clone cn621_8.	994	94
889	Y41293	Homo sapiens	Human soluble protein ZTMPO-1.	4595	99
890	G03714	Homo sapiens		147	63
891	AF208856	Homo sapiens	BM-014	1012	99
892	U29195	Homo sapiens	neuronal pentraxin II	2002	98
893	X68149	Homo sapiens	Burkitt lymphoma receptor 1	1953	100
894	Y94914	Homo sapiens	Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	537	100
895	W61630	Homo sapiens	4 11	326	63
896	M24110	Homo sapiens		481	100
897	Z68747	Homo sapiens		2018	99
898	AF186112	Homo sapiens		619	100
899	AF225420	Homo sapiens		734	100

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
NO:				Score	Identity
900	P60657	Homo sapiens	Sequence of human lipocortin.	1835	100
901	M27288	Homo sapiens	oncostatin M	1297	99
902	W85737	Homo sapiens	Polypeptide with transmembrane domain.	749	100
903	G01349	Homo sapiens		650	99
904	Y00261	Homo sapiens	Human secreted protein encoded by gene 4.	1133	99
905	AF039688	Homo sapiens	antigen NY-CO-3	771	99
906	AB007836	Homo sapiens	Hic-5	2544	100
907	AB017507	Homo sapiens	Apg12	224	100
908	AK000056	Homo sapiens	unnamed protein product	1537	98
909	Y86299	Homo sapiens	Human secreted protein HFOXB55, SEQ ID	427	100
910	AF231023	<del>                                      </del>	NO:214.		.
911	Y14134	Homo sapiens	protocadherin Flamingo 1	7393	99
711	1 14154	Homo sapiens	Vascular endothelial cell growth inhibitor beta	1319	100
912	290420	177	protein sequence.		
712	2,90420	Homo sapions	Human GDF-3 (hGDF-3) polypeptide encoding	1950	100
913	Y19757	Homo sapiens	CDNA.		<u> </u>
914	G03172		SEQ ID NO 475 from WO9922243.	1361	100
915	U14971	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	48
916	AF172854	Home sapiens Home sapiens	ribosomal protein S9	886	90
917	AC005525	Homo sapiens	cardiotrophin-like cytokine CLC	1204	99
918	AF166350		F22162_1	1963	100
919	Y87285	Homo sapiens	ST7 protein	4711	99
1	10/203	Homo sapiens	Human signal peptide containing protein HSPP-	430	100
920	Y36131	Homo sapiens	62 SEQ ID NO:62.  Human secreted protein #3.	<u> </u>	
921	AF193766	Homo sapiens		465	88
922	Y95013	Homo sapiens	cytokine-like protein C17	724	100
923	X75208	Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor	357	100
924	Y96202	Homo sapiens	Protein tyrosine kinase-receptor	5256	100
925	AB039886	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56. down-regulated in gastric cancer	813	98
926	G03368	Homo sapiens	Human secreted protein, SEQ ID NO: 7449.	785	78
927	Y48606	Homo sapiens	Human breast tumour-associated protein 67.	55	50
928	Y36151	Homo sapiens	Human secreted protein #23.	539	100
929	AF110399	Homo sapiens	elongation factor Ts	668	100
930	AF210317	Homo sapiens	facilitative glucose transporter family member	1666	100
		·	GLUT9	2763	99
931	Y73328	Homo sapiens	HTRM clone 082843 protein sequence.	931	100
932	G01959	Homo sapiens	Human secreted protein, SEQ ID NO: 6040.	274	100
933	U47924	Homo sapiens	B-cell receptor associated protein	1469	100
934	G03827	Homo sapiens	Human secreted protein, SEQ ID NO: 7908.	529	93
935	AB039371	Homo sapiens	mitochondrial ABC transporter 3	196	63
936	X56385	Canis	rab8	1064	100
		familiaris		1004	100
937	B08906	Homo sapiens	Human secreted protein sequence encoded by	117	44
			gene 16 SEQ ID NO:63.	]	47
938	M13692	Homo sapiens	alpha-I acid glycoprotein precursor	1064	99
939	Y53886	Homo sapiens	A suppressor of cytokine signalling protein	515	42
			designated HSCOP-6.	"	12-
940	Y16630	Homo sapiens	Human Putative Adrenomedullin Receptor	1904	99
0.11			(PAR).	""	
941	AC005102	Homo sapiens	small inducible cytokine subfamily A member	627	99
~			24		
942	M12886	Homo sapiens	T-cell receptor beta chain	1289	81
943	AF226046	Homo sapiens	GK003	1049	98
944	Y36078	Homo sapiens	Extended human secreted protein sequence, SEQ	667	100
015		<u> </u> _	ID NO. 463.	= -	
945	M22877	Homo sapiens	cytochrome c	565	100
946	W67869	Homo sapiens	Human secreted protein encoded by gene 63	551	93
045	11/60053		clone HHGDB72.		
947	W67859	Homo sapiens	Human secreted protein encoded by gene 53	283	100
· · · · · · · · · · · · · · · · · · ·			clone HBMCL41.		
	11/0670			1	
948	W85726	Homo sapiens	Novel protein (Clone BG33_7).	789	100
	W85726 AJ242015 G04075	Homo sapiens		789 4236 567	100 100

	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:					100
51	AF110645	Homo sapiens	candidate tumor suppressor p33 ING1 homolog	1314	70
52	Y36111		Extended human secreted protein sequence, SBQ ID NO. 496.	402	
53	AB012109	Homo sapiens	APC10	990	100
54	AF246221	Homo sapiens	transmembrane protein BRI	1405	100
	AF054986	Homo sapiens	putative transmembrane GTPase	1883	100
55	W74726	Homo sapiens	Human secreted protein fg949_3.	1879	100
56		Homo sapiens	Human viral receptor protein (ACVRP).	1581	100
57	Y27096		cystinosin	1920	100
58	AJ222967	Homo sapiens	Human secreted protein clone df202_3 protein	587	100
59	Y53052	Homo sapiens	sequence SEO ID NO:110.	283	100
60	G02694	Homo sapiens	Human secreted protein, SEQ ID NO: 6775.	1214	96
61	AF151855	Homo sapiens	CGI-97 protein	250	65
62	U26592	Homo sapiens	diabetes mellitus type I autoantigen		1
63	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	3796	100
64	AF078859	Homo sapiens	PTD004	2089	100
065	AB020315	Homo sapiens	homologue of mouse dkk-1 gene:Acc# AF030433	1466	100
	770 4 557 1	Warra cardons	precursor polypeptide (AA -22 to 1185)	6580	99
66	X04571	Homo sapiens	hepatocellular carcinoma antigen gene 520	993	99
967	AF146019	Homo sapiens	minK-related peptide 1; MiRP1	632	100
968	AF071002	Homo sapiens	membrane-type-5 matrix metalloproteinase	3545	100
969	AB021227	Homo sapiens	memorane-type-5 man x metanoprotentase	1579	100
970	AF180920	Homo sapiens	cyclin L ania-6a	5621	99
971	AF105365	Homo sapiens	K-Cl cotransporter KCC4	739	100
972	AF083248	Homo sapiens	ribosomal protein L26 homolog	6295	100
973	AJ132429	Homo sapiens	hyperpolarization-activated cyclic nucleotide gated cation channel hHCN4	l	
974	W61619	Homo sapiens	Clone HTPEF86 of TM4SF superfamily.	454	100
975	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
976	AF275948	Homo sapiens	ABCA1	11763	99
	AB026891	Homo sapiens	cystine/plutamate transporter	2552	100
977 978	AF117657	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP80	3348	99
979	AF044201	Rattus	neural membrane protein 35; NMP35	1570	92
		norvegicus	li de la litte estada 1	1170	99
980	AF119297	Homo sapiens	neuroendocrine-specific protein-like protein 1	1983	99
981 982	AF155652 W88499	Homo sapiens	potassium channel modulatory factor Human stomach carcinoma clone HP10412-	1553	99
•	}	1	encoded protein.	10010	98
983	Z56281	Homo sapiens	interferon regulatory factor 3	2012	100
984	AB026125	Homo sapiens	ART-4	2160	
985	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	172	70
007	AD022000	Homo sapiens	b-chemokine receptor CCR4	1895	100
986	AB023888		Human H1075-1 secreted protein 5' end.	712	100
987 988	W27291 AF153450	Manduca	juvenile hormone esterase binding protein	226	32
		scxta	VI	194	88
989	G03697	Homo sapiens		1486	100
990	AF204159	Homo sapiens	channel beta 3a subunit		·
991	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
992	AL031266	Caenorhabditi s elegans		327	40
002	Y66749	Homo sapiens	Membrane-bound protein PRO1124.	4730	99
993		Homo sapiens		141	77
994	G01246			5811	99
995 996	AF133845 AF117756	Homo sapiens Homo sapiens	thyroid hormone receptor-associated protein	4999	100
ì	L		complex component TRAP150	284	93
997	W62066	Homo sapiens		725	100
998	Y87173	Homo sapiens	NO:212.		•
999	Y13379	Homo sapiens	Amino acid sequence of protein PRO263.	1654	99
1000	Y95008	Homo sapien:	Human secreted protein vf3_1, SEQ ID NO:56.	676	47
I TANA	AF190167	Homo sapien		1747	100

SEQ	Accession	Species	Description	T Smith-	1%
ID	No.		2 doi:phon	Waterman	Identity
NO:				Score	luctury
1002	G01234	Homo sapiens	Human secreted protein, SEQ ID NO: 5315.	398	96
1003	W73420	Homo sapiens	Human secreted protein encoded by Gene No.	2150	100
		1	24.		100
1004	X12791	Homo sapiens	19kD SRP-protein (AA 1 - 144)	742	100
1005	M23323	Homo sapiens	membrane protein	642	100
1006	X63745	Homo sapiens	KDEL receptor	326	98
1007	Y35997	Homo sapiens	Extended human secreted protein sequence, SEQ	824	99
			ID NO. 382.	1	
1008	AB032918	Hylobates	dopamine receptor D4	92	35
		moloch		1 .	}
1009	Y91680	Homo sapiens	Human secreted protein sequence encoded by	1372	99
1010	1,2,2,2,2,2		gene 81 SEQ ID NO:353.		
1010	AL136125	Homo sapiens	dJ304B14.1 (novel protein)	825	98
1011	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	379	98
1012	Y17531	Homo sapiens	Human secreted protein clone BL205 14 protein.	818	97
1013	G00724	Homo sapiens	Human secreted protein, SEQ ID NO: 4805.	462	100
1014	AF288092	Naegleria	haem lyase	114	37
1015	47046000	gruberi	100		
1015	AB045292	Homo sapiens	M83 protein	3867	99
1016	X15940	Homo sapiens	ribosomal protein L31 (AA 1-125)	644	100
1017	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
1018	AL024498	Homo sapiens	dJ417M14.1 (novel protein)	589	100
1019	X83425	Homo sapiens	Lutheran blood group glycoprotein	3054	99
1020 1021	W03516	Homo sapiens	Prostaglandin DP receptor.	1864	100
	G03960	Homo sapiens	Human secreted protein, SEQ ID NO: 8041.	398	100
1022	Y91689	Homo sapiens	Human secreted protein sequence encoded by	768	100
1023	A E000660		gene 93 SEQ ID NO:362.		
1023	AE000660 AF132965	Homo sapiens	hADV36S1	573	100
1024	W92380	Homo sapiens	CGI-31 protein	1550	100
1025	R66278	Homo sapiens	Human TR-interacting protein S103a.	1466	97
1020	K002/8	Homo sapiens	Therapeutic polypeptide from glioblastoma cell	830	100
1027	X65614	Homo sapiens	line.		
1028	Y41741	Homo sapiens	S100P calcium-binding protein	476	100
1029	AJ001014	Homo sapiens	Human PRO704 protein sequence. RAMP1	1323	100
1030	W63682	Homo sapiens	Human secreted protein 2.	806	100
1031	AK023007	Homo sapiens	unnamed protein product	1354	99
1032	W97900	Homo sapiens	Human SR-BI class B scavenger.	766	100
1033	Y82453	Homo sapiens	Human TGC-440 secretory protein SEQ ID	2672	99
	102.03	110mo sapiens	NO:1.	639	99
1034	Y73473	Homo sapiens	Human secreted protein clone yd178_1 protein	752	93
		Tionio supiciis	sequence SEQ ID NO:168.	132	93
1035	Y86468	Homo sapiens	Human gene 48-encoded protein fragment, SEQ	96	90
	100.00	Tromo suprous	ID NO:383.	90	90
1036	U09813	Homo sapiens	mitochondrial ATP synthase subunit 9 precursor	698	100
1037	AJ242832	Homo sapiens	calpain	3699	99
1038	X66403	Homo sapiens	acetylcholine receptor epsilon subunit CHRNE	2574	100
1039	AJ242730	Homo sapiens	polyhomeotic 2	1310	100
1040	AF169968	Mus	DNA binding protein DESRT	1453	80
	İ	musculus		1433	80
1041	X52563	Bos taurus	permability increasing protein	383	29
1042	G00368		Human secreted protein, SEO ID NO: 4449		
		Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	75	50
1042	G00368		Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613.	75 60	50 53
1042 1043	G00368 G02532	Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B	75 60 1850	50 53 100
1042 1043 1044	G00368 G02532 M94582	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256O22.1 (similar to IGFALS (insulin-like	75 60	50 53
1042 1043 1044 1045	G00368 G02532 M94582	Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))	75 60 1850	50 53 100
1042 1043 1044	G00368 G02532 M94582 AL080239	Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))	75 60 1850 1704	50 53 100 50
1042 1043 1044 1045	G00368 G02532 M94582 AL080239	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit)) HSPC040 protein	75 60 1850 1704	50 53 100 50
1042 1043 1044 1045 1046 1047	G00368 G02532 M94582 AL080239	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))	75 60 1850 1704	50 53 100 50
1042 1043 1044 1045 1046 1047	G00368 G02532 M94582 AL080239 AP125101 W74809	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit)) HSPC040 protein Human secreted protein encoded by gene 81	75 60 1850 1704	50 53 100 50
1042 1043 1044 1045 1046 1047	G00368 G02532 M94582 AL080239 AP125101 W74809	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256022.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit)) HSPC040 protein Human secreted protein encoded by gene 81 clone HMWDN32.	75 60 1850 1704 580	50 53 100 50
1042 1043 1044 1045 1046 1047	G00368 G02532 M94582 AL080239 AP125101 W74809	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4449. Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile submit)) HSPC040 protein Human secreted protein encoded by gene 81 clone HMWDN32. dJ1042K10.4 (novel protein)	75 60 1850 1704 580 176	50 53 100 50 100 100

D C	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
1052	Y21851	Homo sapiens	Human signal peptide-contianing protein (SIGP) (clone ID 2328134).	1643	95
1053	AL163815	Arabidopsis thaliana	putative protein	661	62
	V6/000	Homo sapiens	Human secreted protein encoded by gene 77.	262	100
1054	Y76200	Homo sapiens	TC10-like Rho GTPase	1160	100
1055	AJ276567	Homo sapiens	Human secreted protein encoded by gene No. 54.	154	96
1056	Y27620	Homo sapiens	ribosomal protein	745	100
1057	D14530	Homo sapiens	TADA1 protein	1132	100
1058 1059	AF132000 AL031778	Homo sapiens	di34B21.1 (novel BZRP (benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein)	920	100
1060	AF227135	Homo sapiens	candidate taste receptor T2R9	134	33
1061	Y27575	Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
1062	Z11697	Homo sapiens	HB15	1088	100
1062	AF123757	Homo sapiens	putative transmembrane protein	819	100
1064	AF155135	Homo sapiens	novel retinal pigment epithelial cell protein	2932	99
1065	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	2575	100
1066 1067	¥36087	Homo sapiens	Extended human secreted protein sequence, SEQ	770	85
1068	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein	301	100
1069	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein sequence SEO ID NO:124.	301	100
1070	W64535	Homo sapiens	Human leukocyte cell clone HP00804 protein.	2014	99
1071	X03145	Homo sapiens	pot. ORF III	148	50
1072	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	821	91
1073	X82200	Homo sapiens	enStaf50	249	62
1074	G03213	Homo sapiens	Human secreted protein, SEO ID NO: 7294.	99	47
1075	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	506	55
1076	G03187	Homo sapiens	Human secreted protein, SEQ ID NO: 7268.	424	98
1077	L25899	Homo sapiens	Lribosomal protein L10	332	76
1078	Y91447	Homo sapiens	Human secreted protein sequence encoded by gene 48 SEO ID NO:168.	898	97
1079	G01862	Homo sapiens	Human secreted protein, SEQ ID NO: 5943.	290	89
1080	AB039723	Homo sapiens	WNT receptor frizzled-3	1376	92
1081	AB020527	Homo sapiens	Na/PO4 cotransporter homolog	269	100
1082	L13802	Homo sapiens	ribosmal protein small subunit	499	80
1083	W75098	Homo sapiens	Human secreted protein encoded by gene 42 clone HSXB125.	143	81
1084	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	83	51
1085	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	88	43
1086	AF090942	Homo sapiens	PRO0657	124	64
1087	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	129	41
1088	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	126	36
1089	AF140631	Homo sapiens	G-protein coupled receptor 14	364	82
1090	G04063	Homo sapiens		114	32
1090	S72304	Mus sp.	LMW G-protein	146	83
1092	W88708	Homo sapiens		405	100
1093	W85612	Homo sapiens	Secreted protein clone fh123_5.	4358	97
1094	Y53012	Homo sapiens	Human secreted protein clone pm514_4 protein	1013	99
1095	Y92345	Homo sapiens		_	100
1096	AF090942	Homo sapiens	PRO0657	147	60
1097	L24521	Homo sapiens		166	58
1098	X56932	Homo sapiens	23 kD highly basic protein	490	70
1099	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	83	35
1100	Y02693	Homo sapiens	1 11 44	149	59

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SEQ ID	Accession No.	Species	Description	Smith-	%
NO:				Waterman Score	Identity
1101	AF119851	Homo sapiens		183	72
1102	G04086	Homo sapiens		207	62
1103	G04063	Homo sapiens		91	52
	X74856	Mus musculus	ribosomal protein L28	128	69
1105	G03789	Homo sapiens		130	62
1106	G03133	Homo sapiens		122	48
1107	G03040	Homo sapiens		69	43
1109	AF039942	Homo sapiens		744	99
	AF201951	Homo sapiens	high affinity immunoglobulin epsilon receptor beta subunit	738	94
1110	AF111108	Mus musculus	transient receptor potential 2	223	79
1111	AF119900	Homo sapiens	PRO2822	144	59
1112	Y16589	Homo sapiens		265	39
1113	G02872	Homo sapiens	Human secreted protein, SEO ID NO: 6953.	178	67
1114	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	164	63
1115	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	1217	99
1116	X51394	Xenopus	APEG precursor protein	130	40
		laevis		1	"
1117	M27826	Homo sapiens	neutral protease large subunit	442	65
1118	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	72	60
1119	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	491	97
1120	Y35906	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 155.	244	97
1121	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	65
1122	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	110	90
1123	AF084830	Homo sapiens	two pore domain K+ channel; TASK-2	703	94
1124	AF212862	Homo sapiens	membrane interacting protein of RGS16	442	88
1125 1126	W64469	Homo sapiens	Human secreted protein from clone CW795_2.	191	53
1127	G01361 G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	154	100
1128	Y84320	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	165	100
		Homo sapiens	Human cardiovascular system associated protein kinase-1.	815	99
1129	G02105	Homo sapiens	Human secreted protein, SEQ ID NO: 6186.	88	73
1130	Y32923	Homo sapiens	Transmembrane domain containing protein clone HP01512.	700	100
1131	Y29817	Homo sapiens	Human synapse related glycoprotein 2.	260	91
1132	Y91644	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:317.	525	96
1133	Y91449	Homo sapiens	Human secreted protein sequence encoded by	542	100
1134	ADCCCCC	l	gene 49 SEQ ID NO:170.		
1134 1135	AB017908 X51760	Homo sapiens	4F2 light chain	2399	93
1136	Y99426	Homo sapiens	zinc finger protein (583 AA)	312	55
		Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	917	72
1137 1138	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
1138	AF155106	Homo sapiens	NY-REN-36 antigen	768	91 ·
	AL031055	Homo sapiens	dJ28H20.1 (novel protein similar to membrane transport proteins)	117.	50
1140	AF011359	Bos taurus	regulator of G-protein signaling 7	138	96
1141	Y70018	Homo sapiens	Human Protease and associated protein-12 (PPRG-12).	623	100
1142	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	113	38
1143	AB030235	Canis familiaris	D4 dopamine receptor	89	48
1144	Y94922	Homo sapiens	Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.	539	88
1145	X99962	Homo sapiens	rab-related GTP-binding protein	398	
1146	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	168	96
1147	G03712	Homo sapiens	Human secreted protein, SEQ ID NO: 7793.	512	79 85
1148	Y28279	Homo sapiens	Human G-protein coupled receptor GRIR-1.	705	76
1149	U13642	Caenorhabditi	exon 5 similar to transmembrane domain of S.	247	36
				-11	-v

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D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			cerevisiae zinc resistance protein		
			Human secreted protein, SEQ ID NO: 7519.	117	62
150	G03438		Human secreted protein, SEQ ID NO: 5084.	181.	80
151	G01003		Human secreted protein, SEQ ID NO: 7879.	198	63
152	G03798			95	41
153	X88799	0.,	DNA binding protein	155	96
154	D85245		TR3beta	341	87
155	R74272	Homo sapiens	Tumour suppressor protein, p53.	99	41
1156	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID NO:180.		
157·	G02577	Homo sapiens	Human secreted protein, SEQ ID NO: 6658.	263	98
1158	AF104334	Homo sapiens	putative organic anion transporter	185	42
159	G01393	Homo sapiens	Human secreted protein, SEQ ID NO: 5474.	173	57
160	W75771	Homo sapiens	Human GTP binding protein APD08.	224	81
	AF216833	Homo sapiens	M-ABC2 protein	410	83
1161			Human secreted protein encoded by gene 10	1156	100
1162	W67816	Homo sapiens	clone HCEMU42.	230	70
1163	AF119851	Homo sapiens	PRO1722	113	31
1164	Y87252	Homo sapiens	Human signal peptide containing protein HSPP- 29 SEQ ID NO:29.		1
1165	W64537	Homo sapiens	Human liver cell clone HP01148 protein.	338	82
1166	AF269286	Homo sapiens	HC6	134	64
1167	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	149	51
1168	D90789	Escherichia coli	Dipeptide transport system permease protein DppC.	411	90
	7.6000	Homo sapiens	TG0847 protein.	344	90
1169	R63783	Homo sapiens	Human secreted protein encoded from gene 18.	478	98
1170	Y45274		Mr 110,000 antigen	347	96
1171	D64154	Homo sapiens	organic anion transporter OATP-B	311	67
1172	AB026256	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	60	52
1173 1174	G00357 D87717	Homo sapiens Homo sapiens	similar to human GTPase-activating	178	59
		İ	protein(A49869)	391	78
1175	M64716	Homo sapiens	ribosomal protein	285	67
1176	R08330	Homo sapiens	Human IL-7 receptor clone H6.		72
1177	L06505	Homo sapiens	ribosomal protein L12	242	
1178	AJ251885	Homo sapiens	organic cation transporter (OCT2)	276	88
1179	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	155	71
	G01207	Homo sapiens	Human secreted protein, SEQ ID NO: 5288.	282	90
1180 1181	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	249	62
	<del> </del>		HSPC176	138	90
1182	AF161524	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	282	66
1183 1184	G03789 Y02671	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 22	107	71
	L		clone HMSJW18.	88	69
1185	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	118	46
1186	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	96	37
1187	AB032905	Hylobates concolor	dopamine receptor D4		
1188	G00956	Homo sapiens	Human secreted protein, SEQ ID NO: 5037.	292	78
1189	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	178	79
	G03361	Homo sapiens	Human secreted protein, SEQ ID NO: 7442.	324	76
1190 1191	AF117755	Homo sapiens	thyroid hormone receptor-associated protein	187	70
1192	Y70455	Homo sapiens	Human membrane channel protein-5 (MECHP-5).		67
1193	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	99	42
		Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	192	76
1194	G02607			2001	98
1195	W29661	Homo sapiens	4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	239	69
1196	Y14104	Homo sapiens		149	90
1197	X61972	Homo sapien	s macropain subunit iota	145	51
1198	G00534	Homo sapien		1089	89
1199	Y86260	Homo sapien	NO:175.	l	57
	G02607	Homo sapien	s Human secreted protein, SEQ ID NO: 6688.	154	1 31

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SEQ		Species	Description	Smith-	1%
ID	No.			Waterman	Identity
NO:			:	Score	1 - 1 - 1 - 1
1201	G00838	Homo sapiens		404	50
1202	M27826	Homo sapiens	neutral protease large subunit	202	49
1203	Y73424	Homo sapiens	Human secreted protein clone yi4_1 protein	265	61
1			sequence SEQ ID NO:70.	203	or
1204	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein	625	
j			M160 precursor	023	98
1205	Y36203	Homo sapiens		100	
1206	U78111	Gallus gallus	AQ	219	59
1207	AF095448	Homo sapiens		205	57
1208	AF116715			416	76
1209	AF099137	Homo sapiens		127	75
1210		Homo sapiens		475	95
1210	AF205718	Homo sapiens		423	79
1211	Y/050 CO		suppressor		
1211	Y27868	Homo sapiens		224	70
			107.	1	1."
1212	G00719	Homo sapiens		117	44
1213	G01009	Homo sapiens	Human secreted protein, SEQ ID NO: 5090.	351	73
1214	AF090942	Homo sapiens	PRO0657	124	70
1215	Y14427	Homo sapiens	Human secreted protein encoded by gene 17	99	
1	1		clone HSIEA14.	99	77
1216	G03905	Homo sapiens	Human secreted protein, SEQ ID NO: 7986.	100	
1217	Y57897	Homo sapiens	Human transmembrane protein HTMPN-21.	173	57
1218	J00194	Homo sapiens	hla-dr antigen alpha chain	1173	100
1219	Y59709	Homo sapiens	ma-dr antigen alpha chain	454	78
1220	W81576		Secreted protein 76-28-3-A12-FL1.	470	92
1220	W 013/0	Homo sapiens	EBV-induced G-protein coupled receptor (EBI-	725	100
1221	1110/5/5	<b></b>	2) polypeptide.		i
1221	W96745	Homo sapiens	High affinity immunoglobulin E receptor-like	650	98
L			protein (IGERB).	1.	1
1222	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	135	31
4.5.			ID NO. 160.	]	
1223	Y00278	Homo sapiens	Human secreted protein encoded by gene 21.	260	95
1224	AF161422	Homo sapiens	HSPC304	568	90
1225	U14970	Homo sapiens	ribosomal protein S5	202	95
1226	G01733	Homo sapiens	Human secreted protein, SEQ ID NO: 5814.	610	100
1227	AF099973	Mus	schlafen2	333	
	1	musculus		333	56
1228	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	155	<del>   </del>
1229	AF217188	Mus	YIP1B	155	81
1		musculus	, AM 1.D	801	63
1230	AF176813	Homo sapiens			
1231	X98333	Homo sapiens	soluble adenylyl cyclase	275	100
1232	W74955		organic cation transporter	1704	100
12,52	W /4933	Homo sapiens	Human secreted protein encoded by gene 77	212	53
1233	Y94940	<del>  ,,                                  </del>	clone HOEAS24.	İ	1 1
1233	194940	Homo sapiens	Human secreted protein clone yi62_1 protein	526	100
1004	110000		sequence SEQ ID NO:86.	<b>!</b>	1 1
1234	U76618	Mus	N-RAP	482	82
100-		musculus		ĺ	
1235	AF044924	Homo sapiens	hook2 protein	380	97
1236	G01459	Homo sapiens	Human secreted protein, SEQ ID NO: 5540.	417	100
1237	AF000018	Homo sapiens	adapter protein	164	84
1238	W88633	Homo sapiens	Secreted protein encoded by gene 100 clone	250	
	( .	•	HE8EU04.	230	90
1239	W29660	Homo sapiens	Homo sapiens CH27_1 clone secreted protein.	(07	-20-
1240	AF004161	Oryctolagus	nerovisomal Co dependent as late as will	697	98
	] =	cuniculus	peroxisomal Ca-dependent solute carrier	154	52
1241	Y92710		The state of the s		
1242	Y95002	Homo sapiens	Human membrane-associated protein Zsig24.	709	97
1243	Y44905	Homo sapiens	Human secreted protein vc34_1, SEQ ID NO:44.	908	88
1443	144905	Homo sapiens	Human potassium channel molecule ERG-LP2	325	100
1244	ATORA 450	<del> </del>	partial protein.		- 1
1244	AF284422	Homo sapiens	cation-chloride cotransporter-interacting protein	511	97
1245	Y53629	Homo sapiens	A bone marrow secreted protein designated	1888	93
			BMS115.		- "
1246	AB039371	Homo sapiens	mitochondrial ABC transporter 3	389	97
1247	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	168	39

	No.	-	Description	Waterman Score	Identity
NO:			ID NO. 160.	50010	<del> </del>
1248	AF072509	Rattus	glutamate receptor interacting protein 2	559	90
		norvegicus	tandem pore domain potassium channel TRAAK	661	98
249	AF247042	Homo sapiens	Human secreted protein sequence encoded by	1087	97
1250	B08974	Homo sapiens	gene 27 SEQ ID NO:131.	858	59
1251	L15313	Caenorhabditi s elegans	putative		75
1252	Y29338	Homo sapiens	Human secreted protein clone it217_2 alternate reading frame protein.	278	
1253	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	211	92
1254	G03074	Homo sapiens	Human secreted protein, SEQ ID NO: 7155.	294	83
1255	G01818	Homo sapiens	Human secreted protein, SEQ ID NO: 5899.	253	91
1256	AF286368	Homo sapiens	eppin-l	222	54
1257	AF220264	Homo sapiens	MOST-1	87	93
1257	G02227	Homo sapiens	Human secreted protein, SEQ ID NO: 6308.	281	78
1258	Y07970	Homo sapiens	Human secreted protein fragment #2 encoded from gene 26.	81	94
1260	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain	986	100
			ligand (clone 3TW). zinc metalloprotease ADAMTS6	172	36
1261	AF140674	Homo sapiens		237	67
1262 1263	U28369 Y07049	Homo sapiens Homo sapiens	semaphorin V Renal cancer associated antigen precursor	288	71
			sequence. Human secreted protein #25.	187	80
1264 1265	Y36153 Y78114	Homo sapiens Homo sapiens	Human cytokine signal regulator CKSR-2 SEQ	723	93
	İ		ID NO:2.	191	100
1266	Y13397	Homo sapiens	Amino acid sequence of protein PRO334.	859	95
1267	AF030558	Rattus norvegicus	phosphatidylinositol 5-phosphate 4-kinase gamma		96
1268	U73167	Homo sapiens	candidate tumor suppressor gene LUCA-1	159	76
1269	AF190664	Mus musculus	LMBR2	552	
1270	AL050332	Homo sapiens	dJ570F3.1 (homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP)	820	98
1271	G02126	Homo sapiens	Human secreted protein, SEQ ID NO: 6207.	131	95
1272	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	253	92
1273	AL035661	Homo sapiens	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthethase (acetate-coA ligase))	1280	100
1274	AF064748	Mus musculus	S3-12	3523	61
1275	D17554	Homo sapiens	TAXREB107	377	78
1276	Y30715	Homo sapiens	Amino acid sequence of a human secreted protein.	643	90
1000	A E 1 2 C 2 C 2	Wama anniana	septin 2-like cell division control protein	707	100
1277	AF146760	Homo sapiens	Human PIGR-2 protein sequence.	281	46
1278 1279	X59668	Homo sapiens Oryctolagus	aorta CNG channel (rACNG)	267	85
	1	cuniculus	Human secreted protein, SEQ ID NO: 5132.	489	98
1280	G01051	Homo sapiens		120	43
1281	G03411	Homo sapiens	numan secrete protein, seq 10 No. 1492.	1635	100
1282	AF055084	Homo sapiens	very large G-protein coupled receptor-1	357	98
1283	AF117814	Mus musculus	odd-skipped related 1 protein		
1284	U87318	Xenopus laevis	NaDC-2	535	60
1285	AF061346	Mus musculus	Edp1 protein	452	68
1286	AB030182	Mus musculus	contains transmembrane (TM) region	582	68
1287	A13595	synthetic	immunosuppresive protein PP15	185	97
1000	AF254411	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1	837	100
1288 1289		Rattus	serine/threonine protein kinase TAO1	319	98
1 17.89	AF084205	norvegicus	Southed the Country of the Country o	- I ·	

SEQ	Accession	Species			
ID O	No.	Species	Description	Smith-	%
NO:	1			Waterman	Identity
1290	AF038563	Homo sapien		Score	
1291				523	100
1231	1 70034637	Homo sapiens		468	100
1292	M15888		deaminase		
1293		Bos taurus	endozepine-related protein precursor	937	87
1293	AB010092	Arabidopsis	ATP-dependent RNA helicase-like protein	636	45
1294	A 170000000	thaliana		ł	
1295	AF209923	Homo sapiens	orphan G-protein coupled receptor	1570	100
1295	W67828	Homo sapiens		504	98
1296	1 4 500 1000		cione HFEAF41.	1	1
1296	AC004832	Homo sapiens	protein, similar to	648	65
1297	1/2000		CAA10644.1 (PID:g4164418)	1	""
1297	X80035	Oryctolagus	cysteine rich hair keratin associated protein	575	70
1000	1 00000	cuniculus			1.0
1298	G02645	Homo sapiens		223	97
1299	Y59440	Homo sapiens	Human delta3 fragment #4.	122	32
1300	W70504	Homo sapiens	Leukocyte seven times membrane-penetrating	459	81
1			type receptor protein JEG18.	1 '0'	01
1301	Y67315	Homo sapiens	Human secreted protein BL89_13 amino acid	3916	99
			sequence.	1 32.0	"
1302	M77693	Homo sapiens	spermidine/spermine N1-acetyltransferase	174	96
1303	G01331	Homo sapiens	Human secreted protein, SEQ ID NO: 5412.	254	69
1304	G01491	Homo sapiens	Human secreted protein, SEQ ID NO: 5572.	747	99
1305	AF148509	Homo sapiens	alpha 1,2-mannosidase	602	98
1306	G01658	Homo sapiens	Human secreted protein, SEQ ID NO: 5739.	333	
1307	Y90899	Homo sapiens	D1-like dopamine receptor activity modifying	332	98
L			protein SEQ ID NO:1.	332	98
1308	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	348	
1309	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.		52
1310	AF063243	Bos taurus	ribosomal protein L30	147	66
1311	AF224494	Mus	arsenite inducible RNA associated protein	296	90
1	1	musculus	associated protein	688	70
1312	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	- 1124	
1313	Y99419	Homo sapiens	Human PRO1780 (UNQ842) amino acid	1154	100
	1		sequence SEQ ID NO:282.	1145	78
1314	AF116667	Homo sapiens	PRO1777		
1315	W75100	Homo sapiens	Human secreted protein encoded by gene 44	433	97
	1		clone IIE8CJ26.	807	97
1316	AJ272078	Homo sapiens	APOBEC-1 stimulating protein		
1317	AB041533	Homo sapiens	sperm antigen	789	100
1318	U19617	Mus	Elf-1	2607	98
	İ	musculus		806	92
1319	U82598	Escherichia	ferric enterobactin transport protein		
		coli	torrie enteropaerin d'ansport protein	768	100
1320	D90892	Escherichia	SORBITOL-6-PHOSPHATE 2-		
	[ .	coli	DEHYDROGENASE (EC 1.1.1.140)	709	100
			(GLUCITOL-6- PHOSPHATE	1	
			DEHYDROGENASE) (KETOSEPHOSPHATE		l
		1	REDUCTASE).		
1321	W67847	Homo sapiens	Human secreted protein encoded by gene 41	10.	
	ĺ		clone HPBCJ74.	601	92
1322	AJ276101	Homo sapiens	GPRC5B protein	1	
1323	AJ276101	Homo sapiens	GPRC5B protein	466	93
1324	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	504	97
1325	U91561	Rattus	pyridoxine 5'-phosphate oxidase	1584	100
		norvegious	Pyrmonine a -biospirate oxidase	1277	89
1326	AF125533	Homo sapiens	NADU outochrome he as in the		
1327	Y32206	Homo sapiens	NADH-cytochrome b5 reductase isoform	1606	100
		Tromo sabiens	Human receptor molecule (REC) encoded by	1531	90
1328	AF151048	Homo sapiens	Incyte clone 2825826. HSPC214	<u> </u>	
1329	Y10530			657	85
1330	AF180681	Homo sapiens	olfactory receptor	1645	100
1331	AF111856	Homo sapiens	guanine nucleotide exchange factor	4314	99
	-# 111070	Homo sapiens	sodium dependent phosphate transporter isoform	3591	99
1332	Y13583	Homo series	NaPi-3b	<u> </u>	_
1333	AF078866	Homo sapiens	G-protein coupled receptor		100
	.4 070000	Homo sapiens	SURF-4	1395	100

SEQ	Accession	Species	Description	Smith-	%
D ID	No.	Proces		Waterman	Identity
NO:	110.	1		Score	
1334	Y25755	Homo sapiens	Human secreted protein encoded from gene 45.	1380	96
1334	AF152325	Homo sapiens	protocadherin gamma A5	4742	99
1336	X74070	Homo sapiens	transcription factor BTF3	639	81
	AF095927	Rattus	protein phosphatase 2C	1931	95
1337	AF095921	norvegicus	proudit phosphilities 20	1	
	000000		Human secreted protein, SEQ ID NO: 7958.	621	100
1338	G03877	Homo sapiens	bK223H9.2 (ortholog of A. thaliana F23F1.8)	626	100
1339	AL008582	Homo sapiens	leukemia inhibitory factor receptor	5820	99
1340	X61615	Homo sapiens	A carcinogenesis-inhibiting protein.	7528	97
1341	Y01519	Homo sapiens		2372	100
1342	AF207600	Homo sapiens	ethanolamine kinase	1167	97
1343	U54807	Rattus	GTP-binding protein	110,	1"
		norvegicus		12002	51
1344	AC020579	Arabidopsis thaliana	putative phosphoribosylformylglycinamidine synthase; 25509-29950	3283	
1345	Y28576	Homo sapiens	Secreted peptide clone pc503_1.	944	100
	W74787	Homo sapiens	Human secreted protein encoded by gene 58	1171	100
1346	W /4/6/	110mo sapions	clone HHFHN61.		
1678	166640	Homo sapiens	guanylate binding protein isoform I	2636	87
1347	M55542		28.4 kDa protein	1329	100
1348	AF183428	Homo sapiens	Fas-ligand associated factor 3	167	24
1349	U70669	Homo sapiens	Pas-liganti associated rate of the channel	562	99
1350	AF295530	Homo sapiens	cardiac voltage gated potassium channel	1 502	
		_	modulatory subunit		

# TABLE 3

	-	• .				· · · · · · · · · · · · · · · · · · ·
SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino, acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1	1351	A	2	337	1	HWPQAPHRA***GLLPPRWLGHGLPGGPAAP WAASQWVDGVAGRLPGPAWSWHASGAAPA OPGPL*LLVPGSSGLPDPRDP
2	1352	A	2.7	100	366	IRNSSIRPMKERETKLSAKHMITCSASYDIRGL QIETTVYHHTPIRMAKIQKT/GHHQC**ECGAT GTLIHGWWGCKVVEPLGKTVWQIPK
3	1353	A	40	3	314	. HASAHASVVLKDNSELEQQLGATGAYRARA LELEAEVAEMRQMLQLEHPFVNGADKLRPD SMYVHLNEL*QSLVENMLLTVVDTH\RTPI*R SCNYTLALILFL
4	1354	A	74	2	292	TASALFSCPDGGSLAGFAGRRASFHLECLKR QKDRGGDISQKTVLPLHLVHHQVAHTFGQAT VTCQQARQSPG*RTNPE/ALQWVLPVSDGWH VLPLP
5	1355	A	78	114	850	ENCRVASNLPGVFFSEDTAQSGSYMRISAHPP, NAGGEVSNGPKRKLTLMLNFSLPSSGLNAGA FYALSTLLNRMVIWHYPGEEVNAGRIGLTIVI AGMLGAVISGIWLDRSKTYKETTLVVYIMDT GGAWWCYTFYLGTGDTCG*CFITAG\TMGFF MTGYLPLGFEFAVEL\SYPESEGISSGLLNISA QVFGIIFTISQGQIIDNYGTKPGNIFLCVFLTLG AALTAFIKADLRRQKANKETLEN EWFSYMLGSNMSVYHSP*SLEPLCKVLSES*A
6	1356	A	81	97	376	YLRYPFIRILLNAR*IRKAYKRMSLEIKLLI/RE *CLFOEMGLSLQWLYSARGDFFRATSRL
7	1357	A	93	2	872	TLSSACLIGDAWKELTIVAGAVSNQLLVWYP ATALADNKPVAPDRRISGHVGIIFSMSYLESK GLLATASEDRSVRIWKGGDLRVPGGRVQNIG HCFGHSARVWQVKLLENYLISAGEDCVCLV

COPO ID	TOPOTO	134	1 686		·	
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	woo	in NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	i	USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	j	09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
j		1		peptide		/=possible nucleotide deletion, \=possible
L	L	ł		sequence	i	nucleotide insertion
						WSHEGEILQAFRGHQGRGIRAIAAHERQAWV
1	}	!	!	]	1	ITGGDDSGIRLWHLVGRGYRGLG/DLGSLLO
	1	İ				VP**ARYTQGCDSGWLLATAGSD*YRGPVSL
		]	1			*RRGQVLGAAARG*TFPVLLPAGGSSWSRGL
			1	1		RIVCYGQWGRSCQGCPHQHSNCCCGPDPVS
8	1358	A	106	<del> </del>	1.50	WEGAQLELGPAWL
°	1336	/ A	100	3	350	FSSLLSGRISTLRDETGAILIDGDPAACAPIIKF
		ł		1		LLTBELHLRGVSIYVLRHEAQIYGITPLVCAL
İ	1	ł		ł	1	LI/CRRL*SDSCMRAALNDRGLYQVLILDGLV
9	1359	A	115	49	186	QCLGFVDSDSRKMVSTLT
		``		"	'66	QAWAIFKGKYKEGDTGGPAVWKTRLRCALN KSSEFNEGPERERMDV
10	1360	Λ_	123	2	1249	KGCRTQEKVDRTEVIRTCINPVYSKLFTVDFY
	,	1	1			FEEVQRLRFEVHDISSNHNGLKEADFLGGME
1	1	1				CTLGQIVSQRKLSKSLLKHGNTAGKSSITVIA
		1				EELSGNDDYVELAFNARKLDDKDFFSKSDPF
-	1	l				LEIFRMNDDATQQLVHRTEVVMNNLSPAWK
	1	1	1			SFKVSVNSLCSGDPDRRLKCIVWDWDSNGK
	ļ					HDFIGEFTSTFKEMRGAMEGKOVOWECINPK
1	1	]				YKAKKNYKNSGTVILNLCKIHKMHSFLDYI
			1 1			MGGCQIQFTVAIDFTASNGDPRNSCSLHYIHP
]				'		YQPNEYLKALVAVGEICQDYDSDKMFPAFGF
i		[	1			GARIPPEYTDSHDFAINFNEDNPECAGIQGVV
	1					EAYQSCFPKAPTFTGPTNICPHSSRKVAKFRR
						SEGN*HQGRAFAIIFILVDPGQVGVYSQDMGP DNPGGHFV
11	1361	A	147	614	9	ACARKQLLGRTVFIWFVGQLLGGELKGYSKT
					-	NTTSSRPASSRG\TLSSSSSSSSSLTKDALPSSL
	1			i		KSDSTTITSGLVFPFRSLCVNPAKSSVSESVSSI
						KILLSSSVKYLE*KRTSCCFPDSSESKLSQLSS
			1 1	1		DERVSMGTSSRKPTNSSSSLGALKMSATS\*G
						SGSESPTPFFLTGLQSPPSTRPREPGLTTARNS
12	1262					TTLTRDC
12	1362	A	177	12	416	LIPSEPALDSLVDPRVRSRKQPFVIYPVYDTAI
			] ]			DTKIHFSLLDGNVGEPDMSAGFCPNHKAAM
	,					VLFLDRVYGIEVQDFLLHLLEGGFLPDLRAA
			] [			ASLDT/AEIGAMDFLLS*LFTLCLMMFFFIYPFI NLLTMNVY
13	1363	Ā	249	535	105	WTFHRHLSPAPLIVCDQGTCVVSYYPONIVO
						MPDTQMEQGLN/HLFLDGNA*PHSVECYCPS
	j				[	TFEIAIKITSFVLYFHRYRAPEVLLRSSVYSSPI
					ĺ	DVWAVGSIMAELYMLRPLFPGTSEVDEIFKIC
<u> </u>						QVLGTPKKVSTLVPKLL
14	1364	À	254	572	201	YLLTXIGNLMMLLVINADSCLRTXM*FFLGH
						FFFLDICYSSVTAQDAAEFPVS*KPILVWGYIT
	i				ì	*SFFFIFSWGTNGCLLSAITYACYAAICHPLLS
15	1266		059	105		TMVMNRPLCTATVNATNKMGFLNSQVN
"	1365	A	257	425	68	THAKFLNKKFNIPKLVILPKLVYIVKAIPTKM
1	i			}	1	AIEFLLECDQNIT\KLICENT*KNIAKNI*KRRV
	1			<u> </u>	[	TFTPIET*HPVKQMIKWQ*LTAWLRNRGYKKI
16	1366	A	263	104	481	KQTPNSETAPSVCRNLVFDKCG
	-500	^	203	101	701	FCIFRTTEEDRGGDDCVVSVWTKQRNNSCVK
	- 1				ì	SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV
	į		}		l	GDLSSPNETKYIISLDQDSVVKLENWTDASRV
17	1367	A	298	68	208	RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW
			1			VSSLAMKEMLTKTTM
18	1368	A	300	904	1	LVVGITGTRHHARVIFIFLVETGFPHVGQAGL
		{			ł	ELLTSGDPPALASQSAGITGMSHCARPKGHFG

	000 0	3.464	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	1=Teoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	(	3	ng to first	acid residue	O=Glutemine, R=Arginine, S=Serine,
uence	l	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Ì	ļ	}		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ.		residue of	Seductice	/=possible nucleotide deletion, \=possible
	Í	ĺ	{	peptide	1	nucleotide insertion
	1	l	İ	sequence		IHLK*MFYTMSQKMP*PTINLILLLIIPGNLNIF
						IHLK*MFYIMSQKMP*PIINLILLLIIFONLNIF
	]	l		· ·		KPNMGWLGPKTAFV*KDEVLSGIPFAKGRCR
	\	1	•	İ		WK*DY*C/LQEVTDPIMEKGKKKKRTASFFK
	1 .	1	1		1	GQPHQSTNALLRRCVR*RYHLS\TVETAGLP*
			}	1	1	KNTGHIPGOPFLFKLVFKC*NVICI**QYKW*Q
	i	1	1	Ì	) ·	NIGVKNKSFCPH*SSSPSL*FIGHHSRNF/CSFK
	1	{	ſ	1	1	TEPHSVVQAGGQWRNLSSLQAPPPGLMPLSR
		1	ì		1	ISLMSSWDYRRPPQ
	J			<u> </u>	<del> </del>	NSPSRWAKIQMFEHTFCG*GCG/ER/NVHIHCS
19	1369	Α	302	3	445	NSPSKWARIQWIPERTIFCO GCGLIAVIVILLICO
	l	}	1			WICRLRPLLWRAVREYLSKLKNAELSFDPGV
	1	1	ļ	1	1	SLLRIYAIDMPTSI*DEKEALLFAFLAFHE*HC
	1	1	ì	1		KSRIWAVIQ/CIHLWDWLRKL*CFHRMKFYA
		1				AV*NKPRHLLSHIWKDVQNILLK
20	1370	A	304	†1	1339	PFFCGKEVPLFEONKHPGPRATTSPGA/HARA
20	13/0	1^	304	1 *	1	LLSAGEFTAGVGLSP*AIHSFVWLCTFIQHGA
ı	i	l	1			GGPCHOPGGSPGPWMHTTQAGHLWEGAYPG
	1	i	1		l	GSSTWHQVPGQLGGSWGPRERSLLGSFIKCSP
		1	1	ŀ	1	CPHPPGFRLWMSPNQKPPTENPGVMGRVWR
		J	1			LMPGESPLIWEAEGKEDHLSPEGQGHSE/PVA
		.1	1	ĺ	. [	LWAGEST MEYER TO TO THE BOOK OF THE COLOR
l	ł	1	ì	1	į	PLHSSLGNTVKP*PKNQKPKQNRSRHGQ\GF
	1	1	1.	1	1	MAGQGQSRPAAR*PPCPALTPASHSAGTWPP
	1	1	1	j	1	RICRTVPGGPCPSPSGFRSCRR*GFSA*TRSWP
	1		1			DAEPPSTPDTAPRCCTQSDTSSQGPQ*S*WRR
İ	1	1	1			CRALPGRLCSAPAAGLRRARPRLSESRRGNSP
i	1	)		1		PASPAAASARCPSWGPSCPARPPSRPAAGTEP
1		1	1 .	j	1	AAPSRCTAWLRGEREPGPRPPGRRPRSGRGP
Í	1	1	1			VSFAPEVLSLPAVRQTKSWRWRNEEEITRPW
i .	1	1	Ì			
'	1 .	<u> </u>				ALVRSRGG GSQVLPPPPSQDSATLPQDA*GPRAAPGQPVC
21	1371	A	326	799	1587	GSQVLPPPPSQDSATLPQDA*GRAAAFQFVC
İ	1	1		1	Ì	E*GLQGAGVRRLRGEVLCQPQP*GAL*EQCLP
	1	ļ	i	1	i i	HLSFSPRQGAAPDTEPSAWGPAPTGATGPGLP
Ì		1	1			LRHVRLFSAGAPRGAATPCPPALLHGPAWPP
ł	1	1	ĺ	1		ARPMFRGHPPVRPLGPWGKVAAGPRALCLA
1	ł	1	1		(	GVPAVOGECATKPSG*GL*PAHLRGPPGPEVL
ŀ	1	1		Į.		OWHWOLSAGRDPVPAEDPPL*EGPLGPGGPA
	]	1	i			AAQAEPGADPEPEDKDQAAESRPAGAMSLSA
4	- {	l	i	1	{	QGSGPVGGQGLR
L					<del>-  </del>	PHLENPHPEHSFPGAPLT*STLSWSILSPREPSP
22	1372	A	327	146	652	PHLENPHERIOFPUARE I OILDWOILDFREFOR
		i				GAPCYPGHPHLENPHLEHLLTWRTVTWSTLL
1		1				PGAPCYPEHPHLEHPLTWSTPHLEHPSPGEPL
		1		ł		SCRTPTRSILHRDHPLP*CLSTEESPI*GWGSLP
Į.		1.	Į.	1		APPSTPLVLDVAPPGPQPASSCPGRDSCYSVP
	1			1		GTVVSP
<u></u>		<del></del>	<del> </del>	1200	12	CIVSSCQGTRKPCHLEDANKINKQSPTLEKIES
23	1373	A	348	397	4	LQESL*VKQ*LIVAEKYVQILHPRKKYFQRPL
1 .	1			1	1	NNEKRKMKKRKEEKKKCRERMQRRSKWRR
1	1 .		1		1	NNEKKIMAAKAEEAAACKEKWQKASAWK
1		}		1		EEKKE*RREE\EERKKEKEDRKERRKETSPRG
1	1	1		1	1 '	SRRLLRD
24	1374	A	362	170	352	GRALDTAAGSPVQTAHGLPSDALAPLDDSMP
24	13/4	^	302	1 * " "	1	WEGRTTAOWSLHRKRHLARTLLVSRVRGPQ
				373	128	YLITTILETGYLWKNRHSDQ*KRTENPERDQH
		A	384	3/3	120	KYPKVDFCKSNSMKNRLCNKWHWTNWIFTD
25	1375		1		1	KKINLNLKPHTKLTPNIKKN
25	1375		- 1		ı	I VVINTUTVLUITVT I LINTVVIN
25	1375					THE WAR IN THE COME IS THE STATE OF THE PARTY OF THE PART
	1375	A	397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK
25		A	397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI
		A	397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIPANF
26	1376					EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIPANF KSKATGYMYNI*KLIVVFLYANDEQLEIEMNK
		A	397	383	380	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIPANF KSKATGYMVNI*KLIV\FLYANDEQLEIEMNK IVP\FNGSKNKIAFTNLTKYONIQNRHAENYKI
26	1376					EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIPANF

SEQ ID	SEOID	Met	SEO	Predicted	1 N 0 - 1 - 1	
NO: of	NO: of		ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide		in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	j	USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ı	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
(	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1	1	Į	peptide	1	/=possible nucleotide deletion, \=possible
L				sequence	1	nucleotide insertion
28	1378	A	408	14	427	TICTNKFNNLDEIK/FLERHKLSKLTOEEVENL
i	İ	i	i	i	i	ITLKTSRETELVINK*VIPHKEKPGPDSFTGEF
1		1				YQTFKEEL/II/ILHKLFOTIKYGRILPNSVYETS
ļ	1	}	1	}		TLKPKPEKDL\KENYRPLPLSNIDAK\LNKTLA
29	1200	<del>ا</del>				NRI**HIR
29	1379	A	434	395	128	1YSKMCMERQRLNN*ILKKNKVRGIAVPDVK
	1	1	1	(	1	VYYKPTVIK/TSWIL*KDSHIVEWNRLENI.EID
30	1700		155			PN/IKRLILDKGAEATEWRKDSFFROWO
30	1380	A	455	2	228	FFFETESHSVTQAGVQWCNPGFKRFSCFGLSS
	1	1	ľ		Ì	SWDYRYAPPRP\ANF\*FLVETGFYYVAOAGL
31	1381	A	100	-		KLLSPGDLPALAS
J1	1301	A	462	393	2	QLMFDKGVKNIH\WGWTPPFTK*YWKNWISI
						CRRMNLNPYLSRYIKINSR\KDLTVRPEPIKLV
		1				EENTGKTIQDTGLGK*FIAKTSKAOSTKTNK*
				,		KRQTRYIKLK\KKSTASKENNRVKRQPLE*EK
32	1382	A	474	125	471	IFAN
	1502	1"	7/7	123	4/1	VKPYEIAVFLVKPIEYK*HLLSDPAIPLSGI*LK
		1				EIKAYT/RRICTPMFAAPVSVIA/RN*KQSK/CQ
	l					KQ*YVHRMEYYTTIKRSEILICTTTWVDFRNT
33	1383	A	488	1825	2	ILRETDRIHKTTYDVISLI
		1		1025	2	KSACSFICSEEQPASPSPLKPGTYASET\RPRDP
	İ	l	1 1			HAAGPRRDSSEAETRRPRGA/DGSGTVVKGT
		1				PGSPAPPCSWGHGG\ETEGAG*CPAAPGTDLR
	1	l	1 1			APGGSAGS*\GLPSAGGSRGRKGWRAAGRQP STR*GRPGRHGGRGE*AGHPEPRQSALQSAG
		i	1			L/ASSPEPMGAALAEDGSGDSRGAGPRPQE*P
		1	1			PSVLSRS\GS*G*G*AASGTASSPRSHSSRLGPP
		1	1			SAGFHGLRCGQPPFAAAPPGPWPGTGRPAGG
		1		Į		AGSPPAAAGTAPPATRGAQSRRQNRTAGRNA
	ļ	1	1 1	i		SPQTAAGAGSPVQWALSRATG*TGETGSWC
	ĺ	ĺ	1 1			AGGTHQATHLTAAWVCPPTWSVRPGGSGPA
				I		AGLGR*GRHPAQSPPLPVPRG*PAWPOEAPSP
		1	1 1	1		SPASSEVALSSGSCWPDQAPGPARGSPPAPLA
		[		1		PAWPAAGRGROR*GROSAHPPPRR*STAVSI
·		1	1	j	j	SGTS*WRRSP*AGTRTQQC*SPWLVPACSSRP
			]			L*RGTRRPSTQQSPQTTGTPGRSAGPGHPRS*
			] [	l		GGRSPAGTGHLGAQTVASPH*GHWPTALSCL
}			1	- 1	i	WASASPPGPEAPPQTGACIGTNCRYRAASAR
				1		RSSVAPACA*GWQ*AGSPPAVLRGPP*RVRER
34	1384	A	497	422	2	GALTHRPRAPDE
ł		·- I	"	706	-	APGASVGRAQAAEG*RGGPTGRPPSALGVS/E
				[	1	AGRAGRAGEGRPVPPAYPLCKSAQTSGPPKA
ł	i			ł	ţ	RLS\PPLASCOGRGPPGGAACATCAPPAGPAR
		- 1			İ	SSRCRRRSPPE*GPR*PSRPARPSPGSAASRRQ KLTPCRCQFRGLCA
35	1385	A	509	156	475	PTPYPGE*QAAFLLRGPGLRPPA/DPSLR/HRN
1	ļ	Į		-		LTELVVAVTDENIVGLFAALLAERRVLLTAS
ļ	]	ı				KLSTLTSCDHAFCALLYPMRWEHVLIPTLPPH
				.[		LLDYC*CPPLPRT
36	1386	A	512	3		FFFSFVCHLYCVSPTPGPHGRLATWL/PGLLA
	}	- 1		1		FLOLAAGGQTLCPAGELPGHARAQASGAPGS
]	i	[		1	1	VLIAVPGRRRVHTCGPGPAAPSTRGECPPPAL
	ı				l	CUTTO L DODGE THE COLUMN AND THE COLU
- 1	[	l	1	1		(IH   KPAKPKPV\PKAPAVPORDGGOGGOGGA + - M - I
					1	GHTRPARPRPV\PFAPAVPQEPGGQGHGAA/P PATGHSAPRGCPPARAAPTGSATPAPPPAACA
					ľ	PATGHSAPRGCPPARAAPTGSATPAPPPAACA
						PATGHSAPRGCPPARAAPTGSATPAPPPAACA AFHSAWSVPPAGRQQG*RVPAPAFRRTTPGT PGQHLLDRPGAPPAOGSGPAPAPPPRIAGPA
						PATGHSAPRGCPPARAAPTGSATPAPPPAACA AFHSAWSVPPAGRQQG*RVPAPAFRRTTPGT PGQHLLDRPGAPPAOGSGPAPAPPPRIAGPA
						PATGHSAPRGCPPARAAPTGSATPAPPPAACA AFHSAWSVPPAGRQQG*RVPAPAFRRTTPGT

OFO ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
nuci-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	ļ	peptide	}	/=possible nucleotide deletion, \=possible
		ŀ	}	sequence	1	nucleotide insertion GRPSQSQ*PAGPPGMRGCCLRGW*PSSSGSD
						GPSQSQ*PAGPPGMRGCCLRGW*P333G3D GPGPHPASTWLRAGKTGPSPPACGCA*LPPPS
		1	1 .			VSAAPQSPRTRCPRGCAAAAGLCVLAAAGAS
•		ļ	1	Į		HGA\GLPGVRVHTQRVHIH+GAG/GCQTPRPR
·				]		LRSLPVLGLPAPRCPVSAHPWHRRSGSSCHA
	1	1				ARLVPRHPAPGCP**TG*\PLITGFPEP*A*GLP
	}	1	1	ļ	}	NHQAVGLEASGALQAGHRDELPTMVQLLDH
			ł	l	1	SPDYPLKGRPHAP
		l			<u></u>	FRLPLAAGA/RGAAEPRVAVSMAPDPSAKIH
37	1387	Α	620	828	1	WEASPEMQSKCHQKGKNNQTECFNHVRFLQ
		•		}		RINSTHLYACGTHAFQPLCAAIDAEAFTLPTS
	ļ.	l	1	l .		FEEGKEKCPYDPARGFTGLIIDGGLYTATRYE
		1		1		FRSIPDIRRSRHPHSLRTEETPMHWLNG*EDE
	ì		1	j		AQDDGG*GTISSFLLPWPADHPTPKSPGEPVH
	1					SIPVCCQVRGQPQSGGKESPACLKSLSNCLTH
	ļ				1	\DAEFVFSVLVRESKASAVGDDDKVYYFFTE
	1 .	1		į.		RATEKESGSFTQSRSSHRVARGIPPL
		<u> </u>		<u> </u>	427	FRAMVSSTLKLGISILNGGNAEVQ/QGNRGKG
38	1388	Α	739	1	421	TSEEGKEG*EVPV*LPVSPPLPRPLQKMLDYL
		1	}	1		KDKKEVGFFQSIQALMQTC\GEKVMADDEFT
	1			1		QDLFRFLQLLCEGHNNDFQNYLRTQTGNTTT
	1	ì				INIIICTVDYLLRLQESI
	<u> </u>		5.5	<del> </del>	1030	TI DI TGPLLLGGVPNVPKDFRGRNRQFGGCM
39	1389	A	767	1	1030	RNLSVDGKNVDMAGFIANNGTREGCAARRN
	İ					FCDGRRRONGGTCVNRWNMYLCECPLRFGG
	1	1	İ		İ	KNCFOGEWPASSIPPVTAAWEALLLDVPGTT
			1			VRGLHIOVROPLVVYAAFTVDSHRPLQETVL
ļ	1		1	1	-	RRAPAPASGVPSPSGVGWDR*AGPAEPSPSTP
1	1	1 .	Ì	Ī	1	ATVIISVPWYLGLMFRTR\KEDSVLMEATSGG
	i	1		1	1	PTSFRLOVTGAPCHOGTC*VGARGRDPMLSG
				J	]	LRVTDGEWHHLLIELKNVKEDSEMKHLVTM
ĺ	į	1		İ		TLDYGMDOVSWHLHLLWG*TLPPAQGKTGA
		1			1	SEDKVSVRRGFRGCMQVRGGCGGRGEACPS
			1		1	QAAPRL
40	1390	A	801	69	399	IHKIIIHKEDLNKWKYILCSGMERLSTVMIPVV
40	1390	1	1001	1 00		PQIIYKFNA*Q\VILKFTW*E*GAKITILRKNKL
	1	ì			Ì	RGLVLVPLSTC*VKYLLDKVLPHIKTYYEAR
ļ		1		1	1	VNKSVVLVQVTIM
41	1391	A	835	7	195	SMI KERK VFOFPSCLFFOYITWLGPPYHVLFD
41	1371	^	1 555	1		SSVTNFSIGAK*DILOSVMNCLYAKRIPCVT
42	1392	A	841	<del>-   1</del>	415	GSTHASGYDKTPDFILOVPVAVEGHIIHWIES
42	1372	^	1 04,	1 ^		KASEGDECSHHAYLHDOFWSYWNSLKHRTW
1		i		l	1	OGIGTVASNLSOL*TLNAPFPELLLFRSLARTG
}	l			1		FVLT*\RFGPGLVIYWYGFIQELDCNRERGILL
1	1	1		1	1	KACEPTNIVIL
43	1393	A	845	358	92	PALSPAPVPOKKGSPLPLDPCLGPSSWLLSVG
45	1393	^	1 373	1 555		LGWPRL*PRRGPGDPGSLPATPPLLTPPHTLLP
1		-	- 1	i	1	ORPMLPPSHAGLARPPPPEPISVP
44	1394	A	853	452	1	LPOYCFFPRLSPKSKLVKHSAL**PSALKPPTK
""	1374	1	1 355	1	,	SPRCIPRTSLYFTICC/PPALOL/SPIEDPPAIYRS
1	1				1	PPTHMLRSASOPLNOAPTLVKGHPPSRFLQG
1	!					OVSCPPOPTLPREKPLPLHLRPPPRPAQPPLPR
1	1			}		PLTFSTRRNVDPEIPERFR
15	1206	A	894	379	162	GVYPPTVFDNYSVOTSVDGQIVSLNTWDTAG
45	1395	A	074	1 3"		QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT
1		1		j	1	WLSMSMGK
1	120/		900	$-\frac{1}{1}$	366	TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL
46	1396	A	שעקן	1 4	1 220	THE PARTY OF A PROPERTY OF STREET AT THE IDD
1 70		- 1	- 1		ľ	EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR VFLFHQLNIT**CLHFFIMTTFIAIPFSFLFLGR

ſ	SEO ID	SEQ ID	Met	Lego	I Dunding 1	16 P. 1	
ĺ	NO: of	NO: of	hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	nucl-	peptide	1100	in in	nucleotide	nucleotide location	D-Aspartic Acid, E-Glutamic Acid,
- [	eotide	seq-	1	USSN	location	corresponding	F-Phenylalanine, G-Glycine, H-Histidine,
	seq-	uence		09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
-1	uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1			1	" "	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
٠		l	1	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	1	1	peptide	1	/=possible nucleotide deletion, \=possible
					sequence	1	nucleotide insertion
							D/KSLAMLPRLVSNSWPQVILPP
1	47	1397	A	944	162	2	QLQNLASRGCL*SQLLRRLRRENRLNPGGGG
-		<u> </u>			<u> </u>	J	CSEIAP\CTPAWVTQRDFFRKKK
ļ	48	1398	A	963	216	308	HFTPDRIAIVKNTRDSHCWRGC*EEGAPARC
-	49	1399	A	967	466	1	PRKRESWWGERLP/PRGFPPAAEDAPAPGWK
}		1			i,		GRKHASRTARAHVFHPIRQSIRSPVRGRPGDP
-			1	ł	ļ		RAAHTRSAGTRLQCKASRGG*GKGPAPTR*E
1		l	i i	ł		ļ	GGPGSAPAPLPASSGCSLFPDSSPWTPPPPAPG
-	50	1400	A	973			AAAAQP**TPRCPAALRAGAHIGRVGRPY
1	30	1400	A	9/3	45	421	EKCIQALDVFVFCYIDHSSHCLMSCD*E/DQA
1			1	[			LNFMPLEMEPKMSKLAFGCQRSSTSDDDSGC
		1	ł			1	ALEEYAWVPPGLRPEQIQLYFACLPEEKVPY
1		. ,	}				VNSPGEKHRIKQLLYQLPPHDNEVRYCQSLSE
H	51	1401	A	992	2095	194	E PROPERTY OF A
		1	1 "	''-	2033	154	IRIRHEAARSCLGCAAGHVPAPGLRLLPTVRG
1			l			1	PPGRRGPAAPGCVCY*SGESTFVSHVPQRMA
1					•		WPGSAPPRGFHPLQSQTSPSDTVSSPQLSKEE DGPGWEHPLSSSL*SLGQAGGNH*QPEELAG
						]	WEPRGPPSLAPSSPT/TMWTALVLIWIFSLSLS
							ESHAASNDPRNFVPNKMWKGLVKRNASVET
1			l	1 1			VDNKTSEDVTMAAASPVTLTKGTSAAHLNS
			1				MEVTTEDTSRTDVSEPATSGVAADGVTSIAPT
1				1			AVASSTTAASITTAASSMTVASSAPTTAASST
				1			TVASIAPTTAASSMTAASSTPMTLALPAPTST
i			•				STGRTPSTTATGHPSLSTALAQVPKSSALPRT
		:		]			ATLATLATRAQTVATTANTSSPMSTRPSPSKH
ı							MPSDTAASPVPPMRPQAQGPISQVSVDOPVV
ļ							NTTNKSTPMPSNTTPEPAPTPTVVTTTKAOAR
	ı						EPTASPVPVPHTSPIPEMEAMSPTTQPSPMPYT
							QRAAGPGTSQAPEQVETEATPGTDSTGPTPRS
-							SGGTKMPATDSCQPSTQGQYMV/DHH*APHP
İ	ĺ					· i	GRGRQNSPSGGAVTRGDPFHHSLGFVCPAGL
	ł						*ELQEEGLHPGGLLNQRDVCGLRNVRGAGA
	·						WREAWPLPRPFLLPLRPNQVLPNSFGAIEEIC QMLKHI
	52	1402	A	994	1	462	ESGEFL VSFTLKKPTNVFHHINGMKFFNK/LIF
	ĺ	1		1	_		*SHTDIAFYKIQHPFMLKALTKWA*EGT*PDR
	- (		. 1		ſ		RYLH*SLRLNGEQLKTFPLRSGMR*G/CAILPL
1	- 1		1				VLNAMLSIVPAVVPAGKTRHEKEITCPLIGQE
L						[	EK*FS*FVGDMNTCVENKKESKKLLE
1 5	3	1403	Α	1011	1	630	PEVIQQSAYDSKADIWSLGITAIELAKGEPPNS
	İ	1	ļ	1		- 1	DMHPMRVLFLIPKNNPPTHCWRRLLESPKEV
1	1	į	- [	- 1		ì	*LMLA*TKDPSI\RPTAKELLKHKFIVKNSKKT
		[	i	1		İ	SYLTELIDRFKRWKAEGHSDDESDSEGSDSES
1	[	- 1	Ī	1	1	1	TSRENNTHPEWSFTTVRKKPDPKKVONGAEO
	ŀ		1				DLVQTLSCLSMIITPAFAELKQQDENNASRNQ
5	4	1404	A	1016		200	AIEELEKSIAVAEAAGPG
ľ	. ]	1704	^	1010	1	222	ISIDA*KAFDKIQH/CFMITTLKKLGIDGKYLN
1	ľ	]	]	- 1	Ì	ļ	TIKAIDDRHTVSTILNVEKLKAFL*RSGTRQRF
5	5	1405	${A}$	1033	3		PISGSGARI
۱	-		"	1000	,	366	HASVDGDEGSDDVYYYYTPAILRELQALNTA
1			l	- 1			EAAEHRPEEDRMLSEDPWRPAHMIKGYMPL
	1			1			HNIPHTEVIDVTGLNQSHLYQHLNKGTPMKT
5	6	1406	$\Lambda$	1044	5	429	QKRAA/LYTWHVLEQLEILRQINQQSHGPG
					1		SVLTLQTRSPSKPLS\RKLMDWEVVSRNSISE
	1	j		1	j		DRLETQSRASRSPPVTPNQSQETPVDGKPLAL PPNQSQKNIRYHIHYLHLQYYLDRHISATLPIP
	- 1	İ	- 1	- 1	}	1	SSSGIPTPIAVITDALTDLVELILGQPCSEESGR
L	[	ĺ		- 1	ŀ	İ	APGTLFLLAL
	<del></del>						

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Mct	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN	location	corresponding	i=isoleucine, K=Lysine, L-Leucine,
seq-	uence	ĺ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
	uonoc	l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	]	ł	peptide	bodanis	/=possible nucleotide deletion, \=possible
	1	1	ł		1	ancleatide insertion
	·			sequence	100	GAYAFETNGFPIMLVLTTDKIEGDVGIAGLYD
57	1407	A.	1050	11	430	MHVISLPMAFLLRTLVRCTSYIIPVTHVLSTPV
		l	1			TCLRREKDGVIVDVLSDTASNHNGFPVEEH
	i	1	1	1		TCLKKREKDGVIVDVLSDIASMINGII VBEI
	1	i	l		į	ADDTHPARLQGPTLRSQPMGPLKHKAFEERA
	ì	i	1		ļ	NLGLVQRRLRLED
	1400	A	1058	258	419	LKHRDTPVVGANNRALSCTPLTSLTLCALCPL
58	1408	I A	1038	236	1 722	PCLGCPTXATCRLYOTTVAVVF
	l			<u> </u>	425	LA ESETTSLIGHORMHTGERPYKCKECGKTF
59	1409	A	1064	3	423	KGSSSLNNHQRIHTGEKPYKCNECGRAFSQC
		1	l	1	l .	SSLIQHHRIHTGEKPYECTQCGKAFTSISRLSR
	-	l	1	1		22 I OHHIGH I GENT LEGI GCOLON LOISINGON
	ł	1	ì	(		HHRIHTGEKPFHCNECGKVFSYHSALIIHQRIF
		Į	,	1	-	TGEKPYACKDVGK
<u> </u>	1410	1	1065	204	419	T GCDDGDFT AUTHAGLOAPGPLLAPAGDEGDL
60	1410	14	1005	201		LLLAVQQSCLADHLLTASWGGK/DPIPTKALC
		1	1	1	1 .	EGOEGLPLTV
				<del> </del>	102	RHSRAHLCQPFHLVMRDLLQLGQDIPQGCHY
61	1411	A	1079	3	383	LEENHLIHRDIAARNCLLSCAAPTRAATIGDF
		1	1			GMARYIYRTRYYQLGDRAL/LPRKWMPPEAI
	1	1	i	1	1	GMARYIYRIRY YQLGDRALILIRR WWITER
	1	}	1			LEGIFTYNTDSWTFGVLLWEIFSLGYMPYPGI
	1	1	i i			TN
		+	1080	1	859	VVEFLWSRRPSGSSDPRPRRPASKCQMMEER
62	1412	Α	1000	1 '	1 857	ANI MHMMKI SIKVLLOSALSLGRSLDADHA
	1 .	1	1	ł		PLQQFFVVMEHCLKHGLKVKKSFIGQNKSFF
		1	- 1	1.		GPLELVEKLCPEASDIATSVRNLPELKTAVGE
	1	1	- 1	[		GRAWLYLALMQKKLADYLKVLIDNKHLLSE
	•			İ		GRAWLYLALWORKLYD I LKY LIDYMIDDOL
	1	1	l	1		FYEPEALMMEEEGMVIVGLLVGLNVLDANL
	1	1		j	}	CLKGEDLDSQVGVIDFSLYLKDVQDLDGGK
	- [	1	ì			HERITDVLDQKNYVEELNRHLSCTVGDLQTI
	1	1		1	1	IDGLEKTNSKLQERVSAATDRICSLQEEQQQI
	1	ı	1			REONELIR
						SSFAKHKRIHTGEKPFICLECGKAFTSSTTLTI
63	1413	A	1083	2	615	HRRIHTGEKPYTCEECGKAFRQSAILYVHRR
}	1	1	1	}		HTGEKPYTCGECGKTFRQSANLYAHKKIHT
l	1	ı		l l		HIGERALICGECONTROSANTIANICALIA
1	1	ı	j	1	1	EKPYTCGDCGKTFRQSANLYAHKKIHTG\EK
		1	1	1	<u> </u>	YKCKECGKAFKSYYSILKHKRTHTRGMSYE
1	i	i	1	1	1	DEC/QRSLN/RSSILSNHKIIHNEEK/PLKCEKC
1		1	1		1	KAFNHTSICCRHKKN
L				1	-+	KKQDLSSSLTDDSKNAQAPLALTESHLATLA
64	1414	A	1084	946	1	SSSQSPEAIKQLLDSGLPSLLVRSLASFCFSHI
1	1	1	1	1	}	DOUGLEAUNCLEDGUL BELLE ROLLOW CLOUD
1	1	J		1	1	SSESIAQSIDISQDKLRRHHVPQQCNKMPITA
1	- 1		- 1	1	l .	LVAPILRFLTEVGNSHIMKDWLGGSEVNPLV
1	1	1		1	1	TALLELLCHSGSTSGS\HNLG\AQQDQCKISF
1	ĺ			1	1	FESWLTTGLTTOORTAIE\NATVAFF\LQCI\S
1	İ	1			1	HPNNQKLMAQVLCELFQTSPQRGNLPTSGN
1		1	1	l	1	S\GFIR\RLFLQLMLEDEK\TMFLQSPCPLYK
1	1	1	}	l	1	2/QLIKKTLIOTAL OLG CONTENT IN DIGLE
1		1	ļ	1		RINATSHVIQHP\MYGAGHKFRTLHLPVSTT
ļ		-	1	1		SDVLDRVSDTPSITAKLISKQKDDKKKK
H	1210	<del></del>	1087	103	324	PRAFEFVHTEMIVG/RVQNIHLFTLQVLEDR
65	1415	A	108/	103	327	LFTMSVGSSLWSTYLIHVMALP/DRELLKPN
	1	l			1	SVALHKLSNALV
ì	- 1	1	1			HETCSVTHIVSFSLPFLNPSHPASTPGHTENE
66	1416	A	1095	3	493	HEICSVIHIVSPSLPFLNYSHYASIFUHIENE
1 **		1.			- !	PSLVWFDRGKFYLTFEGSSRGPSPLTMGAQ
1		]	-		1	TLPVAAAFTETVNAYFKGADPSKCIVKITGI
	1	l	1	ł		MVLSFPAGITRHFANNPSPAALTFRVINFSR
1	1				ı	HVLPNPQLLCCDNTQNDANTK\EFWVNMP
1		1.	- 1		1	
ł			- 1	1		MTHLK
1	<b>I</b>	1				
67	1417	A	1098	57	356	LKLTSLGFIIGVSVVGNLLISILLVKDKTLHK
67	1417	A	1098	57	356	LKLTSLGFIIGVSVVGNLLISILLVKDKTLHR PYYFLLDLCCSDILRSAICFPFVFNSVKNGS: WTYGTLTCKVIAFLGVLSCFHTAFMLFCISV

SEQ ID	SEQ ID	Met	T SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	[	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Scrine.
1	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ł	1		Į.	residue of peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	1	1	į	sequence	1	/=possible nucleotide deletion, \=possible nucleotide insertion
ļ	<del> </del>	+	<del> </del>	sequence	<del> </del>	RYL
68	1418	A	1106	1	1326	MGKISATGINMGTKCSWALVWHLESYDPKH
				· •	1.520	YEREGMQDWKTASGQSEEATQQSSQKPQPH
			[		İ	YTTYQSSSFLKYSSESHLLAWRENSSEGSFQF
		{			ļ	PGRSRARPPRTRQQRRGAAAGPGRGAVRLG
				١.	l	HPQSAAQPQLRAAARIPESPAAFPAQPRPGSA
İ		1	1	ì		RNSDASGPASLSRTLGRASSPRPPOAPDVTAP
1		1			1	SPAALAPRAARGGSRAAALAGAEAEEPLRTL
	ì	1 '			1	APRPTRAAAPPPPPPPPPPPLPPGAPPPPVRCVSR
1		ł			1	RARAPPWR/PAATGPPP\RPVAPSRKLGSARAP
ļ	l	1			1	APALQIRKGTSSGLPGRGGGSGPGNNLSSVA
	1	Į.			Ì	GNWRGSSFAVERPGMAKYQGEVQSLKLDDD
1	ľ	1			1	SVIEGVSDQVLVAVVVSFALIATLVYALFRNV HQNIHPENQELVRVLREQLQTEQDAPAATRQ
	ļ	(			1	QFYTDMYCPICLHQASFPVETNCGHLFCGSLT
					ĺ	PNSIW
69	1419	A	1107	2	466	FDTARLHEFGTSITQIFAVDNREDLQKWMEA
		1			i	FWQHFFDLSQWKHCCEELMKIEIMSPRKPPLF
	İ	1 1		:	ļ	LTKEATSVYHDMSIDSPMKLESLTDHOKKIEE
						TNGQFLIGQREESLP/SS/CGPHSLMVTIKWSS
70	1420	A	1111	<b></b>		RKRY/SYPASEPLHDEKGKKRQAPLPPSDK
" .	1420	^	1111	698	23	ALRRLHYVRATKV\FLSFRRPFWREEHIEGGH
1	ļ		ì			SNTDRPSRMIFYPPPREGALLLASYTWSDAAA
j						AFAGLSREEALRLALDDVAALHGPVVRQLW DGTGVVKRWAEDQHSQGGFVVQPPALWQT
			Ì			EKDDWTVPYGRIYFAGEHTAYPHGWVETAV
						KSALRAAIKINSRKGPASDTASPEGHASDMEG
					,	QGHVHGVASSPSHDLAKEEGSHPPVQGQLSL
71	1101					QNTTHTRTSH
71	1421	A	1119	2	385	QKQTLQNGYLDSSMDILYLGSLPPELQVSSDE
1 1		1				PPGPPEQAGLSQFHLEPETQNPETTEEIQSS/LQ
			1	- 1		QEAAAQLPQLPEVVELSSTKA\EAPALPSQSL
72	1422	Ā	1127	1	906	EGVHSSTEQKAPAQQLPAFEEILAPLLIHHE
1		-		•	300	HAQYVGPYRLEKTLGKGQTGLVKLGVHCTT
l 1			- 1		j	GQKVAIKIVNREKLSESVLMKVEREIAILIRLI EHPHVLKLHGVYENKKYFPPDELTSGPSMLA
			ì	i i		QVSPHGKLSARRSWDLLSGFPRYLVLEHVSG
, ,		ì	l			GELFDYLVKKGRLTPKEARKFFRQIVSALDFC
]			1	1	j	HSYSICHRDLKPENLLLDEKNNIRIADFGMAS
	1	ĺ	1	ĺ	1	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR
			i	İ		RADMWSCGVILFALLVGALPFDDDNLROLLE
1	i	1	1	!	j	KVKRGVFHMPHFIPPDCOSLLRGMIEVEPEKR
73	1423	A	1128	1	802	LSLEQIQKHPWYLGGNFIS
	.	-	-120	•	602	LRNALDVLHREVPRVLVNLVDFLNPTIMRQV
	j	- 1	}		ŀ	FLGNPDKCPVQQA/MLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG
[ [	]	1	1		1	SDFLCTEWKASNSVPTSVHQLRPADIKVVAA
] ]	1	- 1			ľ	LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG
	]	1	[		1	GDGNLETHITLPNILKKFNPYLLGFSTSTWEG
	1				í	TAGLNVAAEGARARDMPAQAWDLVERMKN
					Į	SPDINLEKDWKLVTLFIGGNDLCHYCENPEA
174	1404					HLATEYVQHIQQALDILSE
74	1424	A .	1139	60	480	FREPCLLVPGDHOPLREASWLA/LPPIGLWGT
	- 1		}	1	ļ	DSPLCCVEVAIPCNKGAHSVGLKGWLLAOG
	ļ		ļ	,	ļ	VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE
						EQPAADAAVAKGEF/QGEQIAPVPA\IIAAHPE
75	1425	A	1147 2	2	413	AADPAPVHTTAHPKGA
	-	-	'   '	-	743	PFPHQHPQEP\KGSCWPQSALRGQCPGPVLGV TTTSDLCSLQVPVSSHRNPLLDLAAYDQEGR
						1.10DLCOLQ VI VOORKIYLLDLAAYDQEGR

						Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-Aspartic Acid, E-Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	nuclcotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	į	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	to last amino	M=Memonine, N=Asparagne, 1-1 totale,
ience	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ICIICC		1	)	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l	}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	•	I	peptide		/=possible nucleotide deletion, \-possible
	1	i	i			nucleotide insertion
	<u> </u>		<u> </u>	sequence		RFDNFSSLSIQWESTRPVLASIEPELPMQLVSQ
	1	ĺ	i	!		DDESGQKKLHGLQAILVHEASGTTAITATAT
	j	1		1	1	DUESCONTE DE A D
	Į.	l	1			GYQESHLSSAR
76	1426	A	1155	38	410	PIISAPAQDDPILLSFIHCLHANLLCVWRRDVK
, •	1		1	l		PDCKEIWIFWWGDEPNLV\VQYIMNCMLWK
	1	1	1	1	ļ	KDSGKMAFPMNVGRC/FFKEIHNLLERCLMD
	İ	1	1		ļ	KNFVLIGKWFVRPYYKDEKPVNKSEHLSCAF
	1	1	1			l τ
		<u> </u>	1	1.00	350	RFPQGLEDVSTYPVLIEELLSRGWSEEELQGV
77	1427	A	1162	526	330	LRGNLLRVFRQVEKVQEENKWQSPLED
		1	1	<u> </u>		MAESASPPSSSAAAPAAEPGVTTEQPGPRSPP
78	1428	A	1171	1	1293	MACOAOTTOOOAAATAACTU TITOTOTOOT
	1	{			1	SSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQT
	I	1	1	1	1	TSPRNWCIKMVCNPWFECVSMLVILLNCVTL
	ļ	1	}	j		GMYQPCDDMDCLSDRCKILQVFDDFIFIFA
	į	i		1		MEMVLKMVALGIFGKKCYLGDTWNRLDFFI
	ĺ	1	1	1		VMAGMVEYSLDLONINLSAIRTVRVLRPLKA
	ļ	1	1	İ		INRVPSMRILVNLLLDTLPMLGNVLLLCFFVF
-		Į.	1	1		FIFGIIGVQLWAGLLRNRCFLEENFTIQGDVAL
	1		-		<u> </u>	PPAYYQPEEDDEMPFICSLSGDNGIMGCHEIPP
	1	1	1	ł	ì	LKEQGRECCLSKDDVYDFGAERQDLNASGL
	1	1	}	ì		CVNWNRYYNVCRTGSANPHKGAINFDNIGY
	ļ		1	1		CVNWNRYYNVCRIGSANPIRGAINFDINGT
		}	1			AWIVIFQVITLEGWVEIMYYVMDAHSFYNFI
	ĺ		ì	1		YFILLIIVSVREPGLLGGSFSTAQSPKCQGDSFF
		1				GVAAESLLLRGWVLWLPGGG
<del></del>	1420	A	1175	+1	405	PNDFFKDMFPDLPGGPLGPIKAENDYGAYLN
79	1429	\ ^	11/3	1 '	1 705	FISATHLGGLFPPWPLVEERKLKPKASQQCPI
	1		1			CHKVIMGAGKLPRHMRTHTGEKPYMCTICE
		ì	- 1	1	i	VRFTRQDKLKIHMRKHTGERPYLCIHCNAKF
•		}		1	ŀ	VHNYDLKNHMR
	l	ì				EMNELSQQLSQQGGRGASQCPSPPAPTLPNPT
80	1430	A	1182	25	198	EWNET SAGARGAS COLUMN 1711
••	1	1	- [	(		PLCQLQLQRVNTGLPTPPCHPGAGAA
81	1431	A	1186	254	583	KTVLDVGAGTGILSIFCAQAGARRVYAVEAS
0.1	1431	1 ''	1	1		AIWQQAREVVRFNGLEDRVHVLPGPVETVEL
	- 1	1	1	j .		PEOVDAIVSEWMGYGLLHESMLSSVLHARTE
	1	ŀ	ł			VVKDGGFFLPXSSELFM
			1,,,,	<del> </del>	716	DFVDAARNLPLESTKSPAEPSKSVPSLE\DPRA
82	1432	Α	1187	2	716	SSQGLPSQGPVQNQGRRGEQRPKKF/TVIQHT
	1	-				SSFEKSDSLEQPSGLEGEDKPLAQFPSPPPAPF
	1	1		Į.		SSEEKSDSLEGEOUTEGEDATEAGETSTITALL
		1	1	(	[	GRSAHSLQPKLVRQPNIQVPEILVTEEPDRPD
	l			i	1	TEPEPPPKEPEKTEEFQWPQGSQTLAQFPVEK
l		ļ		}		I DPKKKRI GLAKMAOSSGESSFESSVPLFRSI
1	ſ.		1	ţ	\	SQESNVSLSGSSRSALFERDDHGKAEAPSPSF
l	1		İ	1		DMGPKPLGTHMLTV
						ESPGLSKVLRTGAFAYPFLFDNLPLFYRLGLO
83	1433	A	1188	517	804	WGRGHGCGQEALSTSHGYHLFCALLTGFLF.
1	1	-		{	1	WUKUHUCUQEALSI SITU I IELICALI OTTI
Į.		1				SHLPERLAPGRFDYIGHSHQLFHICAVLGTHE
1	}	ŀ	1	}		Q
101	1434	A	1192	45	476	LGDVGFWVERTPVHEAAQRGESLQLQQLIE
84	1434	A	1172	1 75		GACVNOVTVDSITPLHAASLOGQARCVQLL
1	1			1		AAGAOVDARNIDGSTPLCECLRLGQHRVCE
1	1	- {	1	- 1	1	LAVLRGQGQPSPVHSVPPARGLHXREFRMC
1	1	Ĭ	1	1		PUATROZOZI DI LITTO I IL LICODIA ILI
1		-	1	1		GFLFDVGXNLEAHEFHFGEP
85	1435	A	1194	69	410	KRSEEASAPPFPLGGTGAAPTRASLPEQILLP
1 55	1 1 1 1 1 1	**	1 '	- [		SCLEARKSQPDEKLLSALHNSRTWN*EPRRS
1	J			1		HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT
	1	1		1	}	GRSPCPSLPGTTRTNSLL
i		1	1		<del></del> _	LPSHTCGNPGRLPNGIQQGSTFNLGDKVRYS
<u></u>		-+-				
86	1436	A	1215	3	405	NI GEFLEGHAVI TCHAGSENSATWDFPLPSO
86	1436	A	1215	3	405	NLGFFLEGHAVLTCHAGSENSATWDFPLPSO RADDACGGTLRG/AEWHHLQPPLPLG/ATKI

SEQID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	2.00	in in	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine
eotide	seq-	İ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		ł	914	ng to first	acid residue	Q=Ghutamine, R=Arginine, S=Serine,
		ł		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	l	j .	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
1	ŀ					NADCTWTILAELGDTIALVFIDFQLEDGYDFL
\- <del></del>	 	i	<u></u>			EVTGTEGSSLW
87	1437	A	1216	226	964	GTARFGPMVGFGANRRAGRLPSLVLGVLLV
1	ĺ	ľ	i		İ	VIVVLAFNYWSISSRHVLLQEEVAELQGQVQ
ĺ						RTEVARGRLEKRNSDLFAVVGHAQETDRPEG
			į i			GRLRPPQQPAAGQRGPREEM\EDDKVKLQNN
1		ł				ISYQMADIHHLKEQLAELRQEFLRQEDQLQD
						YRKNNTYLVKRLEYESFQCGQQMKELRAQH
		[ ]				EENIKKLADQFLEEQKQETQKIQSNDGKELDI NNQVVPKNIPKVAENVADKNEEPSSNHIPHG
88	1438	A	1218	1	534	PEFGTTISCGYLMATDVSRRPSVHKAVEIEOE
				•	334	RVKSAGAWIIHPYSDFRFYWDLIMLLLMVGN
1		ŀ				LIVLPVGITFFKEENSP\PWIVFNVLSDTFFLLD
						LVLNFRTGIVVEEGAEILLAPRAIRTRYLRTW
1					-	FLVDLISSIPVDYIFLVVELEPRLDAEVYKTAR
						ALRIVRFTKILSLLRL
89	1439	A	1223	1	743	MGFDEVFMINLRRRQDRRERMLRALQAQEIE
						CRLVEAVDGKVGMLTRSNAAPGRHLAMLET
1 1						LVVVAPRFVDADNLILNPDTLSLLIAENKTVV
1						APMLDSRAAYSNFWCGMTSQGYYKRTPAYI
						PIRKRDRRGCFAVPMVHSTFLIDLRKAASRNL
] ]						\AFYPPHPDYTWSFDDIIVFAFSCKQ\AEVQMY
[						VCNKEEYGFLPVPLRAHSTLQDEAESFMHVQ
90	1440	A	1227	2	349	LEVMVPSSPSSAQSMAVVSADHIGLVISYL
1 1	1110	^	1221	-	349	NKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGF
				ļ		GPWDFKFILCRYTSVLFYANMDTSIVVLGLIT/ YDRY/WKVVRHL/WDSWMTGI/SFTRVYLLG
1			ļ	ì		LGARLVWFGKLILAKGGHGGISWL
91	1441	A	1245	3	1937	LGSSDVRAPQRSELGAESPSRMVASQAYNLT
	i					SALTPILTRSRVLNEEPLTLAGF\SRAPANLSD
1	-	ŀ	İ			VVQLIFLVDSNPFPFGYISNYTVSTKVASMAF
			İ			QTQAGAQIPIERLASERAITVKVPNNSDWAAR
		i				GHRSSANSV\VQPQAFVGAVVTLDSSNPAAV
		}	1			LHLQLNYTLLDGRYLSEEPEPYLAVYLHSEPR
		}	ĺ			PNEHNCSASRRIRPESLQGADHRPYTFFISPGT
	1	İ				RDPVGSYRLNLSSHFRWSALEVSVGLYTSLC
	ĺ	ĺ	- 1		ľ	QYFSEEDVVWRTEGLLPLEETSPRQAVCLTR
						HLTAFGTSLFVPPSHIRFVFPEPTADVNYIVML
	ľ	}	}		ļ	TCAVCLVTYMVMAAILHKLDQLDASRGRAIP
	l	- 1				FCGQRGRFKYEILVKTGWGRGSGTTAHVGIM LYGVDSRSGHRHLDGDRAFHRNSLDIFQIATP
	i	- 1	ì		1	HSLGSMWKIRVWHDNKGLSPAWFLQHIIVRD
	1	- 1	1		Į	LQTARSTFFLVNDWLSVETEANGGLVEKEVL
	ļ			1	ļ	AASKASFRVPTPS\AALLRFRRLLVAELQRGF
						FDKHIWLSIWDRPPRSCFTRIQRATCCVLLICL
	1	- 1	j		ļ	FLGANAVWYGAVGDSAYSTGRVSRLNPLSV
,	İ	1	1	-	1	DTVAVGLVSSVVVYPVYLAILFLFRMSRSKV
	l	ļ	į	Ì	.	GWGWGPGSTGNGAWASAPCPEPPLSSAAAR
<del></del>	1442	<del>  </del>	-10/6		-22	GKGVHQRLLGKGQHT
92	1442	Α	1246	5	562	VFDEENILNELNDPLREEIVNFNCRKLVATMP
	1	ļ	l	1	ļ	LFANADPNFVTAMLSKLRFEVFQPGDYIREG
1	ł	ł	- 1		ł	AVGKKMYFIQHGVAGVITKSSKEMKLTDGS
l		-			l	YFGEICLLTKGRRTASVRADTYCRLYSLSVD
	1	- 1	j		ļ	NFNEVLEEYPMMRRAFETVAIDRLDRIGKKN
93	1443	A	1249	180	901	SILLQKFQKDLNTGVFNNQENEILKQIVKH
		^	.2-73	100	201	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGPK ASCSTAGSGSPGLERINGSPAGGSALDERL
1	1		- 1		i	PGRKASCSTAGSGSRGLPP\SSPMVSSAHNPN KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT
		ĺ				ERPGAERPSLLPNGKENSSGTPRVPPASPSSHS
						THE COURT OF THE PROPERTY OF THE PARTY OF TH

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide	)	in	nucleotide	location	F=Phenylalanine, G=Grycine, n=Firstanine, I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	Ì	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	[	[	914 .	ng to first		T=Threonine, V=Valine, W=Tryptophan,
		Ì	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	j	1	j	residue of	sequence	/=possible nucleotide deletion, \=possible
	'			peptide	ĺ	nucleotide insertion
	<u> </u>	<u> </u>	<u> </u>	sequence		LAPPSGERSRLARGSTIRSTFHGGQVRDRRAG
	l	1			1	GGGGGGVQNGPPASPTLAHEAAPLPAGRPRP
	}	1	1	ì	ļ	TTNLFTKLTSKLTRRVADEPERIGGPEVTRRP
	Į.	İ			1	RQEDHLSPGGRGCSEL
		ļ	1061	<u> </u>	385	KFSQWGLTKPKLSNASP/WISLVKKLMKKWS
94	1444	A	1261	3	303	VTQNLTFREQLEAGIRYFDLRVSSKPGDADQ
		l .	1		Ì	EIYFIHGLFGIKVWDGLMEIDSFLTQHPQEIIFL
	1	1	]	1	l	DFNHFYAMDETHHKCLVLRIQEAFGNKLCPA
	1		1		ļ	CR
	L	<del></del>	1000	<u> </u>	550	GPRDNPG\EDPRFEIVEHFGIAWFTFELVARFA
95	1445	A	1282	2	330	VAPDFLKFFKNALNLIDLMSIVPFYITLVVNL
	1		l	1	1	VVESTPTLANLGRVAQVLRLMRIFRILKLARH
			1	1	1	STGLRSLGATLKYSYKEVGLLLLYLSVGISIFS
	1	1		Į.	1	VVAYTIEKEEN\EGLATIPACWWWATVSMTT
	1	1		1		VGYGDVVPGTTAGKLTASACILA
	1	+	1294	<del>                                     </del>	1456	OLLPPSNRENAGLLVGRCLCSAALRPVGDLIT
96	1446	A	1294	1.	1450	SSGOVAVRNAPOAGSAKAGKGKFQDNFEFIQ
1		1	1	1	]	YFKKFFDANCNEKDYNPVAAGQGQETEVAP
ĺ	1		[	1		SIVAPVLNKPNQCPEGYICVKAGRNPNYGYT
	1	1	1			SEDITESWAFLSLFRLMTODYWENLYQLTLRA
	}		ļ			AETTYMIF/LV/LVILLGSLYLVTLILAV/VAMA
		1	1			YEEONOATLEEAEOKEAEFQQMLEQLKKQQ
		1		i		EAAOOAATATASEHSREPSAAGRLSDSSSEAS
	ł	ł	1	ļ	İ	KLSSKSAKERRNRRKKRKQKEQSGGEEKDED
		}	1	1	1	EFOKSESEDSIRRKGFRFSIEGNRLTYEKRYSS
	1	}	ľ	j	)	PHOSLLSIRGSLFSPRRNSRTSLFSFRGRAKDV
	1	1		1	1	GSENDFADDEHSTFEDNESRRDSLFVPRRHGE
	1	ĺ			1	RRNSNLSOTSRSSRMLAVFPANGKMHSTVDC
	1	1	ł	1	1	NGVVSLVGGPSVPTSPVGQLLPEVIIDKPATD
	J	1	Ì	1		DNGTTTETEMRKRRSSSFHVSMDFLEDPSQR
1		1		}		QRAMSIASILTNTVE
97	1447	A	1295	2	2057	IQTQLPTKSSQQLRKGGNCVRCKMQMNFIAE
	1	1				EVLLKYRITFYNNNKGPNMLYIEIKAFVHFMI
			-	ì		NRYLSYGSGPKRFPLVDVLQYALEFASSKPV
	Ì	1	1	1	1	CTSPVDDIDASSPPSGSIPSQTLPSTTEQQGALS
	1	1			1	SELPSTSPSSVAAISSRSVIHKPFTQSRIPPDLP
		1	l	1	1	MHPAPRHITEEELSVLESCLHRWRTEIENDTR
	1 .	1	Ì	ļ	İ	DLQESISRIHRTIELMYSDKSMIQVPYRLHAV
	1	1			ł	LVHEGQANAGHYWAYIFDHRESRWMKYNDI
	1	1		ļ	1	AVTKSSWEELVRDSFGGYRNASAYCLMYIN
			1	1	1	DKAQFLIQE\DLIKTGQPLVGIETLPPDLRDFV
		1	1	1	1	EEDNORFEKELEEWDAQLAQKALQEKLLAS
		}	}	1	1	QKLRESETSVTTAQAAGDPKYLEQPSRSDFSK
}		1	-	1	1	HLKEETIQIITKASHEHEDKSPETVLQSAIKLE
{		- 1	- 1			YARLVKLAQEDTPPETDYRLHHVVVYFIQNQ
		1		1	1	APKKIIEKTLLEQFGDRNLSFDERCHNIMKVA
1	ļ	1		}		QAKLEMIKPEEVNLEEYEEWHQDYRKFRETT
1	1	1	1	1		MYLIIGLENFQRESYIDSLLFLICAYQNNKELL
1	-	1	1			SKGLYRGHDEELISHYRRECLLKLNEQAAELI
		1.				ESGEDREVNNGLIMNEFIVPFLPLLLVDEMER
	ĺ		1	1		KDILAVEDMRNRWCSYLGQEMEPHLQEKLT DFLPKLLDCSMEIKSFHEPPKLPSYSTHELCER
		}				TO THE REPORT OF THE PROPERTY
				ļ		
						FARIMLSLSRTPADGR
98	1448	A	1304	118	453	FARIMLSLSRTPADGR SGPSSRATYLHRKEYSONLTSEPTLLOHRVEH
98	1448	A	1304	118	453	FARIMLSLSRTPADGR SGPSSRAIYLHRKEYSQNLTSEPTLLQHRVEH LMTCKOGSORVOGPEDALOKLFEMDAHGRV
98	1448	A	1304	118	453	FARIMLSLSRTPADGR SGPSSRAIYLHRKEYSQNLTSEPTLLQHRVEH LMTCKQGSQRVQGPEDALQKLFEMDAHGRV WSQDLILQVRDGWLQLLDIETKEELDSYRLD
98	1448	A	1304	118	453	FARIMLSLSRTPADGR SGPSSRAIYLHRKEYSQNLTSEPTLLQHRVEH LMTCKQGSQRVQGPEDALQKLFEMDAHGRV WSQDLILQVRDGWLQLLDIETKEELDSYRLD SIOAMNVALNTCSYNSILS
98	1448	A	1304	118	453	FARIMLSLSRTPADGR SGPSSRAIYLHRKEYSQNLTSEPTLLQHRVEH LMTCKQGSQRVQGPEDALQKLFEMDAHGRV WSQDLILQVRDGWLQLLDIETKEELDSYRLD

[SEO]	D   SEQ I	DTM	t SEQ	Predicted	15000	
NO: of					Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptid		in	nucleotide	location	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine,
eotide	seq-	- [	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	- 1	09/496		to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		٠, ]	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	Ī	- {		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan
Ì		ı	1.	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon
	1	1	1.	peptide	1	/=possible nucleotide deletion. \=possible
<u> </u>			<del></del>	sequence	<u> </u>	nucleotide insertion
	1	1	1	1		DSRLLLFDAPDLRLSPPSGALLQVLDLRDPQF
ĺ	ĺ	- İ	ĺ	1	ĺ	SATPVLASDVIHAOSRDLPRIFRVTTSOLAVPP
1	}	}	- 1	1		TTCTVLLLAESEGERERWLQVLGELQRLLLD
		ł		ļ	·	ARPRPRPVYTLKEAYDNGLPLLPHTLCAAILD
ł			1	ı	j	QDRLALGTEEGLFVIHLRSNDIFQVGECRRVQ
				1		QLTLSPSAGLLVVLCGRGPSVRLFALAELENI EVEVPKIPESRGCQVLAAGSILQARTPVLCVA
						VKRQVLCYQLGPGPGPWQRRIRELQAPATVQ
	1	1	1	į	j	SLGLLGDRLCVGAAGGFALYPLLNEAAPLAL
		-				GAGLVPEELPPSRGGLGEALGAVELSLSEFLL
		- 1	ł	1	1	LFTTAGIYVDGAGRKSRGHELLWPAAPMGW
İ	Į.					GYAAPYLTVFSENSIDVFDVRRAEWVOTVPI.
1	1		İ	1		KK\VRPLNPEGSLFLYGTEKVRLTYLRNOLAE
}	}	- 1	-		1	KDEFDIPDLTDNSRRQLFRTKSKRRFFFRVSE
		ł				EQQKQQRREMLKDPFVRSKLISPPTNFNHLV
100	1450	A	1318	918	190	HVGPANGRPGARDKSP
		1	1	1	190	SLCVPGPVDTGTFAVMSVMVGSVTESLAPQA LNDSMINETARDAARVQVASTLSVLVGLFQV
		1	-	{	ĺ	GLGLIHFGFVVTYLSEPLVRGYTTAAAVQVF
		1		1		VSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKL
				·		PQSKVGTVVTAAVAGVVLVVVKLLNDKLQQ
		1				QLPMPIPGELLTLIGATGISYGMGLKHRFEAG\
		ļ	j			PPVAPNTQLFSKLVGSAFTIAVVGFAIAISI GK
101	1451	- A	1353	220	7.5	IFALRHGYRVDSNQVWVMRDV
1	1	^^	1333	220	445	DWPDLFTYPLIGSPKCFQSARPE\RMYRRTVR
[	1	ļ	ļ	]		SSHGNHALQEVLPRSGHGTEFTKQKHLEAAD HGHPPARMSIFSR
102	1452	A	1363	542	2	AHLLMLNLAL\TDLL\YLTSLPFLIHYYASGEN
		1			_	WIFODFMCKFIRFSFHFNLYSSILFLTCFSIFRY
						CVIIHPMSCFSIHKTRCAVVACAVVWIISLVA
1	1	i i	1			VIPMTFLITSTNRTNRSACLDLTSSDELNTIKW
	1	1				YNLILTA\LLCLPLVIVTLCYTTIIHTLTHGHAN
103	1453	A	1371	2	410	WSCLKQKARRLTILLL
100	1433	1^	13/1	2	410	CHSTESSSDFILPGDYLLGGLCPLHSGCLQV\C
1						SFNEHGYHLFQAMRLAVEEINNSTALLPNITL
1				!		GYQLYDVCSDSANVYATLRVLSLPGQHHIEL
	L	1	1		1	QGDLLHYSPTVLAVIGPDSTNRAATTAALLSP FLVPMLLEO
104	1454	A	1376	3	432	NSRVEDRS/NMSLWTQNITVCPVRNVTRDGG
	1	Í.				FGPWSPWQPCEHLDGDNSGSCLCRARSCDSP
ł	ļ	1		J	}	RPRCGGLDCLGPAIHIANCSRNGAWTPWSSW
		1			- 1	ALCSTSCGIGFQVRQRSCSNPAPRHGGRICVG
105	1455	A	1379		206	KSREERFCNENTPCPVPIF
1	1700	^	13/9	2	396	GLGLLYLIFAAVEGVMRVIGGSNHLAVVLDD
	1		1 1	İ		IILAVIDSIFVWFIFISLAQTMKTLRLRKNTVKF
l		1	1	ļ	j	SLYRHFKNTLIFAVLASIVFMGWTTKTFRIAK
				1	ŀ	CQSDWMERWVDDAFWSFLF\SLILIVIMFLW RPSA
106	1456	A	1383	1 +		EDGHGGWSSRCLVDHAEEGHREPWKRLCIW
	i	1	1		l l	QRGGHEIRFAFYFPGHPLLSPQICLAPETPPRG
		1	i i	ì	ŀ	CPPVSSLHFISLQ/RLPRDCQELFQVGERQSGL
	i	1	1 1	- 1	ļ	FEIQPQGSPPFLVNCKMTSGTFWTCRTDSRVF
102	1177	<del> </del>				QNANPSNAAHSEDQPTP
107	1457	A	1386	719	558	FFFVTRSHSVAQAECSGVFTAHRSLDLVGSSN
108	1458	A	1207	(2)		YPALSLQSSWDHRHTWLIFAFL
	1770	^	1397	631	2	RVAISLLCAAIFISFMVQSAGKRWPTGVMLM
		1		1	1	VVVLFAFLYSWPIQALLPTYLKTDLAYNPHT
		}	] [		-	VANVLSFSGFGAAVGCCV/GGFLGDWLGTRK
		ــــــــــــــــــــــــــــــــــــــ	<del> !</del>			AYVCSLLASQLLIIPVFAIGGANVWVLGLLLF

250 VD T	OFO IN	Mot	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=A enartic Acid E=Glutamic Acid.
	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-		1	USSN	location	corresponding	1=Isoleucine K=Lvsine, L=Leucine,
eotide	seq-	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	l	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threanine V=Valine W=Tryptophan
		ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ		(			Scquence	/=possible nucleotide deletion, \=possible
		1		peptide		nucleotide insertion
	L			sequence		FQQMLGQGIAGILPKLIGGYFDTDQRAAGLG
		ì	1			FTYNVGALGGALAPIIGALIAQRLDLGTALAS
į		ł	1	1		LSFSLTFVVILRNRRPGKSLVR
	l	İ	1	Ĺ		VLVALPDT\VTSETVVTEVLGHRVTLPCLYSS
109	1459	A	1402	15	387	WSHNSNSMCWGKDQCPYSGCKEALIRTDGM
	İ	İ	1			RVTSRKSAKYRLQGTIPRGDVSLTILNPSESDS
	ļ	ł	1	ì	1	RVISRKSAK I REQUIERODVSETIEM SESSE
	ì	1	1			GVYCCRIEVPGWFNDVKINVRLNLQRASTT
110	1460	A	1421	3	350	HEDLSSLLTRGSGNQERERQLKKLISLRDWM
				ł.	1	LAELAFPVGVLATCA*SLLSC*YCVILFPCSCF
		1	1		ļ.	FFHSPDALFSLLLLSCYFPSYCFFYYLFFSSSPL
	1	1		L		CLLLASSPFPLFILLASL
111	1461	1A	1426	2	344	FTSTMTKPFEKESEQPA*ATLAFGAQTSTTAD
111	1	1	1			QCALKPDLSYLNNSSSSSSTPATSAGGGIFGSS
	1	]	ŀ		1 .	TSSSNPPVATFVFGQSSDPVSSYGFVNTAESST
		1	ł			SDSLLFSQDSKLATTS
112	1462	A	1434	46	372	TTSWTTSCTRSCT*SGASSGPGWTPRTTWWR
112	1402	1	]	1		SRRSSORTCSRACSGAWSRTW*RSS*TSSSSC
1	1			ļ		STSCSSSSSRSCGRPGGPLGARGVHITSCLNSC
	}	1	1	j	1 .	MSSSTTSSTTSTF
110	1462	A	1439	3	292	HEDIMTHYDRLVDE*ALNAGKQRYEKMISG
113	1463	1^	1433	1		MYLGEIVRNILIDFTKKGFLLRGQISEMLKTR
1	1	}			1	GIFLTFLLSNFLIVCVLLFYVSFYLFQSCINFVL
	1	<del>                                     </del>	1462	1	396	KQQAVPEPHSSTTTPQEQEQNWYGQDLLNLQ
114	1464	A	1463	1 1	370	<b>ORTKVHLPGHKTGPAVAKDTPEPVKKEFTVP</b>
		1	*		Ì	ATSQGP*SPFSEEPPLPPSNEEVPPTLPP*EPQS
	1	}	)	1	}	EDP*KNA*LKQMHAATTHWQQHQQHQVGC
		1	ł		i	OYHGIMQ
			<del> </del>	1001	+	AGSYPSMVWSCHWGVTQKRRAL*VYSFEEG
115	1465	A	1464	291	1 2	GRRKCGQYWPLEKDSRIRFGFLTVSNLGVEN
ı		1	1		1	MNHYKKSTLEILNPEVNPGFFFLTLWKQGEN
	1	j	ļ			NYCN
	<u> </u>				200	LPPORPA*TDSYSTCNVSSGFLAGQSHNIHLQ
116	1466	A	1465	667	337	YWTKYQVWBWLQHFLDTNQLDANCIPFQEF
l	1		i	1		DINGEHLCSMSLQEFTRAAGTAGQLLYSNLQ
ĺ	1	1	1			HLKWNGDSLFLCLSLPC
1 .						GTSGGPKRVLVTERFPWQNPLPVNRGQAQR
117	1467	A	1479	1	381	VLGPSNSFQRVPLQAQKLVSSHKPGQNQKHK
1	1		1	1		OLQATSVPHPVCMPLNNTQKSKQPLPSAPEN
			-			QLQATSVPHPVCMPLNNTQKSKQPLPSAPEN
1			- [			NPEEELASDPNNEESL*RPWALEDFEIGRPLG
	1 .		1	_		KGK
118	1468	A	1485	3	385	TYLWL*GNPPFYEKNDGGLFELILRAKDEFNS
1	1 - 1 - 2	1 ""		ł		PYWDDMSDSAKHFIRPLTGRDP*KPFPCDQPL
l	1		1			QHPWIEGHTCLDNNIHQAASEPINNNFAESKR
1	1		1	ļ	İ	NLAFLATGVVRHMRKLFMGANLEGPGPTVS
ł	ì			Ì	1	Н
119	1469	+	1486	1	398	GTTSKHH*LARSLIRGPFDHDLKPNAATRDQL
113	1407	^	1,400	1	1	NIIVSYPPTKOLTYEEODLGWKFRYYLTNQE
1		1	1	1	1	KALTKFLKWVNWDLPQEAKQALELLGKWK
1	1	1	1	1		PMDVKDSLELLSSHYTNPTVRRYAVARLRQA
1		1	1	į.		DDEDLLMYL
<u></u>	<del></del>		1400	<del> </del> -	999	MGESPAV*GYFVLAGMNSAGLSFGGGAGKY
120	1470	Α	1497	3	1 333	LAEWMVHGYPSENVWELDLKRFGALQSSRT
	3	1		1	1	FLRHRVMEVMPLMYDLKVPHWDFQTGRQL
1	1	i	1	1		RTSPLYDRLDAQGARWMEKHGFERPKYFVP
		i				I WINE T I DEPONDOUNCE ASSESSMENT OF TAKE 19 1 1 4 1
			1			DONDLI VI EUGALEANDUMEDIMEGEANACCA
						PDKDLLALEOSKTFYKPDWFDIVESEVKCCK
						PDKDLLALEQSKTFYKPDWFDIVESEVKCCK FAVCVIDMSSFTEFEITSTGDQALEVLQYLFS
						PDKDLLALEQSKTFYKPDWFDIVESEVKCCK EAVCVIDMSSFTEFEITSTGDQALEVLQYLFS NDLDVPVGHIVHTGMLNEGGGYENDCSIARI
						PDKDLLALEQSKTFYKPDWFDIVESEVKCCK FAVCVIDMSSFTEFEITSTGDQALEVLQYLFS

	SEQ ID	SEQ II	Met	SEQ	Predicted	1 10 11 11 11	
	NO: of	NO: of		ID NO:	beginning	Predicted end nucleotide	
	nucl-	peptide		in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid,
	eotide	seq-	1	USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	uence		09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
	uence	ļ		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	1	peptide	1	/=possible nucleotide deletion, \=possible
					sequence		nucleotide insertion
		1	1	1	1		MTPDHFPSLFCKEMSVGVANGRVMSMTHT
	101	145:	4		1	<u>                                     </u>	GEPGFMLYIPIEYRWGFTMLSTLVSNS
	121	1471	Ā	1498	3	306	AQFLLVGWDHIL*LIVL*TNLTELGRTTCDON
				j	1		WPNSPDVLNHGCFYMOCLSKDCTIGYVSRE
		l	[	1	1		MLVAHTHTVEEHTGTHLQYVSWPDHSVPDD
i	122	1472	A	1533	121		SSDFVEFEN
- 1		11/2	10	1333	121	329	LGLFSFVWTEVLEEPKDFSCETEDFKTLHCT
		1	1			1	WDPGTDTALGWSKQPSQSYTLFES*VGSGYII
- 1	123	1473	A	1547	111	408	DNFFLA
- 1			1	1.517	***	400	DARTTWKPRNGSSGIWPGDGAK*PPAVEQAE
1		]		1	ĺ	i	RGHVEMIEKLTFLNLHTSEKDKGGNTALHLA
L		L	]	1	-		AKHGHSPAVQVLLAQWQDINEMNEKQQTPL IIVAADRG
1	124	1474	A	1555	1	745	MTFDDDDKNTYGVALVWKKFQTQSLRLSDL
-						1	HRKSHLWRGIVSITLIEGRDLKAMDSNGLSDP
-							YVKFRLGHQKYKSKIMPKTLNPQWREQFDF
-			1	1	·		HLYEERGGVIDITAWDKDAGKRDDFIGRCQV
1	1		ĺ	1			DLSALSREQTHKLELQLEEGEGHLVLLVTLT
- [							ASATVSISDLSVNSLEDOKEREEILKRYSPI RI
			1				FHNLKDVGFLOVKVIRAEGLMAADVTGKSD
		!		l i	i	•	PECVVELNNDRLLTHTVYKNLNPEWNKVETI
1			l				*VALVWKKFOTOSLRLSDLHRKSHI.WRGIVS
	ļ						ITLIEGRDLKAMDSNGLSDPYVKFRLGHOKV
			1				KSKIMPKTLNPQWREQFDFHLYEERGGVIDIT
1			1		ļ		AWDKDAGKRDDFIGRCQVDLSALSREQTHK
1					!		LELQLEEGEGHLVLLVTLTASATVSISDLSVN
	ľ				1		SLEDQKEREEILKRYSPLRIFHNLKDVGFLQV KVIRAEGLMAADVTGKSDPFCVVELNNDRLL
L							THTVYKNLNPEWNKVFTL
	125	1475	Α	1556	57	509	GGPAPNSRYAEP*KNSLAMT*AHADCENYVA
1	1			İ	1	[	CGGLDNICSIYNLKTREGNVRVSRELPGHTGY
1	- 1		1 1	ļ	!		LSCCRFLDDSQIVTSSGDTTCALWDIETAQQT
1				į.		•	TTFTGHSGDVMSLSLSPDMRTFVSGACDASS
H	126	1476	A	1592			KLWDIRDGMCROSFTGHVSDINAVS
		1470	Λ	1392	3	178	KSEKSCVSSLAHFGTSCQRDYDAMVKLVETL
	127	1477	Α	1612	1	100	EMLPTCDLADQHNIKFHYAFALNR*ER
			1	1012	•	497	TESPLLVRPYLPYITKSELHAIMTAGFSTIAGS
1	}		.	l	1	1	VLGAYISFGVPSSHLLTASVMSAPASLAAAKL
		ı	- 1	i		. 1	FWPETEKPKITLKNAMKMESGDSGNLL*AAT
			[	- 1	1	İ	QGASSSISLVANIAVNLIAFLALLSFMNSALA WVGNMFDYPQLSFELICSYIFMPFSFMMGVE
L				İ	ĺ	}	WPDSFM
1	28	1478	A	1619	286	486	CCMNSKAQESVFKNVLCNPPALSEMPDVKA
ı			- 1		l	ı	EDEVDFRASSISEEVAVGSIAATLKMKQGPM
1						_	TOAINR
'	29	1479	A	1627	1	395	PTRGALRYWIFGRFLCNIWAAVDVRCCTATI
	1		- 1	- 1	ĺ	- 1	MGLCIISIDRYVGVSYPLRYPTIVTORRGLMA
		1	1	ŀ	1	ſ	LLCVWALSLVIYIGPLLGWRHPAPEDETICOL
1		1	ł	1	1	1	NEEPGYVLFSTPGSFYLPLAIMLVMN*RVYRV
1	30	1480	Ā	1638			AKTE
ľ		1 100	^	1030	2 4	466	DPRVRTKIVNRKTTIYEIQDKTGSMAVVGKG
l	- 1	1			ĺ	Į.	ECHNIPCEKGDKLRLFCFRLRKRENMSKI MS
	}	J	1		1		EMHSFIQIQKNTNORSHDSRSMALPOEOSOHP
L	[	-		- 1		[ :	KPSEASTTLPESHLKTPOMPPTTPSSSSFTKVT
1:	31	481	A	1651	507	3	KDKDIK*LLFNLYSSVEILPEVLHLKT
	- 1			(		4 .	LAEGGDVFDCVLNGGPLPESRAKALFROMVE AIRYCHGCGVAHRDLKCENALLQGFNLKLTD
	ļ			.		] :	FGFAKVLPKSHRELSQTFCGSTAYAAPEVLQ
L.,						16	GIPHDSKKGDVWSMGVVLYVMLCASLPFDD

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  TDIPKMLWQQKGVSFPTHLSISADCQDLLK RLLEPDMILRPSIEEVSWHPWLAST**KQWQV LSNKVGGESKPKKKK  LVAKSLLYCGCLFFLLQLAKNVGNNSFNDIM EANLTSPSPKPTPSSDM*VFLIY*TYFGAWHV VDAQ  RKHIKLLIQKLSDVP*ECQNNQL*KLTEICEKE
						KKEFKKKMDDQRPEKITEA*SKDKSPMEEEK TEMIRSYIQEVGRYIKRLEEAQSKRLEKLREK HKEIRQPILDEKPKGEGSSSFLSETCHEDTSWF PNFTP
134	1484	A	1666	1276	466	PGSTHASARITTY*L*IILSNATEVDNNFSKPPP FFPAGAPPASSSSSSSSSSSPPTVSTAPPLIPPPGF PPPPGAPPPSLIPTIESGHSSGYDSRSARAFPYG NVAFFHLPGSAPSWPSLVDTSKQWDYYARSS SSSSSSSSSSSSPRDRDRER*RTRERERERDHS PTPSVFNSDEERYRYREYAERGYERHRASRE KEERHRERRHREKEETRHKSSRSNSRRRHESE EGDSHRRHKHKKSKRSKEGKEAGSEPAPEQE STEATPAE
135	1485	A	1673	1	417	PTRPVNSSQAFALVYYTLGALGGNLIAHMGL GYRYWAGIGVLQSCESALTHYRLVANHVAS DISLTGGSVVQRIRLPDEVENPGMNSGMLQE DLIQYYQFLAEKGDVQAQVGLGQLHLHGGR GV*QNHQRAFDYFNLAA
136	1486	A	1678	525		ANTSLSSAAVSAVSPPPCRTSTATTLPPPMPSF FCVFPSPSMSPSPSEFLSCIASVSRVHSLSSSSS GSSSTASSLNFSAIMGSSSATASWVLSTASTPP CPSALPSSPAQES*SLAASSSAWPVAGISPSGA CTFPAGSASGAAKAPSPSWRCPSFRALFSLLD SSSLSL
137	1487	A	1680			AHRDEIQRKFDALRNSCTVITDLEEQLNQLTE DNAELNNQNFYLSKQLDEASGANDEIVQLRS EVDHLRREITEREMQLTSQKQTMEALKTTCT MLEEQVMDLEALNDELLEKERQWEAWRSVL GDEKSQFECRVRELQRMLDTEKQSRARADQ RITESRQVVELAVKEHKABILALQQALKEQK LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREBAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS NSFPVSIVOVNSAGOREEYLLCFHEFGVFVDS

CRO ID	LODA ID	1 1764	Liga			
SEQ ID NO: of	SEQ ID NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-		hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
eatide	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq- uence	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
nerice	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
]		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Ì		1	[	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		İ	peptide		/=possible nucleotide deletion, \-possible
<b> </b>	<del></del>	╂	<del> </del>	sequence	<del> </del>	nucleotide insertion
-	!	!	}	ł		YGRESETDDLKWSRLPLAFAYREPYLFVTHF
	4	1	j			NSLEVIEIQARSSAGTPARAYLDIPNPRYLGPA
i		1				ISSGAIYLASSYQDKLRVICCKGNLVKESGTE
138	1488	⊢ <sub>Ā</sub> —	1686		-	HHRGPSTSRR*PASPLPQYQGQRAFLQGRRK
130	1400	A	1080	2	526	GRPQGPAPGAGSPPESGPGLWAALGCSLVWV
						PLCCLGGAAGRL*ARSGKSGLRRRRAHAGPP
1	ł		1	}	l	PGGPCNSCP*CSAPESGGRGPLPGPGTGGVCS
	-	1	1	1	}	CWTRGCQTTARTAAAAAAPGPAGRRPPGGA
	1	1	]	J	}	PQNGSCAASASQEAAAPPPMCPPGRRWAVAS
139	1489	- A.	1.002			PPETRCPAAPGTRCRRLEAA
139	1409	A.	1693	3	376	LPSMSNCTSCFRLQSRTES*IRQAGHLLGRNE
					•	FIETKALGCAWFSLCYYLVLYFESSHKVDFVF
1	1	1	1	ļ		IV*CFSTPPGAQMTIMSQACAERCNIMRLVDR
140	1400	ļ	1			RWAGIAKGVGTQKIIGRVHLGEQKALGL
140	1490	A	1704	3	376	ERTNKFIKELIMDGKNLIAATKSLSVAQRKFA
			ŀ			HSLRDFKFEFIGDAVTDDERCIDASLREFSNFL
Ì	1	ł			1	KNLEEQREIMVS*EGCKLISQLSRGKKIWIWK
141	1401	<del>                                     </del>	1	<u>_</u>		LVLVEVVKHLSLGTVVHCNGKMRFPEP
141	1491	A	1743	1	362	LITNKVFVARELSCLDVHLDSTGSTAVVADQ
		ł				DKLELELVLKGSYEDTQTSFLGTASAFRFHY
ļ	l	1				MAAL*TELSGRLRSSKSNGWNGDNSTGYLTV
142	1400	<b>├</b>	1.550		<u> </u>	PLRPLTIVKEVTMDVPAPNVRGLNWMG
142	1492	Α	1769	1	406	NNPSTLPRGS*PMSPRTTMGRRRQRRREHKSS
		١.				LSLASSTVGPGGQIVHTETTEVVLCGDPLSGF
		1				GLQLQGGIFATETLSSPPLVCFIEPDSPAERCG
	1				,	LLQVGDRVLSINGLATEDGTMEEANQLLRDA
143	1493	-	1500			ALAHKVV
145	1493	A	1789	1	447	QMLRNGGDQNTVPDYHFADRIRELL*PTEDQ
						KNCIP*DTYLRPSALGNIVEEVTHPCSPGPCPA
1						NELCEVNRKGCTSGDPCLPYFCVQGCKLGQA
		1				SDFIARQGTLIQVPSSAGEVECYKICSCGQSGL
144	1494	A	1814			LENCMEMHCMDLPTDTSALVR
144	1424	^	1014	1	404	PGRRFRPRLSQAGTDSGS*VFPDSFPSAPAEPL
1						PYFLQEPQDAYIVKNKPVELRCRAFPATQIYF
1			[			KCNGEWVSQNDHVTQEGLDEATGLRVREVH
}						IEVSRQQVEELFGLEDYWCQCVAWSSAGTTK
145	1495	A	1827	26	440	SRRAYVRI
1	1423	^	102/	20	448	XVEEKHADTWRSXCLSDFFFHAAKXLCXE*N
			·		l	CGDAISLSVGDHFGKGNGLTWAEKFQCEGSE
1 1			J	J	ļ	THLALCPIVQHPEDTCIHSREVGVVCSRYTDV
1						RLVNGKSQCDGQVEINVLGHWGSLCDTHWD
146	1496		1970	574		PEDARVLCRQLNCGTAL
'70	1420	A	1828	574	333	QHEGGDLRRRQLGEIQLTVRYVCLRAASAC*
]				1		SMAAET*HHVPASGADPYVRVYLLPERKWA
147	1497	<del></del>	1055			CRKKTSVKRKTLEPLFDET
***/	147/	A	1855	1	372	ERLVLTSEHCLVLTLFWPSWTYHTLLLSRQH
1 1	- 1	ĺ	ĺ	- 1		VRRLPKLTHAEHDHLASIMNKLLTNYDNLFE
]	1	.	ļ		i	TSVTYSMG*HGAPTGSEAGANWNH**LHAH
1	1	l	i			YYPPLLRSDTVRKFMVGSQMLAQAQRDLTPE
148	1498		1970			Q
170	1470	A	1879	568	7	LLSALDDKGGTQPSASFSNAPTIVCVTACPAG
}	1	1	1	1	!	IAHTYMAAEYLEKAGRKLGVNVYVEKQGAN
<b> </b>	ł	1	ļ		ĺ	GIEGRLTADQLNSATACIFAAEVAIKESERFN
1 . 1	I	- 1	ŀ	ļ	l l	GIPALSVPVAEPIRHAEALMQQALTLKRSDET
				ı	1	RTVQQDTQPVKSVKTELKQALLSGISFAVPLI
149	1400	-,	1000			VAGGTQVA*AV*RQGISSLHDVQVRTWNS
147	1499	A	1880	611	24	GLNSENALSNEAMERGWQCLRLFAERLODIP
}	J	ļ	J	1		PSQIRVVATATLRLAVNAGDFIAKAQEILGCP
						VQVISGEEBARLIYQGVAHTTGGADQRLVVD

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ		}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	1	/=possible nucleotide deletion, \=possible
		1	j	sequence	}	nucleotide insertion
		<del> </del>				IGGASTELVTGTGAQTT*LFSLSMGCVTWLER
		l.			<b>.</b>	YFADRNLGQENFDAAQKAAREVLRPVADEL
		1				RYHSWKEVRGASVTVQALQEIMMAQGMDE
		ĺ	1	İ	· ·	RITMEIWPVD
150	1500	A	1894	2	750	GRVDFFHTDYRPLIRDSNNYVLDEQTQQAPH
		ı	1			LMPPPFLVDVDGNPHPTKYQRLVPGRENSAD
		l		}		EHLIPQLGYVATSDGEVIEQIISLQTNDNDERS
	l	ì	1	}	t	PESSILDGMIRQLQQQQDQRMGADQDTIPRG
		1	1			LSNGEETPRRGFRRLSLDIQSPPNIGLRRSGQV
	}	1	1	ŀ		EGVRQMHQNAPRSQIATERDLQAWKRRVVV
			1		}	PEVPLGIFRKLEDFRLEKGEEERNLYIIGRKRK
 	l		1		Ì	TLQLSHKSDSVGLVSQSRPRTCRRKYP
151	1501	A	1900	141	785	GKTIQIQTTMQNKYKTVQKQYKTIPKNKKA
	1			ļ	1	MEMQIKKQFQDTCKVQTKQYKALKNHQLEV
1	]	1	] .		}	TPKNEHKTILKTLKDEQTRKLAILAEQYEQSI
j		1	1	1 '		NEMMASQALRLDEAQEAECQALRLQLQQEM
<u> </u>		ł	1	1		ELLNAYQSKIKMQTEAQHERELQKLEQRVSL
ĺ	1	(	1			RRAHLEQKIEEELAALQKERSERIKNLLERQE
	1	1	1			REIETFDMESLRMGFGNLVTLDFPKEDYR
152	1502	A	1915	2	377	LVRLLDTQRDGLQNYEALLGLTNLSGRSDKL
		1	1			RQKIFKERALPDIENYMFENHDQLRQAATEC
Í		ĺ	1			MCNMVLHKEVQERFLADGNDRLKLVVLLCG
		l		ł		EDDDKVQNAAAGALAMLTAAHKKLCLKMT
Ī	1	1	1	[		QVTT
153	1503	Α	1921	1	237	AYQSLRLEYLQIPPVSRAYTTACVLTSAAVQL
		1	1	ŀ	1	ELITPFQLYFIPELIFKHFQIWRLITNFLFFVPFG
1	1	ł	1			FNFLLYMIFLYT
154	1504	A	1928	2	354	EMVEGGEGKMCINTEWGGFGDNGCIDDIRTR
ł		1		1		YDTEVDEGSLNPGKQRYEKMTSGMYLGEIV
	ļ.					RQILIDLTKQGLLFRGQISERLRTRGIFETKFLS
		1		l		QIESDRLALLQVRRILQQLGLD
155	1505	A	1929	2	369	TEIAKIKMEAKKKYEKELTMFQNDFEKACQA
]	}	1	1	1	ļ	KSEALVLREKSTLERIHKHQEIETKEIYAQRQ
		1				LLLKDMDLLRGREAELKQRVEAFESYQLELK
]	ļ	1	1			DDYIIRTYRLIEDDRINIQISGHWQESP
156	1506	A	1935	1	270	VTRKLPIFTVDAFTARAFRGSPAADCLLENEL
1			i	1	į.	DEDMHQKIAREMNLSETAFIRKLHPTDNPAQ
1			1	1		RSCFGLIWFTPTTDLQILTSSILPSIL
157	1507	A	1936	584	305	ESKVNNEKFRTKSPKPAESPQSATKQLDQPTA
1		1	1	1		AYEYYDAGNHWCKDCNTICGTMFDFFTHMH
l		1			L	NKKHTQGQFQKSSDFQKEELQQTFLPPERQG
158	1508	A	1939	1	423	TTHRLNVTAEPPCTSMPIYWMPDVPHRCTTA
ł		1	1	1	1	NTCPVDLTDYCAQNGFYCLVYGFLPYGSLED
]		1	1		1	RLHCQTQACPPLSWPQRLDILLGTARAIQFLH
1	1	1	}	1	1	QDSPSLIHGDIKSSNVLLDERLTPKLGDFGLA
1	1	1			<u> </u>	RFSRFAGSSPIQSSM
159	1509	A	1974	3	401	HTSTARLLLHRGAGKEAVTSDGYTALHLAAR
1	1				1	NGHLATVKLLVEEKADVLARGPLNQTALHL
1	1	1			1	AAAHGHSEVVEELVSADVIDLFDEQGLSALH
1		1	i		1	LAAQGRHAQTVETLLRHGAHINLQSLKFQGG
	1	1.	1		<u></u>	HGPAATLLR
160	1510	A	1982	2	417	KFLKDLEKQYNKEEPHLSEIGSCFLQNQEGFA
1 .	1	1	Ì		}	IYSEYCNNHPGACLELANI MKQGKYRHFFEA
		1	1	ł		CRLLQQMIDIAIDGFLLTPVQKICKYPLQLAEL
1			(			LKYTTQEHGDYSNIKAAYEAMKNVACLINER
1	İ	1	1 _		<u></u>	KRKLESIDKIA
161	1511	A	1984	4	770	RETGSVSLSPSGLEGAESYAVSPILYSSPDVKE
				1		
1	1		1		ļ	LWLETLQGQRHSHTGVKSTPGQSAAILMKLR SSHNASKTLNANNMETLIECQSEGDIKEHPLL

SEQ ID	, ,		SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl- eotide	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
zed-	seq- uence	i	USSN	location	corresponding	
uence	dence		09/496 914	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
dence	1	1	914	ng to first amino acid	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1		residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	1	1	peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				sequence		/=possible nucleotide deletion, \=possible nucleotide insertion
	ļ. ——	<del>                                     </del>	<del> </del> -	Soqueine	<del> </del>	
	ļ	ĺ	1			ASCESEDSICQLIEVKKRKKVLSWPFLMRRLS
1	j	1	Ì		1	PASDFSGALETDLKASLFDQPLSIICGDSDTLP RPIQDILTILCLKGPSTEGIFRRAANEKARKEL
				1	1	KEELNSGDAVDLERLPVHLLAVVFKDFLRSIP
L				1		RKLLSSDLFEEWMGALEMQDEEDRIEALK
162	1512	A	1986	864	501	LLNSGLFSAPDGSNLEMRLTRGGNMCSGRIEI
			İ			KFQGRWGTVCDDNFNIDHASVICRQLECGSA
1	1	ĺ	1	ł	1	VSFSGSSNFGEGSGPIWFDDLICNGNESALWN
<u></u>		<u> </u>			1	CKHQGWGKHNCDHAEDAGVICSSKD
163	1513	Α	2001	419	187	AVDLSIDESSLTGETTPCSKVTAPQPAATNGD
	1	ł				LASRSNIAFMGTLVRCGKAKGVVIGTGENSE
						FGDINLSTFVVHS
164	1514	Α	2012	284	597	SLLCLFPGTSTVVCKPIVIETQLYVIVAQLFGG
			1.			SHIYKRDSFANKFIKIOAIEILKIRKPNDIETFKI
	'	1				ENNWYFVVADSSKAGFTTIYKWERETGFYSH
	1	<u> </u>				QSFTR
165	1515	Α	2013	2	403	EDPEELGHFYDYPMALFSTFELFLTIIDGPANY
1	ĺ	ĺ				NVDLPFMYSITYAAFAIIATLLMLNLLIAMMG
			1			DTHWRVAHERDELWRAOIVATTVMLERKLP
	Ì	1	1 1			RCLWPRSGICGREYGLGDRWILRVEDRQDLN
166	1516	A	2019			RQRIQRYA
100	1310	Α	2019	2	927	CCQREGLGLKAVVQILLSHGRNGLPGEPASS
			1			QGLSAASSTPVFHLALQIDSAPDNIDWVEMLF
	1		) )			NKNMVTERLQNVMVLEQCFSDSSSLYRFLTY
1	1					SYLLAFNVWLLLAPVTLCYDWQVGSIPLVETI
1	i i		1			WDMRNLATIFLAVVMALLSLHCLAAFKRLE
	1		1 1			HKEVLVGLLFLVFPFIPASNLFFRVGFVVAER
ļ			1 1			VLYMPSMGYCILFVHGLSKLCTWLNRCGATT
j	]		1 1			LIVSTVLLLLLFSWKTVKQNEIWLSRESLFRS
				ĺ	•	GVQTLPHNAKVHYNYANFLKDQGRNKEAIY HYRTALNNNKAWDYLCWRFRKTLTDLP
167	1517	A	2025	696	71	AAASAASSLTVTLGRLASACSHSILRPSGPGA
`			[ ]	1		ASLWSASRRFNSQSTSYLPGYVPKTSLSSPPW
			1			PEVVLPDPVEETRHHAEVVKKVNEMIVTGQY
	ľ		1	1		GRLFAVVHFASRQWKVTSEDLILIGNELDLA
[			1			CGERIRLEKVLLVGADNFTLLGKPLLGKDLV
1	}			-		RVEATVIEKTESWPRIIMRFRKRKNFKKKRIV
						TTPQTVLRINSIEIAPCLL
168	1518	A	2046	2	366	HLQVAARVFMPLQAVDSAPKPLKGOAOAPO
						RLQGAARVFMPLQAQVKAKASKPLQMQIKA
					ļ	PPRLRRAARVLMPLQAQVRAPRLLOVOSOVS
169	1510		1			KKQQAQTOTSEPODLDOVPEEFOGODOVIR
103	1519	Α	2049	1	945	QNLEDREVLNGVQTELLTSPRTKDTLSDMTR
·	}			- 1		TVEISGEGGPLGIHVVPFFSSLSGRILGLFIRGI
		1		1	1	EDNSRSKREGLFHENECIVKINNVDLVDKTFA
					1	QAQDVFRQAMKSPSVLLHVLPPQNREQYEKS
' I	1				l	VIGSLNIFGNNDGVLKTKVPPPVHGKSGLKTA
				- 1	[	NLTGTDSPETDASASLQQNKSPRVPRLGGKPS
İ	1	l	1	1	ļ	SPSLSPLMGFGSNKNAKKIKIDLKKGPEGLGF
			į	1	ł	TVVTRDSSIHGPGPIFVKNILPKGAAIKDGRLQ
}	!	- 1	}		l	SGDRILEVNGRDVTGRTQEELVAMLRSTKQG
170	1520	Ā	2050	262		ETASLVIARQEGHFLPRELVMFRSQSH
	1520	ra	2030	363	1	PVATHLTKILNSDEHAVVISSAKTLCETVKDF
l		-	-			VAKVEKTYDKTLENAVVADAVASKCSVLNE
İ	ł					KLEQLLQALHTDSQAAPVLPGLSPLIVEEDAV
171	1521	A	2055	139	675	ESSSEESLGESKEQLGDDVTKPSSQKA
ĺ		-				IPSRPWLGRITGLDPAGPLFNGKPHQDRLDPS
ļ		1	- 1	ļ	ŀ	DAQFVDVIHSDTDALGYKEPLGNIDFYPNGG LDQPGCPKTILGGFQYFKCDHQRSVYLYLSSL
		—		<u>_</u>		PPA OCENTILIOUS LEVEN MENT AND AND AND AND AND AND AND AND AND AND

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RESCTITAYPCDSYQDYRNGKCVSCGTSQKE
						SCPLLGYYADNWKDHLRGKDPPMTKAFFDT AEESPFCMYHYFVDIITWNKNVR
172	1522	A	2056	3	361 '	LIQHKSAVEYAQSHLSLVSMCKESHKCSEPK MEWKVKIRSDGTRYITKRPVRDRILKERALKI KEERSGLTTDDDTMSEMKMGRYWSKEERKQ HLVRGKEQRRRREFMMRIRLKCLKES
173	1523	A	2060	1	387	GTRILSMQIPFVGFQPIRTSEHMAAAGVFALL QAYAFLQYLRDRLTKQEFQTLFFLGVSLAAG AVFLSVIYLTYTGYIAPWSGRFYSLWDTGYA KIHIPIIASVSEHQPTTWVSFFFDLHILGCTFPA G
174	1524	A	2071	74	443	LLMGPKAKKSGSKKKKVTKAERLKILQEEEE RRLKEEEEARLKYEKEEMERLEIQRIEKEKW HRLEAKDLERRNEELEELYLLERCFPEAEKLK QETKLLSQWKHYIQCDGSPDPSVAQEMNT
175	1525	A	2083	139	486	AALTWSQPQEFWPMEMQPIVTDMVTVHWV AESSTVGWLCALFRVTHVGVGATGHGVVCG RRVLCGLPLPSPAPMPIMSLPEGESRKEREVQ RLQFPYLEPGHELPATTLLAFLAAV
176	1526	A	2092	3	587	EGSVNFKFGVLFAKDGQLTDDEMFSNEIGSEP FQKFLNLLGDTITLKGWTGYRGGLDTKNDTT GIHSVYTVYQGHEIMFHVSTMLPYSKENKQQ VERKRHIGNDIVITVFQEGEESSPAFKPSMIRS HFTHIFALVRYNQQNDNYRLKIFSEESVPLFG PPLPTPPVFTDHQEFRDFLLVKLINGEKATLET PCI
177	1527	A	2103	44	427	GKGQVSLEGRPHRGPLCLGSWWPGSRVPGC CDGAWLAWACWVFGNDFPSPASAACSALLG CSVSTACLCVPLCSGSPLAPFRRTAALQEGLR RAVSVPLTLAETVASLWPALQELARCGNLAC RSDLO
178	1528	A	2104	2	409	ALQSTLGAVWLGLLLNSLWKVAESKDQVFQ PSTAASSEGAVVEIFCNHSVSNAYNFFWYLHF PGCAPRLLVKGSKPSQQGRYNMTYERFSSSL LILQVREADAAVYYCAVEVPNTDKLIFGTGT RLQVFPNIONPD
179	1529	A	2111	1	312	PTRSSTRPPSLFVHASAKGGEKEEGDDGHYL MRTESHTGLKKGGNANLVFMLKRNTEPKKG SYHFDLERLRAAHILFEREQEHLAPGGISMPL PPPLPLACLG
180	1530	. A	2116	3	366	TSIKRAIETTDVTRSFGWDSSEAWQQHDVQE LCRVMFDALEQKWKQTEQADLINELYQGKL KDYVRSLECGYEGWRIDTYLDIPLVIRPYGSS QAFASVVCTFHLTACVSLHRIHNSTVV
181	1531	A	2117	2 .	386	YGLGAHFGRLFIQAGINENDFYDGAWCAGR NDLQQWIEVDARRLTRFTGVITQGRNSLWLS DWVTSYKVMVSNDSHTWVTGKNGSGDMIFE GNSEKEIPVLNELPVPMVARYIRINPQSWFDN GSICI
182	1532	A	2123	1	493	RTKTDVYILNLAVADLLLLFTLPFWAVNAVH GWVLGKIMCKITSALYTLNFVSGMQFLACISI DRYVAVTKVPSQSGVGKPCWIICFCVWMAAI LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKAL IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS
183	1533	A	2140	3	561	RQAWHEAFKVRKBILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF VYGIDKFMEDLKDMLGFAPSRYYYYMWKYI

SEQ ID	SEQ ID	137.	1 050	<del></del>	·	
NO: of	NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
1	l	i		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l		peptide		/=possible nucleotide deletion, \=possible
		l	1	sequence	ļ	nucleotide insertion
	1	1		<del></del>	<del> </del>	SPLMILSILIASVVNMGLSPPGVNAWIEDVAS
		1	1	1	1	EEFLSYPTWGLAVCASLDVFAILPVPVAFIGR
		l				RFSLIDDGAGPFCSAAYTTTGCRTPYL
184	1534	A	2145	3	538	HELTVAAADRGQPPQSSVVPVTVTVLDVND
			1		j	NPPVFTRASYRVTVPEDTPVGAELLHVEASD
			1	i	i	ADPGPHGLVRFTVSSGDPSGLFELDESSGTLR
1	1	ı	1	ļ		LAHALDCETQARHQLVVQAADPAGAHFALA
1		l				PVTIEVQDVNDHGPAFPLNLLSTSVAENOPPG
100						TLVTTLHAIDGDAGAFGRLRYHL
185	1535	Α	2151	2	671	LDKLLDRMENYNIFNEYILKQVAATYIKLGW
		ļ	j			PKNNFNGSLVQASYQHEELRREVIMLACSFG
		l				NKHCHQQASTLISDWISSNRNRIPLNVRDIVY
		1				CTGVSLLDEDVWEFIWMKFHSTTAVSEKKIL
		}				LEALTCSDDRNLLNRLLNLSLNSEVVLDQDAI
		1				DVIIHVARNPHGRDLAWKFFRDKWKILNTRI
						ROKTLEFDFAEPLILAFPIILYTAIDNPPLVREH
186	1536	A	2153	2	400	E
100	1550	^	2133		400	GPMCDKHSAFAEKFHAGFIDYIVHPLWETWA
İ		ļ	1			HLALPDAQDILYTLEDNRNWVDSMIPQSPSPP
Į.		1	1 .			LDEQNRDWQGLLENLHVELTLDEEDSEGPEK
						EGEOQTYFTSSKTLCGIVPQNTDSLGETGIHIC AHDKSP
187	1537	A	2158	227	442	FNCFRVASDSFLENSSLLIMILPLRNATQEFIIR
	1		2.50	221	772	PGAVAYTCNPSTLGGWGGWITRSGVRDQPG
1		1				OHGGTPS
188	1538	A	2167	3	486	AHLGGAWLTQRSLGSWAAPGPARAAKEVVA
			1	_	100	CIPQNQKMNIWRMKTSKHLQLLSFVLGAVSP
l	1					AVVVPYMMVLQENGYGVEGIPTLLMAASS
						MDDILAITGFNTCLSIVFSSGCARSSGSRNSKS
ļ						LRTPLGTICEGCDDSSIFSHLDHSSKWSSTYG
						HSGA
189	1539	Α	2168	2	412	EFLSSNQITQLPNTTFRPMPNLRSVDLSYNKL
Ì			1 1	1		QALAPDLFHGLRKLTTLHMRANAIQFVPVRIF
1				ŀ		QDCRSLKFLDIGYNOLKSLARNSFAGLFKLTE
			1 1			LHLEHNDLVKVNFAHFPRLISLHSLCLRRNKV
					ľ	AIVVSSLDW
190	1540	A	2179	64	399	MRLNONTLLLESFGXXRPYTSEHAPTYHOW
1			1 1		i	MKADELLRWTTSEPLTLEHEYAMORTWLED
			1			AYECTFIVLDAEKRHAQPGATEESCMVGDVN
101	-2-72					LFLTDLEDLTLGEIEVLIAEP
191	1541	A	2190	1	469	CLDRAAGIRHERNVIYINETHTRHRGWLARR
						LSYVLFIQERDVHKGMFATNVTENVLNSSRV
						QEAIAEVAAELNPDGSAQQQSKAVNKVKKK
,						AKRILQEMVATVSPAMIRLTGWVLLKLFNSF
			1			FWNIQIHKGQLEMVKAATETNLPLLFLPVHR
192	1542		2100	24		SH
174	1542	A	2197	26	157	PSKXGGIRLLLTGTQLYGRFGSALAPLGDLDR
193	1543	_	222			DGYNGEGREEPY
193	1343	A	2236	2	383	EYFPNSIWRSLFSTMDLGDIGFYTYRILQALS
	ŀ			i	1	YTHSKGIMHRDVKPLNILCNSPRNKVILADW
					l	GLAEFYHPMRKYSVHVATRYYKSPEILLDYE
	1				1	YYDYSLDIWAVGVILLELLTLKLHVFEGGDN
194	1544	A .	2241	105	400	EQ
***	17-77	n	2241	105	409	RKGVGKMPTSEGRPGQERSDWVTSYKVMGS
	1			ł	ļ	NDSHTWVTVKNGSGDMIFEGNSEKEIPVLNE
	]				į	LPVPMGARYIRINPQSWFDNGSICMRMEILGC
195	1545	<u> </u>	2245		672	PLPDPNNY
.,,	1747	A	2245	1	672	MGVASDWTKRIEYQPGSGSMPLFPSIHLETCD
						GAVSSLQIVTELQTNYIGKGCDRETYSEKSLQ

SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine O=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- eotide	peptide seq- uence	nod	in USSN 09/496	nucleotide location correspondi	location corresponding to last amino	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq- uence	dence		914	ng to first amino acid residue of	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
•				peptide sequence		/=possible nucleotide deletion, \=possible nucleotide insertion KLCGASSGIIDLLPSPSAATNWTAGLLVDSSE
						MIFKFDGRQGAKIPDGIVPKNLTDQFTTTMW MKHGPSPGVRAEKETILCYSDKTEMNRHHY ALYVHNCRLVFLLRKDFDQADTFRPAEFHW KLDQQALAKVDGQPGKSITRQLQEMPVTIQG
196	1546	A	2256	1	396	ISLKPS FRGTPVSGLTNRDTLAVIRHFREPIRLKTVKP
150	1540	^	2230			GKVINKDLRHYLSLQFQKGSIDHKLQQVIRD NLYLRTIPCTTRAPRDGEVPGVDYNFISVEQF KALEESGALLESGTYDGNFYGTPKPPAEPSPF
197	1547	A	2259	43	594	QPDPV   QLAIEIGVRALLFGVFVFTEFLDPFQRVIQPEEI   WLYKNPLGQSDNIPTRLMFAISFLTPLAVICV
					İ	VKIIRRTDKTEIKEAFLAVSLALALNGVCTNTI KLIVGRPRPDFFYRCFPDGVMNSEMHCTGDP DLVSEGRKSFPSIHSSFAFSGLGFTTFYLAGKL HCFTESGRGKSWRLCAAILPL
198	1548	A	2275	3	404	TCTTVVVIPRMLVDFLSESKTISLPECATQMFF FLGFASNNCFIMAAMSYDRYTAIHNPLQYHT LMTRKICLQMMMASWMVGFLFSLCIIVTVFN LSLCDLNTIQHYFCDISPVVSLACNYTFYHEM AIFVLSA
199	1549	A	2315	1	375	LTOMPFIHALSAIESTILLAMAFDRYVAICHPL RHAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLI KRLAFCHSNVLSHSYCVHQDVMKLAYADTL PNVVYGLTAILLVMGXDRMFISLSYFLII
200 .	1550	A	2334	2	409	PRVRPQQRKMSFFFKTELGEKLVTKFLFETDF SDDPMLPSPDQLKKKAPFTNKKLKAHQTPVD ILKQKAHQLASMQVQAYNGGNANPRPANNE EEEDEEDEYDYDYESLSDDNILEDRPENKSCH DOLOFEYKEEM
201	1551	A	2350	3	512	ISWEAQIAEIIQWVSDEKDARGYLQALASKM TEELEALRSSSLGSRTLDPLWKVRRSQKLDM SARLELQSALEAEIRAKQLVQEELRKVKDAN LTLESKLKDSEAKNRELLEEMEILKKKMEEK FRADTGKLMLCDSALFEYKYFSNECFYFLFD LIVTLEAPTEFQIQY
202	1552	A	2351	1	1003	PSSYSSDELSPGEPLTSPPWAPLGAPERPEHLL NRVLERLAGGATRDSAASDILLDDIVLTHSLF LPTEKFLQELHQYFVRAGGMEGPEGLGRKQA CLAMLLHFLDTYQGLLQEEEGAGHIIKDLYL LIMKDESLYQGLREDTLRLHQLVETVELKIPE ENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGS DEIFCRVYMPDHSYVTIRSRLSASVQDILGSV TEKLQYSEEPAGREDSLILVAVSSSGEKVLLQ PTEDCVFTALGINSHLFACTRDSYEALVPLPE EIQVSPGDTEHRVBPEDVANHLTAFHWELFR CVHELEFVDYVFHGE
203	1553	A	2361	2	403	NNLNCAEPLFEQNNSLNVNFNTQKKTVWLIH GYRPVGSIPLWLQNFVRILLNEEDMNVIVVD WSRGATTFIYNRAVKNTRKVAVSLSVHIKNL LKHGASLDNFHFIGGSLGAHISGFVGKIFHGQ LGRITGLDP
204	1554	A	2390	280	476	SPSLLPQCLMSLSDLSLSPAPPSHLSPRCPSPQ AGSRLGAMRRCAREMDATPMPPAPSCPSERV T
205	1555	A	2400	543	745	AAVALRDISWQQPYPMDFYAGSSLGPWTVN HGQDRRPHAPGRPARGKVQEGSARPPSAVAC EDCSCR

SEQ ID	Tepan	3.64	LODO	Thursday	1 8 11 1	
NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in in	nucleotide	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
eotide	seq-	1	USSN	location	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	ì	09/496	correspondi	corresponding to last amino	
uence	451150	1	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline,
		l	7,4	amino acid	of peptide	Q=Glutamine, R=Arginine, S=Serine,
1	1	İ	1	residue of	sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
		-		peptide	acquotice	/=possible nucleotide deletion, \=possible
	1	1	1	sequence		nucleotide insertion
206	1556	A	2406	122	485	DLSPDSREDHPQGHRRLLPKRPVRGSLMPQH
i	1	1			1.	THHPCPVSSTTNDTPDQIWVSVGSLRMGTGG
	1	1	1		1	MGANASTSPRCWDLSSGNKKWIIQVPILASIV
1.	1		' '	1		ESRGGLLATGVGGMCACVPRNQPLTGT
207	1557	A	2409	289	418	LWTLYRHKQQVQHNHSNRLSCRPSQEDRAT
1	ľ	l			'''	HTIMVLDKENTLS
208	1558	A	2413	64	492	VQGTGXXFIAFTEAMTHFPASPVWAGMFFL
	İ	1				MLINLGLGSMIGTMAGITTPIIDTFKVPKEMFT
}						GGCCVFAFLVGLLFVQRSGNYFVTMFDDYSA
1		-				TLPLTLIVILENIAVAWIYGTKKFMQELTEML
						GFRPYRFYFYMWKFVSP
209	1559	A	2417	3	877	EKERLLDEWFTLDEVPKGKLHLRLEWLTLMP
į	1		1			NASNLDKVLTDIKADKDQANDGLSSALLILY
1	ĺ	1			l	LDSARNLPIRYKTNEPYWEENFTFFIHNPKRQ
	} .					DLEVEVRDEQHQCPLGNLKVPLSOLLTSEDM
	ļ		}		· ·	TVSQRFQLGNSGPNSTIKMKIALRVLHLEKRE
į.	ł	1	1.			RPPDHQHSAQVKRPSVSKEGRKTSIKSHMSG
1	ļ		1 1			SPGPGGSNTAPSTPVIGGSDKPGMEEKAOPPE
ĺ		[			f	AGPQGLHDLGRSSSSLLASPGHISVKEPTPSIA
1		1	1 1		]	SDISLPIATQELRQRLRQLENGTTLGQSPLGQI
210	1560	<del></del>	+			QLTIP
210	1300	A	2422	35	456	REFAASDLEPFTPTDQPISPEATTQPSCIKRQRA
1			1 ' 1			AGNPGSLAATIDHKPCSAPLEPKIQASRNQRW
		İ	] ]			GAVRAAESLTDIAEPASPQVHETPIDASQTQK
ĺ		ļ				VEPASKSRFTPELQAKVSHSRERALSTMDATP
211	1561	A	2431	1	764	HHAQPQRGEG
		' '	2431	*	704	RRYSQKLIQHTACQLLRTYPAATRIDSSNPNP
			1 1			LMFWLHGIQLVALNYQTDDLPLHLNAAMFE
						ANGGCGYVLKPPVLWDKNCPMYQKFSPLER
						DLDSMDPAVYSLTIVSGQNVCPSNSMGSPCIE
			1 1	j		VDVLGMPLDSCIIFRTKPIIIRNTLNPMWNEQF LFHVHFEDLVFLRFAVVENNSSAVTAQRIIPL
				Į.		KALKRGYRHLQLRNLHNEVLEISSLFINSRRM
			j l			EENSSGNTMSASSMFNTEERKCLQTHRVTVH
			1 1	J		GVPG
212	1562	A	2436	1	411	GIRGTTGHLGCPINDDPSLTLTVSWVMEDKPI
			1 1			YIGNGTKKEDDSLTIFAVAKRDHVSDTCGAC
			[			TDLDHNLDKGYLTVLGEQATPTNRLGALPKG
	1		1	l		RANRTRDLELTYLAERIVRLTWIPGDANNRPI
	1000					TDYDCQIEEHQ
213	1563	Α	2445	1	1294	MSSIGCLWVSRSSQIDGLTAEKSGPEKPHGT
ı	1			- 1		WLMPELHPKEQILELLVLEOFLSILPEELOIWV
	l			1		QQHNPESGEESVTLLEDLEREFDDPGOOVPAS
İ				i		PQGPAVPWKDLTCLRASQESTDIHLOPLKTO
1	1			i	1	LKSWKPCLSPKSDCENSETATKEGISEEKSOG
į						LPQEPSFRGISEHESNLVWKQGSATGEKLRSP
	ļ			ŀ		SQGGSFSQVIFTNKSLGKRDLYDEAERCLILT
1	- {		}	ļ	Į	TDSIMCQKVPPEERPYRCDVCGHSFKOHSSLT
	İ				1	QHQRIHTGEKPYKCNQCGKAFSLRSYLIIHOR
			' I	ł	ł	IHSGEKAYECSECGKAFNOSSALIRHRKIHTG
	-				1	EKACKCNECGKAFSQSSYLIIHQRIHTGEKPY
	}	1			İ	ECNECGKTFSQSSKLIRHORIHTGERPYECNE
-	1	- 1	1	1	j	CGKAFRQSSELITHQRIHSGEKPYECSECGKA
214	1564	<del>,</del>	2461			FSLSSNLIRHQRIHSG
217	1704	A	2461	1 T	615	GIPGSTISSSRNIFLEDDLAWQSLIHPDSSNTPL
1	ł	}	1	1		STRLVSVQEDAGKSPARNRSASITNLSLDRSG
1	- 1	- 1		1		SPMVPSYETSVSPQANRTYVRTETTEDERKII
1		-	1	1		LDSVQLKDLWKKICHHSSGMEFODHRYWLR
						THPNCIVGKELVNWLIRNGHIATRAQAIAIGQ

		-	1 600		1 - 10 - 10 - 1	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	Ì	in		location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence	l	<u> </u>	914	ng to first	acid residue	
	i .	1	ł	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l	ľ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	1	ł	peptide	<u>.</u>	/-possible nucleotide deletion, \-possible
	<u> </u>	<u> </u>		sequence		nucleotide insertion
			1			AMVDGRWLDCVSHHDQLFRDEYALYRPLQV
					i	LFSVYCQLECSKLIL
215	1565	Α	2464	3	2932	GPGVRSSQDGMADVFVHLRTAWPRCSFISGQ
		ļ.				HGPGRHGRRVCSSQDSMADVFVHLRTAWPT
	ł		ŀ		Ì	CSLISGQHGPGESVSYEDDDIPAPASLLHVNA
			ľ			AAPALTNPTAPVLCTAPNNTAQKEKVPSGMR
		ļ				QRPAGVRISSRTPDLTCAVSTHSTVPGVRISSC
	ł	ł	}		Ì	TPDLTCAVSIHSTVPSVCISSCTPDLTCAVSTH
	i .		1	<u> </u>		STVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
	l		1			TPDLTCAVSIHATVPGVRISSCTPDLTCAVSIH
	l	l			1	ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
		i				TPDLTCAVSIHSTVPGVRISSCTPDLTCAVSIH
		1	ļ		1	ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
	l	1	1			TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
	1 .	İ .	1			ATVPGVRISSCTPDLTCAVSIHATVPGVRISSC
	l	ļ.	İ		 	TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
	ł	1		1	1	ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
				İ		TPDLTCAVSIHATVPGVRISSCTPDLTCAVSTH
		l			:	STVPGVRISSRTPDLTCAVSIHATVPGVHISSC
	ł	ł			Ì	TPDLTCAVSTHSTVPGVRISSRTPDLTCAVSIH
		i	l.			STVPGVCISSRTPDLTCAVSIHSTVPSVHISSCT
	Į	1				PDLTCAVSIHSTVPGVRISSRTPDLTCAVSTHS
	ļ	l	ł		İ	TVPGVHISSCTTDLTCAVSIHATVPGVHISSCT
		1				PDLTCAVSTHTTVPGVRISSRTPDLTCAVSIHS
	Į.		1			TVPGVRISSCTPDLTCAVSTHSTVPGVRISSRT
	1	1	1	i	İ	PDLTCAVSTHLTVPGVRISSRTPDLTCAVSIHA
	İ	İ				TVPGVHISSCTPDLTCAVSIHATVPGVRISSRT
	Į	ł			-	PDLTCAVSIHATVPGVHISSCTPDLTCAVSTHS
	1	]			1	TVPGVRISSRTPDLTCAVSIHSTVPGVHISSCT
	1	1				PDLTCAVSTHSTVPGVHISSCTPDLTCAVSTH
		1		1		
	ļ	1	1	ļ	i	STVPGVHISSRTPDLTCAVSIHATVPSVHISSC
	L	Ļ		<u> </u>		TPDLTCAVSIHSTVPGLLTSVSQTSTG
216	1566	A	2477	1	414	FRTKSYRKGSYRCIVSEWIAEQGNWQEIQEK
	ł	1	1	}		AVEVATVVIQPTVLRAAVPKNVSVAEGKELD
			]	ł		LTCNITTDRADDVRPEVTWSFSRMPDSTLPGS
		1	1			RVLARLDRDFLVHSSPHVALSHVDARSYHLL
	1	1	<u> </u>			VRDVSKENSGYYY
217	1567	A	2480	2	460	CRTLCEGPQRFEEYEYLGYKAGLYEAIADHY
		1				MQVLVCQHECVRELATRPGRLSPIENFLPLHY
1		1		l		DYLQFAYYRVGEYVKALECAKAYLLCHPDD
1	1			1	ļ	EDVLDNVDYYESLLDDSIDPASIEAREDLTMF
1		1			1	VKRHKLESELIKSAAEGLGXSYTEPNYW
218	1568	A	2483	140	383	AFSSPHPSPAPQFPECGFYGLYDKILLFKHDPT
		1		1		SANLLQLVRSSGDIQEGDLVEVVLSASATFED
l	1		1	1	1	LOIRPHALTVHSYRAP
219	1569	A	2489	3	428	SSRLVLLAGAAALASGSQGDREPVYRDCVLQ
		1		1	1	CEEONCSGGALNHFRSRQPIYMSLAGWTCRD
		1	1	1		DCKYECMWVTVGLYLQEGHKVPQFHGKWP
Į i	1	1	1	1	1	FSRFLFFQEPASAVASFLNGLASLVMLCRYRT
l		1	1	1		FVPASSPMYHTCVAFAWVS
1000	1500	<del> </del>	2400	1	1297	MDGEAVRFCTDNQCVSLHPQEVDSVAMAPA
220	1570	Α	2498	1	1297	
1	1			1		APKIPRLVQATPAFMAVTLVFSLVTLFVVDH
ļ	1	1	1			HHFGREAEMRELIQTFKGHMENSSAWVVEIQ
	1	1	1		1	MLKCRVDNVNSQLQVLGDHLGNTNADIQMV
ſ	1	1	1	1	1	KGVLKDATTLSLQTQMLRSSLEGTNAEIQRL
•	1		1			
			1		İ	KEDLEKADALTFQTLNFLKSSLENTSIELHVL
				]		SRGLENANSEIQMLNASLETANTQAQLANSS

SEQ ID	CEOTO	137.	LOPA	I built and	1	
NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A-Alanine O-Cysteine,
nucl-	peptide	1100	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
		}	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	peptide	] · •	/=possible nucleotide deletion, \=possible
		L	1	sequence	1	nucleotide insertion
		!	Ţ	!		FDNTSAEIOFLRGHLERAGDEIHVLKRDLKM
					]	VTAQTQKANGRLDQTDTQIQVFKSEMENVN
l		l	ł	Į.		TLNAQIQVLNGHMKNASREIQTLKQGMKNA
	1	]	1			SALTSQTQMLDSNLQKASAEIQRLRGDLENT
221	1571	<u> </u>	0.501			KALTMEIQQEQSRLKTLHVVITSQEQLQRTQ
221	1571	A	2501	3	500	RVRLNNDGLSPLMMAAKTGKIGIFQHIIRREV
	1	Ì		}	ĺ	TDEDTRHLSRKFKDWAYGPVYSSLYDLSSLD
·	1	1	i i			TCGEEASVLEILVYNSKIENRHEMLAVEPINE
	1			ļ	1	LLRDKWRKFGAVSFYINVVSYLCAMVIFTLT
	ļ	ļ				AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFT
222	1572	A	2508		1 462	GVLFFFTN
****	.1312	^	2308	3	395	DAHCQRKLAMQEFMEINERLTELHTQKQKL
		1				ARHVRDKEEEVDLVMQKVESLRQELRRTER
		1	1		!	AKKELEVHTEALAAEASKDRKLREQSEHYSK
			1			QLENELEGLKQKQISYSPGVCSIEHQQEITKL KTDLEKKS
223	1573	A	2544	2	412	NDPAIISNFSAAVVHTIVNETLESMTSLEVTK
		1	2577	-	. 412	MVDERTDYLTKSLKEKTPPFSHCDQAVLQCS
		}	]		ĺ	EASSNKDMFADRLSKSUKHSIDKSKSVIPNID
		İ				KNAVYKESLPVSGEESQLTPEKSPKFPDSQNQ
		1				LTHCSLSAA
224	1574	A	2552	401	1	GASLCFISTAFTVLTFLIDSCRFSYPERPIIFLSM
		1	1		-	CYNIYSIAYIVRLTVGRERISCDFEEAAEPVLI
						QEGLKNTGCAIIFLLMYFFGMASSIWWVILTL
						TWFLAAGLKWGHEAIEMHSSYFHIAAWAIPA
						VK .
225	1575	A	2563	724	1	MSARKERREKGEEEGEGEKDGDEDEKEEEKE
		}	]		*	GLGEEEEKEAGKKKKKOEEKEKEKGAVYSR
						VARICKNDMGGSQRVLEKHWTSFLKARLNC
						SVPGDSFFYFDVLQSITDIIQINGIPTVVGVFTT
			1 1			QLNSIPGSAVCAFSMDDIEKVFKGRFKEQKTP
			]			DSVWTAVPEDKVPKPRPGCCAKHGLAEAYK
			1			TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFT
226	1576	A	2571	449	3	KTRVRYRLTAISVDHSAGPYH
		4.	23/1	TT)	,	EGVLFVYGNYVGDVMNFEMAAEMAQEVAIP TRTVLTTDDISSSPIEDRDGRRGVAGNFFIFKV
						AGAACDRGMSLEACEAVTRKANRRTYTMG
			1			VALEPCSLPQTRRHNFEIGAEEMEIGMGIHGE
J			l i			RGVIREKMMPADAIVDHIMDRIFS
227	1577	Α	2575	3	1197	VLSDLCLFYYRDEKEEGILGSILLPSFQIALLTS
				_		EDHINRKYAFKAAHPNMRTYYFCTDTGKEM
	j					ELWMKAMLDAALVQTEPVKRVDKITSENAP
- 1			[		f	TKETNNIPNHRVLIKPEIQNNQKNKEMSKIEE
ŀ	l		}			KKALEAEKYGFQKDGQDRPLTKINSVKLNSL
ļ					ļ	PSEYESGSACPAQTVHYRPINLSSSENKIVNVS
- 1	1		1			LADLRGGNRPNTGPLYTEADRYIQRTNSMQQ
i	- 1	i			ļ	LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS
	ì				ł	HRAQIMARYPEGYRTLPRNSKTRPESICSVTP
ŀ	ļ					STHDKTLGPGAEEKRRSMRDDTMWQLYEW
l	j			1	ļ	QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT
	Ì			1	ł	MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI
						QRGDVTIDRRHRAHHPKVK
228	1578	A	2583	3	330	LPFLGLGSVLPQGMVMASPEMNPTICSVFEA
i	i			-	.	HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE
l	- 1	ł	1	i	.	KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD
220	1570	<u>,                                    </u>				PTMGIKPHLWWVAA
229	1579	A	2589	1	448	DDKNAQGIKRHVKPTSGNAFTICKYPCGKSR
ł	ŀ					ECVAPNICKCKPGYIGSNCQTALCDPDCKNH
						GKCIKPNICQCLPGHGGATCDEEHCNPPCQH

SEQ ID NO: of No: of	VRHC VCMFI NPPER SKEPGA ELGW GIAAS RPLS
mucle cotide code sequence uen	VCMFI NPPER SK NEPGA ELGW GIAAS
sequence uen uence uen uence uen uence uen uence uen uence uen uence uen uen uen uen uen uen uen uen uen ue	VCMFI NPPER SK NEPGA ELGW GIAAS
uence       914       ng to first amino acid residue of peptide residue of peptide sequence       acid residue of peptide sequence       Q=Glutamine, V=Valine, W=Tryptophan, Y=Typtopha	VCMFI NPPER SK NEPGA ELGW GIAAS
amino acid residue of peptide sequence   T=Threonine, V=Valine, W=Tryptophan, Y=Iyrosine, X=Unknown, *-Stop codon, Y=Iyrosine, X=Unknown, *-Stop codon, Y=Iyrosine, X=Unknown, *-Stop codon, Y=Iyrosine, X=Unknown, *-Stop codon, Y=Iyrosine, X=Unknown, *-Stop codon, Y=Iyrosine, X=Unknown, *-Stop codon, Y=Iyrosine, X=Ixroperation   GGTCLAGNILCTCPYGFVGPRCETMVCI	VCMFI NPPER SK NEPGA ELGW GIAAS
residue of peptide sequence	VCMFI NPPER SK NEPGA ELGW GIAAS
peptide sequence	VCMFI NPPER SK NEPGA ELGW GIAAS
Sequence	VCMFI NPPER SK NEPGA ELGW GIAAS
GGTCLAGNLCTCPYGFVGPRCETMVCI	VCMFI NPPER SK NEPGA ELGW GIAAS
ENGGQCLTPDICQCKPGWYGPTCSTA	VCMFI NPPER SK NEPGA ELGW GIAAS
230	NPPER SK NEPGA ELGW GIAAS RPLS
1581	NPPER SK NEPGA ELGW GIAAS RPLS
231	SK IEPGA ELGW GIAAS IRPLS
WEKIAEAVPGRTKKACIKRYKVADLRI   232   1582   A   2596   1   391   STVTGQPRILDTAGHQQPFLELKIRAI   GRARRITPTCEPATPL.CCRDHYVNFQ   RDWILLPEGYQLNYCSGQCPTHLAGSP   FHSAVFSLLKANNPWPGRTSWCVPTAF   LLYL     233   1583   A   2601   184   403   LLFSDEIIMAAPLRIADVTSGLIGGEDGF   YNGKETTLGDMTGKCKSWITPCPEEKV   NSIPYWERIT     234   1584   A   2614   178   335   PLTLCLPENNKPPQADAVPDKELTLPVI   DGSKSSDDQKIISYLWEKTQ     235   1585   A   2616   2   896   DVLEVYGTGVASTRHEMGTLDKHKEL   AKFLNVEAAMVFGMGFATNSMNIPAL   CLILRDEVNHTSLVLGARLLGATIGIFK   QSLEKLLRDAVIYGQPRTRAWKKILII   YSMEGSIVHLPQIIALKKKYKAYLYIDE   GAVGPTGRGVTEFFGLDPHEVDVLMG   FGASGGYIAGRKARILSPPACLVPNTGS   RLTRDLQMNEAMVALVTDRLQGWNSG   WDRADKFGDLVDYLRVHSHSAVYASS   AEQIIRSLKLIMGLDGTTQ     236   1586   A   2621   1   392   NTSSFPAQPSSPARPSLPHLSQHPSNPLI   ADHPQCGRFLPLHEPEPLCPSPSLSYPTI   WSSPFSSHHGCPPGLYPFTSSKTIQPPG   KMLCIPPGRQQLRGAQSMPGHGALSPI	SK IEPGA ELGW GIAAS IRPLS
232 1582 A 2596 I 391 STVTGQFRRLDTAGHQQPFLELKIRAI GRARRRTPTCEPATPLCCRRDHYVNFQ RDWILLPEGYQLNYCSGQCPTHLAGSP FHSAVFSLLKANNPWPGRTSWCVPTAI LLYL  233 1583 A 2601 184 403 LLFSDEIIMAAPLRIADVTSGLIGGEDGI YNGKETTLGDMTGKCKSWITPCPEEKV NSIPYWERIT  234 1584 A 2614 178 335 PLTICLPENNKPPQADAVPDKELTLPVI DGSKSSDDQKIISYLWEKTQ  235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLVIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSW WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGIDGTTQ  236 1586 A 2621 I 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFTSFKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	IEPGA ELGW GIAAS RPLS
GRARRÄTPTCEPATPLCCRRDHYVNFQ RDWILLPEGYQLNYCSGQCPTHLAGSP FHSAVFSLLKANNPWPGRTSWCVPTAI LLYL  233 1583 A 2601 184 403 LLFSDEIIMAAPLRIADVTSGLIGGEDGH YNGKETTLGDMTGKCKSWITPCPEEKY NSIPYWERIT  234 1584 A 2614 178 335 PLTLCLPENNKPPQADAVPDKELTLPVI DGSKSSDDQKIISYLWEKTQ  235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLIGATIGIFK QSLEKLLRDAVIYGQPRTRAWKKILII YSMEGSIVHLPQIIALKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSW WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	ELGW GIAAS RPLS
RDWILLPEGYQLNYCSGQCPTHLAGSP FHSAVFSLLKANNPWPGRTSWCVPTAH LLYL  233 1583 A 2601 184 403 LLFSDEIIMAAPLRIADVTSGLIGGEDGH YNGKETTLGDMTGKCKSWITPCPEEKY NSIPYWERIT  234 1584 A 2614 178 335 PLTLCLPENNKPPQADAVPDKELTLPVI DGSKSSDDQKIISYLWEKTQ  235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNS WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFTSPKTIQPPO KMLCIPPGRQQLRGAQSMPGHGALSPI	GIAAS RPLS
FHSAVFSLLKANNPWPGRTSWCVPTAILLYI   233   1583   A   2601   184   403   LLFSDEIIMAAPLRIADVTSGLĪGGEDGI YNGKETTLGDMTGKCKSWITPCPEEKV NSIPYWERIT     234   1584   A   2614   178   335   PLTLCLPENNKPPQADAVPDKELTLPVI DGSKSSDDQKIISYLWEKTQ     235   1585   A   2616   2   896   DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMGFGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSW WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ     236   1586   A   2621   1   392   NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFTSPKTIQPPGKMLCIPPGRQQLRGAQSMPGHGALSPI	RPLS
233 1583 A 2601 184 403 LLFSDEIIMAAPLRIADVTSGLĪGGEDGH YNGKETTLGDMTGKCKSWITPCPEEKV NSIPYWERIT  234 1584 A 2614 178 335 PLTLCLPENNKPPQADAVPDKELTLPVI DGSKSSDDQKIISYLWEKTQ  235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSI WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	
233 1583 A 2601 184 403 LLFSDEIIMAAPLRIADVTSGLIGGEDGIG YNGKETTLGDMTGKCKSWITPCPEEKYNSIPYWERIT  234 1584 A 2614 178 335 PLTLCLPENNKPPQADAVPDKELTLPVIDGSKSSDDQKIISYLWEKTQ  235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFKQSLEKLLRDAVTYGOPRTRAWKKILIIYSMEGSIVHLPQIIALKKKYKAYLYIDEGAVGPTGRGVTEFFGLDPHEVDVLMGFGASGGYIAGRKARILSPPACLVPNTGSRLTRDLQMNEAMVALVTDRLQGWNSWWDRADKFGDLVDYLRVHSHSAVYASSAEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLIADHPQCGRFLPLHEPEPLCPSPSLSYPTIWSSPFSSHHGCPPGLYPFTSPKTIQPPGKMLCIPPGRQQLRGAQSMPGHGALSPI	VYV
YNGKETTLGDMTGKCKSWITPCPEEKY NSIPYWERIT  234 1584 A 2614 178 335 PLTLCLPENNKPPQADAVPDKELTLPVI DGSKSSDDQKIISYLWEKTQ  235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGOPRTRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSI WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	- · - ·
NSIPYWERIT  234 1584 A 2614 178 335 PLTLCLPENNKPPQADAVPDKELTLPVI DGSKSSDDQKIISYLWEKTQ  235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGOPRTRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSI WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	NVLO
234 1584 A 2614 178 335 PLTLCLPENNKPPQADAVPDKELTLPVDGSKSSDDQKIISYLWEKTQ 235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMGFGASGGYIAGRKARILSPPACLVPNTGSRLTRDLQMNEAMVALVTDRLQGWNSWDRADKFGDLVDYLRVHSHSAVYASSAEQIIRSLKLIMGLDGTTQADATASAEQIIRSLADATASAEQIIRSLA	
235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYJIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNS WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	STTL
235 1585 A 2616 2 896 DVLEVYGTGVASTRHEMGTLDKHKEL AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSG WDRADKFGDLVDYLRVHSHSAVYASS AEQURSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	
AKFLNVEAAMVFGMGFATNSMNIPAL CLILRDEVNHTSLVLGARLLGATIGIFK QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNS WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	EDLV
QSLEKLLRDAVIYGQPRTRRAWKKILII YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSG WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	VGKG
YSMEGSIVHLPQIIALKKKYKAYLYIDE GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSI WDRADKFGDLVVPLRVHSSAVYASS AEQIIRSLKLIMGLDGTTQ  1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	AYM
GAVGPTGRGVTEFFGLDPHEVDVLMG FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNS WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	VEGV
FGASGGYIAGRKARILSPPACLVPNTGS RLTRDLQMNEAMVALVTDRLQGWNSG WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTG WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	AHSI
RLTRDLQMNEAMVALVTDRLQGWNSG WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTG WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPL	<b>IFTKS</b>
WDRADKFGDLVDYLRVHSHSAVYASS AEQIIRSLKLIMGLDGTTQ  236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPC KMLCIPPGRQQLRGAQSMPGHGALSPI	
236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLI ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPC KMLCIPPGRQQLRGAQSMPGHGALSPI	
236 1586 A 2621 1 392 NTSSFPAQPSSPARPSLPHLSQHPSNPLL ADHPQCGRFLPLHEPEPLCPSPSLSYPT WSSPFSSHHGCPPGLYPFPTSPKTIQPPC KMLCIPPGRQQLRGAQSMPGHGALSPL	MSPPI
ADHPQCGRFLPLHEPEPLCPSPSLSYPTI WSSPFSSHHGCPPGLYPFPTSPKTIQPPC KMLCIPPGRQQLRGAQSMPGHGALSPL	DT 40
WSSPFSSHHGCPPGLYPFPTSPKTIQPPG KMLCIPPGRQQLRGAQSMPGHGALSPI	
KMLCIPPGRQQLRGAQSMPGHGALSPL	
	DDII
237 1587 A 2628 398 1 DLVCKISGFGRGPRDRSEAVYTTMSGR	SPAI.
WAAPETLOFGHFSSASDVWSFGIIMWE	
GERPYWDMSGQDVIKAVEDGFRLPPPI	
LMHRLMLDCWOKDPGERPRFSQIHSIL	
QDPEPPNV	
238 1588 A 2631 I 1104 WSPCSLTCGVGLQTRDVFCSHLLSREM	NETV
ILADELCRQPKPSTVQACNRFNCPPAW	YPAQ
	SFLE
LPETFCSASKPACQQACKKDDCPSEWL	
TECSTSCGEGTQTRSAICRKMLKTGLST	
TLCPPLPFSSSIRPCMLATCARPGRPSTK	
AAARKYYIQTRRQRKLHFVGGGFAYL	
VVLRCPARRVRKPLITWEKDGQHLISS*	
VAPFGYLKIHRLKPSDAGVYTCSAGPA	
VIKLIGGNRKLVARPLSPRSEEEVLAGR	REHF
KEALQTHKHQNGIFSNGSKAEKRGLAA	REHF KGGP
RYDDLVSRLLEQGAPCSSSKKKN	REHF KGGP
239 1589 A 2636 1 678 MKPDNILLDEHGHVHITDFNIAAMLPR	REHF KGGP NPGS
TMAGTKPYMAPEMFSSRKGAGYSFAV	REHF KGGP NPGS ETQIT
SLGVTAYELLRGRRPYHIRSSTSSKEIVI TVVTVPSAWSOEMVSI I VKI I EDNIDIV	REHF KGGP NPGS ETQIT DWW
TVVTYPSAWSQEMVSLLKKLLEPNPDO LSDVQNFPYMNDINWDAVFQKRLIPGE	REHF KGGP NPGS ETQIT DWW ITFET
GRLNCDPTFELEEMILESKPLHKKKKRI	REHF KGGP NPGS ETQIT DWW HTFET QRFSQ
EKDMRKCDSSQTCLLQEHLDSVQKEFI	REHF KGGP NPGS ETQIT DWW HIFET ORFSQ IPNK
KVNRDCI	REHF KGGP NPGS ETQIT DWW HTFET QRFSQ IPNK AKK
240 1590 A 2639 389 3 ELLDPTTPMRTKCIELLYAALTSSSTDQ	REHF KGGP NPGS ETQIT DWW HTFET QRFSQ IPNK AKK
LWQNFAREIEEHVPTLYSKNIKKYKTC	REHF KGGP NPGS ETQIT DWW HTFET PRFSQ IPNK AKK UNRE
ANI,KNPRNSHI,QQNLJ,SGTTSPREFAE	REHF KGGP NPGS ETQIT DWW HTFET RFSQ IPNK AKK IINRE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Scrine,
	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
]	1	i	Į.	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
!	!	ļ		!		EMANKELKOLRASYTESCIOEHYLPOVIDGTL
		<u> </u>		L		Y
241	1591	A	2640	392	3	IRLTILRCVFMRLATICVLVFTLGSKITSCDDD
	·		i		]	TCDLCGYNQKLYPCWETQVGQEMYKLMIFD
	[	1	[		Ĭ	FIIILAVTLFVDFPRKLLVTYCSSCKLIQCWGQ
			1			QEFAIPDNVLGIVYGQTICWIGAFFSPLLPAM
242	1592	A	0640	40.5	ļ <u>.                                    </u>	Y
242	1392	Α	2642	405	1	YFKNTTLLLVGVICVAAAVEKWNLHKRIALR
1		ĺ	1			MVLMAGAKPGMLLLCFMCCTTLLSMWLSNT
		1			l	STTAMVMPIVEAVLQELVSAEDEQLVAGNSN
		ł				TEEAEPISLDVKNSQPSVELIFVNEDILDFLMK
243	1593	A	2646	412	2	SPLMISQACI
		l ''	2040	712	*	CLAMIKGIQSSGKIIYFSSLFPYVVLICFLIRAF
			1			LLNGSIDGIRHMFTPKLEIMLEPKVWREAATQ
			i		!	VFFALGLGFGGVIAFSSYNKRDNNCHFDAVL
			1 1			VSFINFFTSVLATLVVFAVLGFKANVINEKCIT ONSETV
244	1594	A	2650	1	1271	MTTTLIGLLKTARLLRLVRVARKLDRYSEYG
			-05,0	•	12/1	AAVLMLLMCIFALIAHWLACIWYAIGNVERP
			1			YLTDKIGWLDSLGQQIGKRYNDSDSSSGPSIK
		1	1			DKYVTALYFTFSSLTSVGFGNVSPNTNSEKIF
i j						SICVMLIGSLMYASIFGNVSAIIQRLYSGTARY
i 1						HMQMLRVKEFIRFHQIPNPLRQRLEEYFQHA
						WTYTNGIDMNMVTNGTCSSCTSDDGHFILVS
			l i			NHHQGGLIYSWNDAASMQRPFNHIKSSLLGS
						TSDSNLNKYSTINKIPOLTLNPSEVKTEKKNSS
						PPSSDKTIIAPKVKDRTHNVTEKVTQVLSLGA
]						DVLPEYKLQAPRINKFTILHYSPFKAVWDWLI
						LLLVIYTAIFTPYSAAFLLNDREEQKRRECGY
						SCSPLNVVDLIVDIMFIIDILINFRTTYVNONEE
245	1595		2666	205		VVSDPASV
243	1393	Α	2656	385	2	NLTWWPLFRDVSFYIVDLIMLIIFFLDNVIMW
İ			1	,		WESLLLLTAYFCYVVFMKFNVQVEKWVKQ
	ĺ	- 1			i	MINRNKVVKVTAPEAQAKPSAARDKDEPTLP
İ		1	1			AKPRLQRGGSSASLHNSLMRNSIFQNKIHTLD
246	1596	A	2660	200	506	PHV
		**	2000	200	200	VLVLQMNYYQMLIIYYVLFFKVNEFLAFEGPI
						LLDMRIKHLIKTNQLSQATALAKLCSDHPEIG IKGSFKQTYLVCLCTSSPNGKLIEEVSMFSFIS
	1	]				NYFLS NYFLS
247	1597	A	2678	3	267	DAWVKNDIIFNQTERKQKISENLKHLASVRV
		-		·	~~'	VQKNLVFVVGLSQRLADPEVSPLVFFVILIFF
	ł	l				VSLSYLEIFDPAQLCDSSEHIIS
248	1598	Ā	2687	1	404	DFTTLAAMMRTLFSLFGDVRSDVHRFSVTLF
	ĺ			-		GAAIKSVKNPDKKSIENQVLDSLVPLLLYSQD
	1		1	1	1	ENDAVAEESRQVLTICAQFLKWKLPREVYSK
-		1	•	į	- 1	DPWHIKPTEAGTICRFFEKKCKGKINILEQTL
			1			MYSKNPKL
249	1599	A	2692	1	440	FRRRRRRERDCAAQGARRHCRHLAECKLV
Ī			1			SFPIGIYKVLRNVSGQIHLITLANNELKSLTSK
			1		l	FMTTFSQLRELHLEGNFLHRLPSEVSALQHLK
1	ĺ	- 1	1	ŀ	1	AIDLSRNQFQDFPEQLTALPALETINLEENEIV
					j	DVPVEKLAAMPALRSINL
250	1600	A	2693	459	21	LLPGSLGVPILHSQPWDPSPQCPHRAPSTPRRL
	j	İ	Í		ľ	PPLGALSQALTFLSRAAKNHSQDPGKGTKPFP
Ì				ĺ	ļ	AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF
1		Ì			İ	NSPWHPATLPGALGPQLSQAAPSPIPPPCLMG
	[					ISSCPDLKLTKSSTP
251	1601	A	2694	2	404	FVFDLKLRVPGFAALLIHGASSVPGPETVRLR
						The state of the s

SEQ ID	CEATA	Met	CEO	Predicted	Desilered and	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	SEQ ID NO: of	hod	SEQ ID NO:	beginning	Predicted end nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
1	İ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
-	<b>,</b>		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide		/-possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
<del> </del>	<del></del>		<del>                                     </del>			OKRKKKAPDHSSGRKEELVTTHTVDKLETKK
· .						PVGRVLCGLSGELLHSLLLPRRKTEKRALGSH
	i				1	RKAGFPEHPVAPEPLSNSCQISKEGREQVLSEI
ļ						GAGDCL
252	1602	A	2697	421	1	PQKSHSGAYQCFATRKAQTAQDFAIIALEDG
1		1				TPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPT
		ľ				VTWALDDEPIVRDGSHRTNQYTMSDGTTISH
		ļ				MNVTGPQIRDGGVYRCTARNLVGSAEYQARI
1		i				NVRGPPSIRAMRNIT
253	1603	A	2698	65	401	ACCOWRRTLIPAKSTTVSCTISTPHHPFRGSYS
	1		}			FDDHITDSEALSRSSHVFTSHPRMLKRQPAIEL
	1			,		PLGGEYSSDVPRPLSTQLSSSLLGYFSTLMTG
		]				AAFTNNIASSTIIL
254	1604	Α	2699	438	301	GQIHSQDDPPFIDQLGFGVAPGFQTFVACQEQ
						RVRGPWEAGPGVGY
255	1605	Α	2700	1	842	LQNREDSSEGIRKKLVEAEELEEKHREAQVS
1	ļ					AQHLEVHLKQKEQHYEEKIKVLDNQIKKDLA
						DKETLENMMQRHEEEAHEKGKILSEQKAMIN
· <b>[</b>	l	1				AMDSKIRSLEQRIVELSEANKLAANSSLFTQR
İ					<i>'</i>	NMKAQEEMISELRQQKFYLETQAGKLEAQN
1						RKLEEQLEKISHQDHSDKNRLLELETRLREVS
}						LEHEEQKLELKRQLTELQLSLQERESQLTALQ
1		ŀ				AARAALESQLRQAKTELEETTAEAEEEIQALT
						VGLGSNIFRLLKASARMSVELALSILAHP
256	1606	Α	2701	2	405	FVGGPGADPPVAVMWDPRAARMDLTAYAE
	1	İ	1			LLKESGNQVLKNGNFSLAIRKYDEAIQILLQL
			ļ			YQWGVPPRDLAVLLCNKSNAFFSLGKWNEA
						FVAAKECLQWDPTYVKGYYRAGYSLLRLHQ
			<u> </u>			PYEAARMFFEGLR
257	1607	Α	2702	2	399	FVESASSRPPGCFSGDGRFWLVSEGSRRGWD
	ļ	}	1			FNPSFSFLDPRYSVGGDENIGTVTTLANILREF
			]			NPSLKGFSVGTGKETSPNAFLNQAVAGGRAE
!			1			DLPVQARRLVDLMKNDTRIHFQEDWKIITLFI
	1.000					GGNDL
258	1608	Α	2709	1	1097	SVGARQGEARDRIRRFFPKGDLEVLQAQVERI
(		1				MTRKELLTVYSSEDGSEEFETIVLKALVKACG
		1		'		SSEASAYLDELRLAVAWNRVDIAQSELFRGDI
1		ł				QWRSFHLEASLMDALLNDRPEFVRLLISHGLS
1	}	1				LGHFLTPMRLAQLYSAAPSNSLIRNLLDQASH
		1			·	SAGTKAPALKGGAAELRPPDVGHVLRMLLG
ļ	J.	1	1			KMCAPRYPSGGAWDPHPGQGFGESMYLLSD
		1				KATSPLSLDAGLGQAPWSDLLLWALLLNRA OMAMYFWEMGSNAVSSALGACLLLRVMAR
1	]	1	<i>.</i>	] ,		LEPDAEEAARRKDLAFKFEGMGVDLFGECYR
1	İ	1				SSEVRAARLLLRRCPLWGDATCLQLAMQAD
	1	j	}			ARAFFAQDGVQSLPTQKWWGDMARR
259	1609	A	2721	1	403	VYLGAGPGLFFSNEGAKEGEKANIPKLMLPR
1237	1009	) ^	2121		נטד	GGFSQREMVTGERSPSPEEEEEEEEEGFGERA
	1		1			SCRRGLFRVRLTRVGLAAPSKASRGQEGDAA
ļ						PKSPVREKSPKFRFPRVSLSPKARSGSGDQEE
ĺ	ĺ	1				GGLRVRLP
260	1610	A	2728	1	477	
200	1010	Ι ^	2128	"	4//	LLGGDLRYHLQQNVHFTEGTVKLYICELALA
	1	1				LEYLQRYHIIHRDIKPDNILLDEHGHVHITDFN IATVVKGAERASSMAGTKPYMAPEVFQVYM
		ł				
		1				DRGPGYSYPVDWWSLGITAYELLRGWRPYEI HSVTPIDEILNMFKVERVHYSSTWCKGMVAL
		l	1		]	LRK
261	1611	A	2730	3	547	LTITDFILVLYRYYRSPLVQIYEIEQHKIETWR
201	1011	1 🙃	2130	٠ .	) J4/	EIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIH
L		<u> </u>		L	!	TITING OF TITING OF THE OWN AND THE WAY IN

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide	ì	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	i	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
.			1	peptide		/=possible nucleotide deletion, /=possible
<b>  </b>			<b></b>	sequence	<del> </del>	nucleotide insertion
1 1					ł	RLPVLDPVSGNVLHILTHKRLLKFI,HIFGSLLP
						RPSFLYRTIQDLGIGTFRDLAVVLETAPILTAL DIFVDRRVSALAVVNECGTHPODERLGLGW
					ĺ	GLGEPGSEERLFPAAITSR
262	1612	A	2733	3	431	GPEFPGSAKLVFLDLSYNNLTOLGAGAFRSA
					1 -0.	GRLVKLSLANNNLVGVHEDAFETLESLOVLE
			•			LNDNNLRSLSVAALAALPALRSLRLDGNPWL
}					ļ	CDCDFAHLFSWIQENASKLPKGLDEIQCSLPM
1						ESRRISLRACRRPASRV
263	1613	Α	2736	2	343	PARISGVDPPVRKATKGGENCSFEDNKNWQF
						LWGLNGNFNFFKEPWGGRNNHAKGFRTTW
		i				ARSSSQNNRTFQNNRNFLRLQRDSQKKGQFA
						RLISPLVNLPQSPGGLEFQYQAT
264	1614	A	2738	2	245	RAMLKCLREGQPPPSYNWTRLDGPLPSGVRV
						DGDTLGFPPLTTEHSGIYVRHDTNEFSSRDSH
						DTVDVLDPPEDSGKQVDL
265	1615	Α	2752	2	388	AAGDAPLRSLEQANRTRFPFFSDVKGDHRLV
1 1		1				LAAVETTVLVLIFAVSLLGNVCALVLVARRR
	-					RRGATACLVLNLFCADLLFISAIPLVLAVRWT
ł l						EAWLLGPVACHLLFYVMTLSGSVTILTLAAV
266	1616		0055	100		SLER
200	1010	A	2755	192	1	AFREVGGYWGLLCEHLYAIPSKTSEGNWTAK
,		1				LQGYLPLQDAFHIFQDPLTGDLPWPELILGLP
267	1617	A	2760	434	714	A SEL EN ONISTRES DA DINTENTONI E PROCESCIONA
""	.017	^	2/00	734	/14	ASRLEKONSTPESDYDNTPNDMEPDGMGYM
		1	1			HRTSVPGEGLPRARDLAGLGQQKQFTTHTPP LYFQTHKGLKDSSIRSEVTCLGISQCWRKGFF
268	1618	A	2762	1	405	IACTFCGQDEWSPERSTRCFRRRSRFLAWGEP
				-		AVLLLLLLSLALGLVLAALGLFVHHRDSPL
	1		}			VQASGGPLACFGLVCLGLVCLSVLLFPGQPSP
	1	İ				ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE
		]				LPLSWAE
269	1619	Α.	2772	3	243	TRPAEKIQYLVLFFVMSHPSQAYDKLSLSDHL
		}	. 1			LIAVLNLLRREVSEHGRHLQQYFNLFVMYAN
						LSKNLSFSEFCFDVSY
270	1620	A	2789	1	486	ELQSQQACTHTKETEQLRSQLQTLKQQHQQA
	ŀ	- 1	I		ł	VEQIAKAEETHSSLSQELQARLQTVTREKEEL
	Į	į	Ì			LQLSIERGKVLQNKQAEICQLEEKLEIANEDR
	ĺ	l				KHALERFEQEAVAVDSNLRVRELQRKVDGIQ
	. }		1			KAYDELRLQSEAFKKHSLDLLSKERELNGKL
271	1621	A	2705	<del>,                                    </del>	560	RHLSP
2/1	1021	A	2795	1	568	KEKRVTVQLPTESIQKNQEDKLKMVPRKQRE
	-	- 1			I	FSGSDRGKLPGSEEKNQGPSMIGRKEERLITE
	- 1	- !	}	*	j	RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN
			]			FQQTQIQTAESKAEHKKLPQPYNSLQEEKCLE VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE
	ł					SQRDDGKGALNIVEFLRKREELHQILSTVKQP
272	1622	A	2797	8	523	KCMQGKYAGAMESEPCVCTEADFDCDYGYE
		- 1	2,3,	~	120	RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNST
		ł	- 1	ĺ		GYRKVVSNNCTDGVREQYTAKPQKCPGKAP
				l		RGLRIVTADGKLTAEOGHNVTLMVOLEEGD
l			1			VQRTLIQVDFGDGIAVSYVNLSSMEDGIXHV
İ		- 1				YQNXGIXRXTVQVDNSLGS
273	1623	A	2801	72	395	HPSRSNVGPRQLTVWNTSNLSHDNRRKYIFS
İ		j		.	1	DEEGQNQLGIRIHQDIPLPPRRRELPALRTTNG
. ]	i	- 1	]	}	]	KADSLNVSRNSVMQELSELEKQIQVIRQELQL
	1					
		_	_ ]	J	ļ	AVSRKTELEEYH
274	1624	A	2805	168	320	

LOROTO	1 000 10	T 3 7 4	1 000	Des It is 1	N 41 4 4	(A. Alada C. C. a.)
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in NO.	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-		USSN	location		F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
	uence	1	09/496	correspondi	corresponding to last amino	
seq- uence	dence	ł	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
dence	1		717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
[	[	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		1	1	peptide	sequence	
Ī				sequence		/=possible nucleotide deletion, \=possible nucleotide insertion
275	1625	A	2812	208	321	GSLATCQLSEPLLWFILRVLDTSDALKAFHD
2/3	1023	^	2012	200	321	MGKIIFO
276	1626	Ā	2813	41	266	AGRSLHGAGDRAWVGISPTDWSPKVVELCK
270	1020	Α .	2013	41	200	
	·	1				KYQQQTVVAIDLAGDETIPGSSLLPGHVQAY QVGPVRRNGEAGPG
277	1627	A	2817	3	410	
12"	1027	Α	2017	) 3	1 410	VLQERLDNFQRKCIQLASSTEGKVDKLLMRN
ļ	ļ	1				LFISYLHTPKHKQHEVLQAMGSILGITGEEME
	1		1			PLFQEEHGTATRWMTGWLEGGSKSVPKTPL
ŀ					}	GLNQQPALNGSFSELFVKFLKTESLSSTLPTX
278	1628	A	2821	238	457	LPPHNSPGKIK
2/0	1028	Α.	2021	238	437	GLSGPSCSCPHSPLPTIISRAQLETALKWRNYE
						VKLRLLLHLEELQMEHDIRHYDLESVPMTWD
279	1629	<u> </u>	0000	240		PVDQNPRLV
2/9	1029	A	2822	342	1	PLIPANLPAHSNPLQPLPSLPHPFLPATHKFPT
	i	1				TPPTFSSVPPPLPSLSSILHHSPLHSELNPHLQS
		1				CRLPSRPSVSRELPPQSGPASSVPLAPTPLPDS
280	1630	<del>  .                                     </del>	0006	307	-	VPSQRHPTXPPPAS
280	1050	A	2825	307	77	PSMVWSYHWGVKQKRLALCVFSFEEGGRRK
	<u> </u>	[				CGQYWPLEKDSRIRFGFLTVTNLTGAVGEPG
281	1631	<u> </u>	0000	01	201	VAFQCDGQRRREPTC
281	1631	Α	2827	81	381	KMGTAVWVPKEKEKRDKASQEGGDVLGAR
l	İ	ľ				QDCTPSLKSLVATGNLLDLEETAKAPLSTVSA
1		l		·		NTTNMDEVPRPQALSGSSVVWVSGCVASRS
282	1632	<b> </b>	2830	401	150	VILSLTSG
202	1032	A	2830	471	160	KLPXDKYELEPSPLTQYILERKSPHTCWQVFV
						TSSGKYNELGYPFGYLKASTTLTCVNLFVMP
		ļ				YNYPVLLPLLDDLFKVHKLKPNLKWRQAFDS
283	1633	A	2835	462	148	YLKTLPPYYL VSPALSLTPTIFSYSPSPGLSPFTSSSCFSFNPEE
203	1033	] ^	2033	402	140	MKHYLHSQACSVFNYHLSPRTFPRYPGLMVP
		ļ				
		1				PLQCQMHPEESTQFSIKLQPPPVGRKNRERVE SSEESAP
284	1634	A	2836	2	384	KTLPRTLLDILADGTILKVGVGCSEDASKLLQ
204	1034	[ ^	2030	2	304	DYGLVVRGCLDLRYLAMRQRNNLLCNGLSL
	l	ŀ				KSLAETVLNFPLDKSLLLRCSNWDAETLTED
		1				QVIYAARDAQISVALFLHLLGYPFSRNSPGEK
	[	ſ				KR
285	1635	A	2843	20	271	PIRPYYSYSGLDRDCSWLPLAKAWLPDVMIL
200	1033	^	2073	20	2/1	VCDRVSEDGINRQQAQEWCIKHGFELVELSP
		1		!	!	EELPEEDGKCLCVRRKYGTYI
286	1636	A	2845	197	278	TAEDVLTVAYEHGVNLFDTAEVYAAGK
287	1637	Ā	2851	2	427	FVAEVRREWAKYMEVHEKASFTNSELHRAM
207	103/	^	2031	-	741	NLHVGNLRLLSGPLDQVRAALPTPALSPKDK
	j '					AVLQNLKRILAKVQEMRDQRVSLEQQLRELI
		l				QKDDITGSLVTTDHSQMKKLFEEQLKKYDQL
		1	1			KVYLEQNLAAQDRVLCALT
288	1638	À	2859	2	469	FVNLGILTCIECSGIHREMGAHISRIQSLELDK
200	1038	^	2037	-	107	
		l				LGTSELLPAKNVGNNSFNDIMEANLPSPSPKP
		l				TPSSDMTVRKEYITAKYVDHRFSRKTCSTSSA
		[				KLNELLEAIKSRDLLALIQVYAEGVELMEPLL
289	1639	A	2861	2	454	EVASCODATA DAS DE COMO A ESPECITO A TANDA
207	1039	^	2001		434	FVASGGPATARMSDSQFFCVAEERSGHCAVV
		[	1			DGNFLYVWGGYVSIEDNEVYLPNDEIWTYDI
			] .			DSGLWRMHLMEGELPASMSGSCGACINGKL
		1				YIFGGYDDKGYSNRLYFVNLRTRDETYIWEK
290	1640	A	2868	1	378	ITDFEGQPPTPRDKLSCWVYKDRLIYFG
200	1040	^	2000	•	310	FRQGQLYKVFLHGSQGQVYHSQQVGPPGSAI
		[				SPDLLLDSSGSHLYVLTAHQVDRIPVAACPQF
	L	<u> </u>	1ل		L	PDCASCLQAQDPLCGWCVLQGRCTRKGQCG

SEQ ID	SEQ ID	Met	SEQ	Predicted	I Designation 1	
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1.00	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	i		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			Į.	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	ļ ·	/=possible nucleotide deletion, \=possible
L			1	sequence	j .	nucleotide insertion
1	1	1				RAGQLNQWLWSYBEDSHCLHIQSLLPGHHPR
201	<del> </del>	1	1	<u> </u>	<u> </u>	QE
291	1641	A	2870	1	385	FRYMPNNRQQLLRKRHIGNDIVTIVFQEPGAL
	[	ĺ		Į		PFTPKSIRSHFQHVFVIVKVHNPCTENVCYSV
	1	1				GVSRSKDVPPFGPPIPKGVTFPKSAVFRDFLL
1				ļ		AKVINAENAAHKSEKFRAMATRTRQEYLKD LA
292	1642	A-	2877	3	188	RPTRPPPATTQSPESTMDTSLKKEKSAILDLYI
	1.7.2	''	20//	13	100	PPPPAVPYSPRYVAVHCHGMLVSCWCHL
293	1643	A	2878	<del>                                     </del>	427	REKEEEVBEEEDKVVKETEKEAEQEKEEDSL
				•	127	GAGTHPDAAIPSGERTCGSEGSRSVLDLVNYF
1.		i		ł	l	LSPEKLTAENRYYCESCASLQDAEKVVELSQ
i		ļ		1	-	GPCYLILTLLRFSFDLRTMRRRKILDDVSIPLL
<u> </u>				f		LRLPLAGGRGQAYDL
294	1644	A	2879	109	245	QLCCFCFRQTTLIVYILSFIGMVIFTFTLDLRYI
L	<u> </u>				<u> </u>	IIVFVTGGVLG
295	1645	Α	2880	3	320	LASSQHGILNNLSLLFSICKTCIRTMDHHCPRA
		İ				NNCVGEQNHRFFCALHCKSKHFCIEFTLNTNF
	ŀ		j .		1	FNCFLPGAEKSTIDAPFSLQPFLQDSKYNTALS
296	1646	A	2000		260	LSESISQ
290	1040	A.	2892	209	363	SQYSHSLDYHLLQVTKNPFTLGDSSNPGQTE
297	1647	A	2893	8	424	RLQEFSQKMDQVRGHWPVST
-5,	1047	^	2093	•	424	SPXTLXLDTFILLGIQDNILVLILATPPFMAGG
		Ì	1			KLYSTMGRFLRDRKNPACREMAVVLLANLA QGDSLAARAIAVQKGSIGHLLGFLEDSLAAT
						QIQQSQASLLHMHNPPFEPTSVDMMRRACRA
						LLALAKVDDNHSEF
298	1648	A	2894	310	445	FWIYFPSFFMTGYLPLGFEFAVEITYPESEGTS
						SGLLNASAQVNL
299	1649	A	2898	1	492	KIKAKNLTNYDLCSIFLGTSTLLVWVGVIRYL
ł						GYFQAYNVLILTMQASLPKVLRFCACAGMIY
ļ		1	j l			LGYTFCGWIVLGPYHDKFENLNTVAECLFSL
			1 . [			VNGDDMFATFAQIQQKSILVWLFSRLYLYSFI
			1 1			SLFIYMILSLFIALITDSYDTIKKFQQNGFPETD
300	1650	Ā	2901	1	445	LQEF
300	1030	^	2501	1	445	PVWWNSLNGASEVTFSVHVKDGGSFPKTDST
1	. 1		1			TVTVRFVNKADFPKVRAKEQTFMFPENQPVS
						SLVTTITGSSLRGEPMSYYIASGNLGNTFQIDQ LTGQVSISQPLDFEKIQKYVVWIEARDGGVPP
			1			FSSYEKLDITVLDVNDNAPIF
301	1651	Α	2902	162	433	THFICLPLGYCFPLLDKDLQLPSGFNCNFDFLE
						EPCGWMYDHAKWLRTTWASSSSPNDRTFPG
				j		KPAVSEDMKELRPACSTYFNPRFPYKL
302	1652	Α	2909	2	412	<b>OPQMLCKKIYFIWVTRSQCQFEWLADIMQEV</b>
				i		EENDHQDLVSVHIYVTQLAEKFDLRTTMLYI
				i	ļ	CERHFQKVLNRSLFTGLRSITHFGRPPFEPFFN
			1 1		İ	SLQEVHPQVRKIGVFSCGPPGMTKNVEKACQ
303	1653	- <u>A</u>	1 2014		450	LVNRQDRAHFM
303	1000	A	2914	291	453	KLNRWLCFFYSWSFGILLYEMVTLGAPPYPE
304	1654	A	2926	179		VPPTSILEHLQRRKIMKRPSSCS
	1007	^	2720	1/7	354	PGVPSQALRKAESLKKCLSVMEAKVKAQTAP
305	1655	<u>A</u>	2938	135	438	NKDVQREIADLGEVGAASLPPSSGPGA
		**	2,50	133	730	GMGYLHAKGILHKDLKSKNVFYDNGKVVIT
			]			DFGLFSISGVLQAGRREDKLRIQNGWLCHLA PEIIRQLSPDTEEDKLPFSKHSDVFALGTIWYE
					İ	LHAREWP
306	1656	A	2944	2	329	VRWNSCVNCSCAFGNGASLSTSLGESSGCLW
	ļ					EIGKWLSCSLLSFPSPLAVLITFCIVTVLGREA
					. [	LTKGALWAVFLLAGSALLCAEVTGVIWROPE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	peptide seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ислес		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
dono			7.1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
İ	J		<u> </u>	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
				sequence	Ì	nucleotide insertion
						SKTKLSFKVSSSA
307	1657	A	2950	2	411	NYLCIAKNSAGSAMGKTRLVVQVPPVIENGL
					Ì	PDLSTTEGSHAFLPCKARGSPEPNITWDKDGQ
	1	l	l	l	ł	PVSGAEGKFTIQPSGELLVKNLEGQDAGTYT
						CTAENAVGRARRRVHLTILVLPVFTTLPGDRS
			}	}		LRLGDRLWLR
308	1658	A	2951	1	407	PTRPPRVRFDNEFDAESQRKRTTSVSKMERM
				ŀ		DSSLPEEEEDEDKEAINGSGNAENRERHSESS
		ĺ				DWMKTVPSYNQTNSSMDFRNYMMRDETLEP
		l	ł	1	1	LPKNWEMAYTDTGMIYFIDHNTKTTTWLDP
,						RLCKKAKAPEDC
309	1659	A	2954	2	179	QDFLTLTLTEPTGLLYVGAREALFAFSMEALE
<u> </u>			<u> </u>			LQGAVRGGAVGGSRACQRARPRGAVLG
310	1660	A	2959	-1	419	QDMMERAIIDTFVGHDVVEPGSYVQMFPYPC
						YTRDDFLFVIEHMMPLCMVISWVYSVAMTIQ
ļ		1	<u> </u>	1		HIVAEKEHRLKEVMKTMGLNNAVHWVAWFI
	1	1				TGFVQLSISVTALTAILKYGQVLMHSHVVIIW
311	1661	A	2963	3	166	LFLAVYAVATIMFCF
311	1001	A	2903	3	465	MKPQMPGLGAPNGYGPGRGRAGVPGGPERR PWVPHLLPFSSPGYLGVMKAQKPGAGEGMK
		1	ł	1	1.	PQKPGLRGTLKPQKSGHGHENGPWPGPCNA
		,	1			RVAPMLLPRLPTPGVPSDKEGGWGLKSQPPS
	1	ĺ				AVONGKLPGHOPPNGYGPGAEPGFNGGLEPO
1		}	1			KI
312	1662	A	2967	3	405	WLAQEWSPCTVTCGQGLRYRVVLCIDHRGM
	2002				'	HTGGCSPKTKPHIKEECIVPTPCYKPKEKLPV
l	1		ł	i	Ì	EAKLPWFKQAQELEEGAAVSEEPSFIPEAWS
		Ì				ACTVTCGVGTQVRIVRCQVLLSFSQSVADLPI
			1			DECEGPKPA
313	1663	A	2969	2	430	VVADNCRQGYLDALRFLERRGLTKEPVLWT
	1	1			1	LVSKEPPAPADGNWDAGCDQRRKGGLSLNW
	ĺ	l				KVPHVQVKDVPNFEQLSPELEAALKKACTRD
	Ĭ	ĺ	İ	ĺ		PSRWARFWHSGPGQVLTYLLLPCTLPFEYIYF
						RSRRLVVWLPDVPADLWWMQ
314	1664	A	2971	422	33	LDXSHNALQRLRPGWLAPLFQLRALHLDHNE
	,		1			LDALGRGVFVNASGLRLLDLSSNTLRALGRH
'		ŀ	1	1		DLDGLGALEKLLLFNNRLVHLDEHAFHGLRA
'		1		1		LSHLYLGCNELASFSFDHLHGLSATHLLTLDL
215	1665	-	2072	<del>                                     </del>	505	SSNRM
315	1665	A	2973	1	525	ITVSTHASGSPFGLEPQSGWLWVRAALDREA
1				[		QELYILKVMAVSGSKAELGQQTGTATVRVSI LNONEHSPRLSEDPTFLAVAENOPPGTSVGRV
İ		1	1		· ·	FATDRDSGPNGRLTYSLQQLSEDSKAFRIHPQ
1	1	ł	1	1	1	TGEVTTLQTLDREQQSSYQLLVQVQDGGSPP
				1		RSTTGTVHVAVLDLNDNT
316	1666	A	2978	2	400	ELVVELVSAGKSGPERNTYEVOVVTGNVPKA
١	1000	1 .	//	-	1 ~~	GTDANVYLTIYGEEYGDTGERPLKKSDKSNK
				1		FEOGOTDTFTIYAIDLGALTKIRIRHDNTGNR
		l .			1	AGWFLDRIDITDMNNEITYYFPCQRWLAVEE
[		ĺ	{		(	DDGQLSRE
317	1667	A	2981	3	440	VLNCQGRPTRPVRINGDGQEVLYLAESDNVR
]		l		*	"	LGCPYVLDPDDYGPNGLDIEWMQVNSNPAH
[	[		[	{	[.	HRENVFLSYQDKRINHGSLPHLQHRVRFAAS
	I	1	1	1		DPSQYDASINLMNLQVSDTATYECRVKKTTM
1		1	1	J	]	ATRKVIVTVQARPAVPMCWTEGQ
318	1668	A	2995	119	414	LPEKEFPIIRKSSSLKVTKCLFTEQPKPIIILRFA
		1		1		ENYDARLLRIDIANTLREQVQELFNKTYGKQ
İ						RRTPGEGHVAAVDREVAGFPVPAEGISGETIH
319	1669	A	2999	2	332	GFFAYTYGRLVVVEDLHSGAQQHWSGHSAEI
<u> </u>				·	<del></del>	

OPA m	T OPO TO	114	1.000			
SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1.	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
1	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		peptide		/=possible nucleotide deletion, \=possible
	ļ	<u> </u>		sequence		nucleotide insertion
!	}	}	}	}		STLALSHSAQVLASASGRSSTTAHCQIRVWD
	l	l		ŀ		VSGGLCQHLIFPHSTTVLALAFSPDDRLLVTL
320	1670	A	3000	693	200	GDHDGRTLALWGTGHL
320	1070	Ι^	3000	093	322	IDESTGLITVNYLDYETKTSYMMNVSATDQA
}		l		ļ	l	PPFNQGFCSVYITLLNELDEAVQFSNASYEAA ILENLALGTEIVRVQAYSIDNLNQITYRFDAY
		i				TSTQAKALFKIDAITVRGWGQGAPFFPI
321	1671	A	3001	6	383	RIPRGKACXTVLORSTGELEGFASSRLPPOPC
	1	1		] ~	303	GWGQSSDLLSRIDLDELMKKDEPPLDFPDTLE
	l	1	1		}	GFEYAFNEKGQLRHIKTGEPFVFNYREHLHR
		L				WNQKRYEALGEIITKYVYELLEKDCNSKKVS
322	1672	A	3007	192	447	ERVRNSLFPGRGDSQCACCPSSPVWVFLETGF
	l .					LFPWLFLQVEVIKKAYMQGEVEFEDGENGK
202						DGAASPRNVGHNIYILAHOLARH
323	1673	A	3019	18	245	KELLFYHLIVNNINFFNTRYAKIHIPIIASVSEH
	ŀ	ŀ				QPTTWVSFFFDLHILVCTFPAGLWFCIKNIND
324	1674	Ā	3020	502	505	ERVFGKRGF
324	10/4	^	3020	523	797 .	LCYFSARYHQRKIFGILYIFTLSAINRKEPNLFI
						YLFIFFEMESHSYTHAGVQRHNLNSLQPLPPG
325	1675	A	3022	2	156	FKRFSCLCFLSSWNYRGAPPGPANF
	10.10	**	5022	-	. 150	NDFLPLYFGWVLTKKSSETLRKAGQVFLEEL GNHKAFKKELRQCRWQVGAL
326	1676	A	3023	38	172	KMVRGSKKLISFFPGGPYGILAGRDPSKGLAT
						FCLNKEALKDEFE
327	1677	A	3027	1	385	LTLEFLLLPAASELAHGKRLACCIVDHKLPEC
						GFYGLYDKILLFKHDPTSANLLOLVRSSGDIO
						EGDLVEVVLSASATFEDFOIRPHALTVHSYRA
						PAFCDHCGEMLFGLVRQGLKCDGCGLNYHK
328	1678	A	3030	13	660	RC
320	10/6	Α	3030	13	569	TTRPTISCQRPGPGLAAGMI.PYTVNFKVSART
					ļ	LTGALNAHNKAAVDWGWQGLIAYGCHSLV VVIDSITAQTLQVLEKHKADVVKVKWAREN
						YHHNIGSPYCLRLASADVNGKIIVWDVAAGV
						AQCEIQEHAKPIQDVQWLWNQDASRDLLLAI
						HPPNYIVLWNADTGTKLWKKSYADNILSFSF
						D
329	1679	A	3038	90	744	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAED
	'			*		GNIEYKKLVNPSQYRFEHLVTQMKWRLQEG
				.		RGEAVYQIGVEDNGLLVGLAEEEMRASLKTL
1	1	- 1	ļ			HRMAEKVGADITVLREREVDYDSDMPRKITE
Ì	ì			- 1		VLVRKVPDNQQFLDLRVAVLGNVDSGKSTL
					1	LGVLTQGELDNGRGRARLNLFRHLHEIQSGR
					Ì	TSSISFEILGFNSKGEVHGINGTQWGQTLRMG W
330	1680	A	3040	3	397	LCSTLLLLTIPSWVLSQITLKESGPTLMKPTET
	}			i		LTLTCTFSGFSLNTSGVGVAWIROPPGKALE
	[	. [			ĺ	WLALIYWDDDKRYSPSLNDRLTIAKDTSRNO
,	ľ			-		VVLTMTNMGPVDTATYYCAQFARGARGSN
221		l				WFDPWGQ
331	1681	Α	3043	3	1509	AGIRHEAPPTTSNRHRRQIDRGVTHLNISGLK
			1			MPRGIAIDWVAGNVYWTDSGRDVIEVAOMK
			1		1	GENRKTLISGMIDEPHAIVVDPLRGTMYWSD
}		J	- 1			WGNHPKIETAAMDGTLRETLVQDNIQWPTG
			- 1			LAVDYHNERLYWADAKLSVIGSIRLNGTDPI
- 1						VAADSKRGLSHPFSIDVFEDYIYGVTYINNRV
- 1	ŀ					PKIHKFGHSPLVNLTGGLSHASDVVLYHQHK QPEVTNPCDRKKCEWLCLLSPSGPVCTCPNG
I			1			KRLDNGTCVPVPSPTPPPDAPRPGTCNLQCFN
					!	GGSCFLNARRQPKCRCQPRYTGDKCELDQC

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide deletion, \=possible nucleotide insertion  WEHCRNGGTCAASPSGMPTCRCPTGFTGPKC TQVCAGYCANNSTCTVNQGNQPQCRCLPG FLGDRCQYRQCSGYCENFGTCQMAADGSRQ CRCTAYFEGSRCEVNKCSRCLEGACVVNKQS
332	1682	A	3045	3	952	GDVTCNCTDGRVAPSCLTCVGHCSNGGSCT MNSKMMPECQCPPHMTGPRCEEHVFSQQQP GHIASILIP TTTISNFHTQVNRTYCCGTYRAGPMRQISLVG
332	1002	C	3045		732	AVDEEVGDYFPEFLDMLEESPFLKMTLPWGT LSSLRLQCRSQSDDGPIMWVRPGEQMIPTAD MPKSPFKRRRSMNEIKNLQYLPRTSEPREVLF EDRTRAHADHVGQGFDWQSTAAVGVLKAV QFGEWSDQPRITKDVICFHAEDFTDVVQRLQ LDLHEPPVSQCVQWVDEAKLNQMRREGIRY ARIQLCDNDIYFIPRNVIHQFKTVSAVCSLAW HIRLKQYHPVVEATQNTESNSNMDCGLTGKR ELEVDSQCVRIKTESEEACTEIQLLTTASSSFP PASE
333	1683	A	3046	497	167	SACSTGPELPGRATRSLTRPANQKGCDGDRL YYDGCAMIAMNGSVFAQGSQFSLDDVEVLT ATLDLEDVRSYRAEISSRNLAVSAPVDTCVG CSSKTWKVAPFVRAWWRP
334	1684	A	3053	37	276	VITDLEEQLNQLTEDNAELNNQNFYLSKQLD EASGANDEIVQLRSEVDHLRREITEREMQLTS QKQVRRVNKVVRSLEDF
335	1685	A	3054	2	846	WDAWGDWSDCSRTCGGGASYSLRCLTGR NCEGQNIRYKTCSNHDCPPDAEDFRAQQCSA YNDVQYQGHYYEWLPRYNDPAAPCALKCH AQGQNLVVELAPKVLDGTRCNTDSLDMCISG ICQAVGCDRQLGSNAKEDNCGVCAGDGSTC RLVRGQSKSITVSPEKREENVIAVPLGSRSVRI TVKGPAHLFIESKTLQGSKGEHSFNSPGVFVV ENTTVEFQRGSERQTFKIPGPLMADFIFKTRY TAAKDSVVQFFFYQPISHQWRQTDFFPCTVT CGGG
336	1686	A	3058	54	347	VVGKQEAGAHSDSCCLLHTPPRLTPAHSRKA LRNSRIVSQKDDVHVCIMCLRAIMNYQVSRG AWDWRLGSPACPHWGLHKLPRLWDPLSLYP VLCWGT
337	1687	A	3059	2	709	ILTSLVELTRFETLTPRFSATVPPCWVEVQQE QQQRRHPQHLHQQHHGDAAQHTRTWKLQT DSNSWDEHVFELVLPKACMVGHVDFKFVLN SNITNIPQIQVTLLKNKAPGLGKVNGLRLCPF LEDHKEDILCGPVWLASGLDLSGHAGMLTLT SPKLVKGMAGGKYRSFLIHVKAVNERGTEEI CNGGMRPVVRLPSLKHQSNKGYSLASLLAK VAAGKEKSSNVKNENTSGTRK
338	1688	A	3060	85	384	KAFYNYHVLELLQMLVTGGVSSQLEQHLDK DKVYGVADSCTSLLSGRNRCKLGLLSLHETIL SDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDE EELNP
339	1689,	A	3063	236	362	CFLCLSGDFMVMTIFFNVSRRFGYVAFQNYV PSSVTTMLSWY
340	1690	A	3065	3	1249	DLWQFTPLHEAASKNRVEVCSLLLSYGADPT LLNCHNKSAIDLAPTPQLKERLAYEFKGHSLL QAAREADVTRIKKHLSLEMVNFKHPQTHETA LHCAAASPYPKRKQICELLLRKGANINEKTKE FLTPLHVASEKAHNDVVEVVVKHEAKVNAL DNLGQTSLHRAAYCGHLQTCRLLLSYGCDPN

NO: of peptide sequence uence    NO: of peptide sequence   Particl	COROLID	T OFF A VIN	137.	1 <del>252</del>		1	
nuclocide older sequence uence USSN (1948) location (1948) loc	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
Sequence			noa			1	
Sequence			1	1 —			
1691   1691   A   3070   1   547	1		ĺ				l=Isoleucine, K=Lysine, L=Leucine,
		ucito	1	1			M=Methionine, N=Asparagine, P=Proline,
	uches	1		714			Terresine Velling Werner,
		İ					V-Turneine V-Linkneum terten ander
	}	ļ				sequence	/www.ible mudestide deletion /www.ible
ISLGGFFALQMINENVOQULQEGISLGNESS   DRQLLEAKAGDUETVIKLETVQSVONESDE   GRQSTPLHFAAGYNRVSVVEYLLQHGADVH   AKDKOGUVPLENACSYGHYEVAELLVYCHOG   GRQSTPLHFAAGYNRVSVVEYLLQHGADVH   AKDKOGUVPLENACSYGHYEVAELLVYCHOG   AVVNVADLWKFTLEHEAAKGKXEKICKLUQ   HGADPITKKNRDGNTPLDLVKDGDTDIQDLE   GDAALLDAKKGCLARVKKLSSPDNVGTLA   GDAALLDAKKGCLARVKKLSSPDNVGTLA   GDAALLDAKKGCLARVKKLSSPDNVGTLA   GDAALLDAKKGCLARVKKLSSPDNVGTLA   GDAALLDAKKGCLARVKKLSSPDNVGTLA   GDAALDAKKGCLARVKKLSSPDNVGTLA   GDAALDAKKGCLARVKKLSSPDNVGTLA   GDAALDAKKGCLARVKKLSSPDNVGTLA   GDAALDAKKGCLARVKKLSSPDNVGTLA   GDAALDAKKGCLARVKKLSSPDNVGTLAGK   GVLIFFORQLARGKSVTSPRNVGTLA   GVLIFFORQLARGKSVTSPRNVGTLA   GVLIFFORQLARGKSVTSPRNVGTLAGK   GVLIFFORQLARGKSVTSPRNVGTLARK   GVLIFFORQLARGKSVTSPRNVGTLAGK   GVLIFFORQLARGKSVTSPRNVGTSLARGK   GVLIFFORQLARGKSVTSPRNVGTSLARGK   GVLIFFORQLARGKSVTSPRNVGTSLARGK   GVLIFFORQLARGKSVTSPRNAKTRIR   AYSOVRPLVASDDDFSGRNVSRGVLDHAB   GROLDGFTTTOGKLMTYKLMABWATDAK   GRUNTUPALBELTGRIGLGVG   GVSTLVAAGLLAATRGLGFM   GVSTLVAAGLGFM   GVSTLVAAGLLAATRGLGFM   GVSTLVAAGLAATRGLGFM		1		1			
DROLLEAAKAGDVETVKKLCTVQSVNCRIDA			<del>                                     </del>	<del> </del>	Joquenee		
GRQSTFLIFRAGYNRVSVEYLLQHSCHEAGHOWNADLWKFTPLIFEAAAKOKYSECKLLLQ	!	i	i	i	i	i	DBUI I EVYK VCDALLAKKI CLAVOSAVICEDIE
ALDKOGU-PLIHNACSYGHTEV-RELLVKHGA			İ	1	1	1	
1691   A   3070   1   547   GVLIPSEQNOLFADIAGNESYTSEHNYQTLIA     341   1691   A   3070   1   547   GVLIPSEQNOLFADILAGIESVTSEHNYQTLIA     342   1692   A   3073   463   3   RINKCREPBADILAGIESVTSEHNYQTLIA     343   1692   A   3073   463   3   RINKCREPBADILAGIESVTSEHNYQTLIA     344   1694   A   3075   250   1   LIVIALATPAVMASILAGVESVGPADILAGVEGRICAGV		1	1		,		
HGADPTKKNRDGNTPLDLVKDGDTDQQLIST   GDAALDAAKSGCLARVKLSSPDNVNCRD   TQGRISTPLHLAGK			i				VVNVADI WKETPI HEAAAKGEVETCELLI O
GDAALLDAKKGCLARVKKLSSPDNYNCRD TQGRISTPLHLAGK							HCADETYKNIPOCNIPI DI VKDCDTDIODI ID
1691   A   3070   1   547   GVLIPSPICHLIAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICHULAGK   GVLIPSPICH   GVLIPSPICHULAGK   GVLIP		[	ſ			1	CDVVII DVVARCCI VBARAI GGDDIDIÓDETE
1691   A   3070   1   547		1	1	1		!	
NYINYDRISEEESVIRILSYNIDGHI.SEKYHTI	341	1691	A	3070	1	547	
RTVKFLRSATIPVVELMDVGGRILDMEWGPD   NRQAAFDMVCTMLEKRVRHKILYLGSKDDT   NRQAAFDMVCTMLEKRVRHKILYLGSKDDT   NRQAAFDMVCTMLEKRVRHKILYLGSKDDT   NRQAAFDMVCTMLEKRVRHKILYLGSKDDT   NRQAAFDMVCTMLEKRVRHKILYLGSKDDT   NRQAAFDMVCTMLEKRVRHKILYLGSKDDT   NRQAAFDMLUPGDTISLIGUTSLRIDYNE   IDDNRVTAEEVDILLREGGKLAPVMAATRIR   AYSGVRPLVASDDDPSGRNVSRGIVLDDHAE   RDGLDGFITTIGGKLMTYRLMAEWATDAVC   RKLGNTRYCTTADLALPGSQEPAKVP   RKLGNTRYCTTADLALPGSQEPAKVP   RKLGNTRYCTTADLALPGSQEPAKVP   RKLGNTRYCTTADLALPGSQEPAKVP   STLVAAFLIAATRGLGFM   WSTLVAAFLIAATRGLGFM   WSTLVAAFLIAATRGLGFM   WSTLVAAFLIAATRGLGFM   WSTLVAAFLIAATRGLGFM   STLVA		1		1 50,0	1 *	377,	
NRQAAPDWCTMLERKYRHKILYLGSKIDDT							PTVKEI DEATIDATE MOVOCEDI DAGVOED
RDEGRYQGYCDAMMIHNI.SPLRMMPRAISSI					•		MBUT TERRATIL A AEPAID A GONDUL
HLRMOLMRDALSANPDLDGVFCTN		j	ļ				BDEOBACCACD WAY THE SDI DYVIDD Y ISSI
1692   A   3073   463   3   RINRCRESDADIL VPGDTISLIGTTSLRIDYNE   IDDNRVTAEEVDILLREGEKLAPVMAKTRILR   AYSGVRPLVASDDDPSGRIVNSGRIVLDHABE   RDGLDGFITTGGKLMTYRIMAEWATDAVC   RKIGNTRPCTADIALPGSQPAKVP     343   1693   A   3075   250   1   LLIYLAIFAPVAMSALAGVKSVQQVRIRAAQS   LGASRAQVLWFVLIPGALPEILTGIRIGLGVG   WSTLVAAELLAATIGLGFW     344   1694   A   3076   2   138   LYFDAYLQSLQVAAISTFCCLLIGYPLAWAV   AHSKPSTRNILLL     345   1695   A   3078   469   3   LKIRGQREIGEDRYMQALPDVEQAVTHAC   VINQAAATGGDARQLVGYLVSQSGLPLDTSA   LQAQLREILPFIMVPVVLLQLPQPLPLIAGT   LQAQLREILPFIMVPVVLLQLPQPLPLIAGT   LANGARGAPKAGSETIIAAAFS   SLLGCDVQDADADFALGGHISLAMKLAT   VINGAAATGGDARQLVGYLVSPNIMI   ERIEDVFTRQSNFSADIAHERTPTINLTCTIL   ALSQSRSQKELEDVLYSNLEELTRMAKMYSD   MLFLAQADNNQLIPEKKMLNILAHEVGKVFD   QFBALPE     347   1697   A   3084   3   340   NELTFEAEISKLYTKVHPAYRTILLEKQALE   DERKAKINGRYTAMPKTQQEIVRLTRDVESQQ   QVYMQLINKEQELKITEASTVGDVRIVDPAIT   QPGYLKPKKGLIII.GAI     348   1698   A   3086   723   10   TQAMVWQQKACAEDDPQLSGRHWLHAATL   YNIAAYPHLKGDDLABQAQALSINRAYBEAA   QRLPGTMRQMEFTVPGGAPTIGFLHMPKGDG   QPGYLKPKKGLIII.GAI   TQAMVWQCKACAEDDPQLSGRHWLHAATL   YNIAAYPHLKGDDLABQAQALSINRAYBEAA   QRLPGTMRQMEFTVPGGAPTIGFLHMPKGDG   QPGYLKPKKGLIII.GAI   TQAMVWQCKACAEDDPQLSGRHWLHAATL   YNIAAYPHLKGDDLABQAQALSINRAYBEAA   QRLPGTMRQMEFTVPGGAPTIGFLHMPKGDG   QPGYLKPKKGLIII.GAI   TQAMVWQCKACAEDDPQLSGRHWLHAATL   LESPRLKAVACLGPVVHTLLSGLKCQQVPE   MYLDVLASRLGMHDASTKSSTEMIQHVLK   ALPNYWWDHTRIVAAFGFFGANVAYRLAY   LESPRLKAVACLGPVVHTLLSGLKCQQVPE   MYLDVLASRLGMHDASTKSSTEMICH   SUMWLAGVOGGAPSINA   SUMWLAGVOGGAPSIN			1				
IDDNRVTAEEVDILLREGEKLAPVMAKTRILR	342	1692	A	3073	463	3	
343   1693   A   3075   250   1   LIYIAIPAENASMATDAVC   RKLONTRPCTTADLALPGSQEPAKVP   RKLONTRPCTTADLALPGSQEPAKVP   RKLONTRPCTTADLALPGSQEPAKVP   RKLONTRPCTTADLALPGSQEPAKVP   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAELIAATRGJOFFM   STUVAAATGGDARQL VGYLLVGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQL VGYLLOGQAVTHAC   VINQAAATGGDARQA VGRAFMAKMYSD   VINTSKDLDVRLOGQAVALSNAKMYSAA   VINQAAATGGARGAVAA   VINQAAATGGARGAVAACAGAPQAALSNAYBAAA   QRLFGTIMRQMEFTYPGAPTITLERQAAELIAATRG VGRAFMAAYHLKGDDLAQAALSNAYBAAA   QRLFGTIMRQMEFTYPGAPTITLIAGATGLAGAVALAATA   LESPRILKAVACLOPVYHTILLSGLKCQQQVPE   MYLDVLASRIGMHDASTKSSTRENH   AALTIVEPVILAGATUAAVVGIGAWTILAAVRLAG   SILWIWLAAAVVGIGAWTILGAGFSV   GFGVAMSQALOPFSLRAGVASSTLGJAQVCG   SILWIWLAAAVVGIGAWTILAAVVGIGAWTILGAGFSV   GFGVAMSQALOPFSLRAGVASSTLGJAQVCG   SILWIWLAAAVVGIGAWTILSSDSVETPDNERKASISVFK   NQRGJQYTILSSDSVETPDNERKASISVFK   NQRGJQYTILSSDSSVETPDNERKASISVFK   NQRGJQYTILSSDSSVETPDNERKASISVFK   NQRGJQYTILSSDSSVETPDNERKASISVFK   NQRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILSSDSSVETPDNERKASISVFK   NGRGJQYTILLSSDSSVETPTNERKASISVFK   NGRGJQYTILLSSDSSVETPTNERKASISVFK   NGRGJQYTILSSDSSVETPTNERKASISVFK   NGRGJQYTILSSDSSVETPTNERKASISVFK				****		١	
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348 1698 A 3086 723 10 TQAMVWQQKACAEDDPQLSGRHWLHAATI. YNIAAYPHLKGDDLAEQAQALSNRAYEEAA QRLPGTMRQMEFTVPGGAPITGFLHMPKGDG PFPTVLMCGGLDAMQTDYYSLYERYFAPRGI AMLTIDMPSVGFSSK WKLTQDSSLLHQHVUK ALPNVPWVDHTRVAAFGFRFGANVAVRLAY LESPRLKAVACLGPVVHTLLSGLKCQQQVPE MYLDVLASRLGMHDASTKSSTRENH  349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV GFGVAMSQALGPFSLRAGVASSTLGIAQVCG SSLWIWLAAVVGIGAWNM  350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD							QVYMQLLNKEQELKITEASTVGDVRIVDPAIT
349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV GFGVAMSQALGPFSLRAGVASTLGIAQVCG SSLWIWLAAVVGIGAWMM 350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYPK NQRGIQYIDLSSDSBDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD							
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QRLPGTMRQMEFTVPGGAPITGFLHMPKGDG PFPTVLMCGGLDAMQTDYYSLYERYFAPRGI AMLTIDMPSVGFSSK WKLTQDSSLLHQHVLK ALPNVPWVDHTRVAAFGFRGANVAVRLAY LESPRLKAVACLGPVVHTLLSGLKCQQQVPE MYLDVLASRLGMHDASTKSSTRENH  349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV GFGVAMSQALGPFSLRAGVASSTLGIAQVCG SSLWIWLAAVVGIGAWNM  350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD							YNIAAYPHLKGDDLAEQAQALSNRAYEEAA
AMLTIDMPSVGFSSK WKLTQDSSLLHQHVLK ALPNVPWVDHTRVAAFGFRFGANVAVRLAY LESPRLKAVACLGPVVHTLLSGLKCQQVPE MYLDVLASRLGMHDASTKSSTRENH  349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV GFGVAMSQALGPFSLRAGVASSTLGIAQVCG SSLWIWLAAVVGIGAWNM  350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK  351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD							QRLPGTMRQMEFTVPGGAPITGFLHMPKGDG
349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTI.ICAGFSV GFGVAMSQALGPFSLRAGVASSTLGIAQVCG SSLWIWLAAVVGIGAWNM 350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD							
LESPRLKAVACLGPVVHTLLSGLKCQQQVPE MYLDVLASRLGMHDASTKSSTRENH  349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTI.ICAGFSV GFGVAMSQALGPFSLRAGVASSTLGIAQVCG SSLWIWLAAVVGIGAWNM  350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK  351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD							
349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTI.ICAGFSV GFGVAMSQALGPFSLRAGVASSTLGIAQVCG SSLWIWLAAVVGIGAWNM 350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD					· [	j	ALPNVPWVDHTRVAAFGFRFGANVAVRLAY
349 1699 A 3087 2 249 RIRSSDPEITLAGTPLHAAYLIGMTI.ICAGFSV GFGVAMSQALGPFSLRAGVASSTLGIAQVCG SSLWIWLAAVVGIGAWNM 350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD					[	ł	
350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYPK NQRGIQYIDLSSDSBDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	240	1200					
350 1700 A 3099 3 424 EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK 351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	349	1699	A	3087	2	249	RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV
1700   A   3099   3   424   EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR ANTPDSDITEKTEDSSVPETPDNERKASISYFK NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK     351   1701   A   3108   2   404   IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	1				i	ł	
ANTIPOSDITEKTEDSSVPETPONERKASISYFK NQRGIQYIDLSSDSBDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK  351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	250	1500					
NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK  351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	300	1700	A.	3099	3	424	EAPEATPQPSQPGPSSPISLSAEEENAEGEVSR
NQRGIQYIDLSSDSEDVVSPNCSNTVQEKTFN KDTVIIVSEPSEDEESQGLPTMARRNDDISELE DLSGMEDLK  351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	ļ					]	ANTPDSDITEKTEDSSVPETPDNERKASISYFK
KDTVIIVSEPSEDEESQGLPTMARRNDDISELE						ł	NQRGIQYIDLSSDSBDVVSPNCSNTVQEKTFN
351 1701 A 3108 2 404 IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD						1	KDTVIIVSEPSEDEESQGLPTMARRNDDISELE
MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	251	1501					
MFGIVVMVIETELSWGAYYKAPLYSLALKCL ISLFTIILLGLTIVYHAREIQLFMANYGADDWR SALTYEPIFLILLEALRGVIHATPCRVSLSLWD	331	1701	A	3108	2	404	IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG
SALTYEPIFLILLEALRGVIHATPCRVSLSLWD							
GLDLP		1					
							GLDLP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
	:	1	1	residue of	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	scquara	/=possible nucleotide deletion, \=possible
1		i .		sequence		nucleotide insertion
352	1702	A	3110	341	2	AQLAEVCPPQTLLTTNTSSISITAIAAEIKNPER
		l				VAGLHFFNPAPVMKLVEVVSGLATAAEVVE
		J	•		ļ	QLCELTLSWGKQPVRCHSTPGFIVNRVARPY
!		,	<b>.</b>			YSEAWRALEEQVAAPEVI
353	1703	A	3111	3	188	HFSLFRIAFAVFLTYMTVGLPLPVIPLFVHHEL
						GYGNTMVGIAVGIQFLATVLTRGYAGRLA
354	1704	A	3116	367	225	WQLFHLNGTFLNIGETDTESCVNGWVYDRSS
		L	L			FPFSNMTEVRGLVFLS
355	1705	Α	3117	101	53	VINLVYLISSPRPELKPVDKESEVVMKFPDGF
		1	1			EKFSPPILQLDEVDFYYDPKHVIFSRLSVSADL
			i		ĺ	ESRICVVGENGAGKSTMLKLLLGDL\APVRGI RHAHRNLKIGYFSQHHVGAAGT*TFSACGNL
ļ .						LGTQVFLGRPEEEY\RHQLGFGMGISGELGHA
						SSLPACLGGOKEAEVAFCSDGLLPCPNFL\IL\
		ĺ	ĺ	ĺ		DEPTNHLGHGRAIEALGPCLQTISGVGVILVS
				,		HE*SALSRLVCRE\LWVC*GRSTSPF
356	1706	A	3121	137	466	RGGRDWGEHNQRLEEHQARAWQGAMDAG
]						AASREHARWQGTGLAPGTRVAVAPTCVQGL
1		l				PQERSVCRPFFSSRWREGPVWALGAGAHGKP
						RWSGGVRCVVRGGRWFTPAPH
357	1707	A	3124	1249	229	MLEAPGPSDGCELSNPSASRVSCAGQMLEVQ
		ł	l	ł	ł	PGLYFGGAAAVAEPDHLREAGITAVLTVDSE
1						EPSFKAGPGVEDLWRLFVPALDKPETDLLSH
						LDRCVAFIGQARAEGRAVLVHCHAGVSRSV AIITAFLMKTDQLPFEKAYEKLQILKPEAKMN
1		l			ľ	EGFEWQLKLYQAMGYEVDTSSAIYKQYRLQ
		ļ				KVTEKYPELQNLPQELFAVDPTTVSQGLKDE
		i		1		VLYKCRKCRRSLFRSSSILDHREGSGPIAFAH
[		İ		l ·	i	KRMTPSSMLTTGRQAQCTSYFIEPVQWMESA
		١ .				LLGVMDGQLLCPKCSAKLGSFNWYGEQCSC
]			1			GRWITPAFQIHKNRVDEMKILPVLGSQTGKI
358	1708	A	3127	816	139	EVETLGPRTPGP/EAQSPTPGSCPGWQEPSPGP
		1	1	1		TPPP*LSGPGPQGAPVLGKLLPDPEETPAGKTP
					ļ	LGKHFWWGL\PVTSANFSPGAAA*FGGALSPP
,			1	ļ		GGDL/GHMLLQGPPSPFRLQQQ*QTPPGSHSP
1		ł	l	i	ł	PTANREINPGPAAAADTRSCWGHKRSWRGW RGLAPWRLGFGSPGIP*PAPAGIP/GRPTWEGG
						KGAGGKPSETLTRSPPVWRGKRGSANGFLSW
		]		1	}	VQILQ
359	1709	A	3132	3	191	HEHLLLLLCVFLVKSQGVNDNEEGFFSARG
		]	]	<b>l</b>	1	HRPLDKKREDAPNLRPALAD\ITVCDYRAQIA
1					1	*AASTPKRAASIAHNAVSCR*AQIA
360	1710	A	3134	1	286	REPPRPALLFF*DRVSLCCPGWNAVVQSQLT
		1	1	1		AAPTSQVQ/SDSPTFPSSWDYRHVPEYPANFL
	·			ĺ	1	*RQGFPMLPRLVSNSWAQTVHPPRPPKVLDL
			<u> </u>	<u> </u>		QA
361	1711	Α	3135	56	1449	PVPAPRVSPSARGAPGRPRLPGVRGPRHS/WA
		1		j	<u> </u>	AD*RGSRM/PPRAPAPSPTGP/APGGKKVRGR
				ļ		VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N
,			1	1	1	GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD
		1		1	1	PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ
					1	APGLPHRTSIRPGWRRLTEPEAWARRHRRPW
		ĺ	1		1	GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT
1		ì	1	1	1	PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ
				1	1	SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA
			1			GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT
1			1	1	1	F/LIPSPT*MSPALVIQPPVPPTQMGLRISGLPR
L	L	<u>L</u>	<u> </u>	<u>L</u>	<u> </u>	QG*PSGAPW*LPGLAQLAFQCHLPHDEVGPP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  RNQSPLGNDTLSSGLPMGPRRQVWPLARVG
362	1712	A	3136	1270	274	GHSSPREPQVLKKPLWGQTDIAGVGSASLYP DNL  RVGMVLGTREVGDSTPPPSPPLYPFTGNEFVQ HNTWQLSRYYPSDLRTDSSNYNPQELWNAG CQMV*GGSRDWEEGVEEQQVGNKFSSDGR VGECSRKLLG*EMLSVDITSRYRAPSTYLLNS LKEGLEGLHGESCSSFLLGPSVAMNMQTAGL EMDICDGHFRQNGGCGYVLKPDFLRDIQSSF HPEKPISPFKAQTLLNQVISVQQLPKVDKTKE GSIVDPLVKVQIFGVRLDTARQETNYVENNG FNPYWGQTLCFRVLGPDFPMLRFGKMDYDW KSRNDLLGKTPCPGTCMQQGYRIIHLLSKDG ISLRPASIFVYICIQEGLEGDES
363	1713	С	3139	60	248	MFAGSYGKSMFSFSKKVLNCLPKWRYHFVIA PAMNESPLAPHLHQHLVFSVFQVLTILIGV**
364	1714	Α .	3140	57	418	SAFKTLQLPAFSLYFDLGSLKLLILRIHTSIVK NHKVESPRTMSPG*DPQSFLQIPQPRPPQLRV GLTSGLIQHFHSPSSCQFPLLRGPPPPRQPPLGI SGASLCPVLSPPR*PLOPSSL
365	1715	A	3145	122	413	LLPYPSLFVFLRQCHFVT\RLECNGVVSAHCN LHLPGSSDSPASAS*VAGTTGVCHHTRLIF\VF LV*TGFHYVAQAGLELLTA*S\PPQLPKVVGL QA
366	1716	A	3150	247	2	VGEKLHDIRFGNDFDMTPKAQATKEKIDKLN FIKIKKLCIEGYY/NREPQNGRKIFANYVS\DK GLMATIYEELLKLSNKLIQ
367	1717	A	3152	3	2367	QKLKQNQPKRAHVEDGGSRSKQGNEQSKKT PIEKSDFAAATHPRAFYLSKPDETPNAWMSD SGTGLTYWKLEEKDMHHSLPETLEKTFISLSS TDVSPNQVLTLDPTLHMKPKQQISGIQPHGLP NALDDRISFSPDSVLEPSMSSPSDIDSFSQASN VTSQLPGFPKYPSHTKASPVDSWKNQTFQNE SRTSSTFPSVYTITSNDISVNTVDEENTVMVAS ASVSQSQLPGTANSVPECISLTSLEDPVILSKIR QNLKEKHARHIADLRAYYESEINSLKQKLEA KEISGVEDWKITNQILVDRCGQLDSALHEATS RVRTLENKNNLLEIEVNDLRERFSAASSAKI LQERIEEMRTSSKEKDNTIIRLKSRLQDLEEAF ENAYKLSDDKEAQLKQENKMFQDLLGEYES LGKEHRRVKDALNTTENKLLDAYTQISDLKR MISKLEAQVKQVEHENMLSLRHNSRIHVRPS RANTLATSDVSRRKWLIPGAEYSIFTGQPLDT QDSNVDNQLEETCSLGHRSPLEKDSSPYGSST SLLIKKQRETSDTPIMRALKELDEGKIFKNWG TQTEKEDTSNSLL*INPRQTETSVNASRSPEK CAQQRQKTLNSASQRSSSLPPSNRKSSTPTKR EIMLTPVTVAYSPKRSPKENLSPGFSHLLSKN ESSPIREKTYSEKATDNHVNHSSCPEPVPNGV KKVSVRTAWEKNKSVSVEQCKPVSVTPQGN DFEYTAKIRTLAETERFFDELTKEKDQIEAAL SRMPSPGGRITLQTRLNQVKCLSLNLL
368	1718	Α	3163	2	2350	EFKSGCGAGLVAAGAVLVLYPASRAGERT RVPGSPAPSSLPLHSPGACGTEVDMDPQRSPL LEVKGNIELKRPLIKAPSQLPLSGSRLKRRPDQ MEDGLEPEKKRTRGLGATTKITTSHPRVPSLT TVPQTQGQTTAQKVSKKTGPRCSTALATGLK NQKPVPAVPVQKSGTSGVPPMAGGKKPSKRP AWDLKGQLCDLNAELKRCRERTQTLDQENQ

SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide seq- uence	seq- uence		USSN 09/496 914	location correspondi ng to first amino acid residue of peptide	corresponding to last amino acid residue of peptide sequence	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
		,		,		QLQDQLRDAQQQVKALGTERTTLEGHLAKV QAQAEQGQQELKNLRACVLELEERLSTQEGL VQELQKKQVELQEERRGLMSQLEEKERRLQT SEAALSSSQAEVASLRQETVAQAALLTEREER LHGLEMERRRLHNQLQELKGNIRVFCRVRPV LPGEPTPPPGLLLFPSGPGGPSDPPTRLSLSRSD
	!			·		ERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDE VFEEIAMLVQSALDGYPVCIFAYGQTGSGKTF TMEGGPGGDPQLEGLIPRALRHLFSVAQELSG QGWTYSFVASYVEIYNETVRDLLATGTRKGQ GGECEIRRAGPGSEELTVTNARYVPVSCEKEV
2						DALLHLARQNRAVARTAQNERSSRSHSVFQL QISGEHSSRGLQCGAPLSLVDLAGSERLDPGL ALGPGERERLRETQAINSSLSTLGLVIMALSN KESHVPYRNSKLTYLLQNSLGGSAKMLMFV NISPLEENVSESLNSLRFASKVEPSVLFGTAQS
						NRKWKTDPDLCVCVCVCVCVCVCVCVCVP MSMYRVRGGRVAGGCFIGWRAPCPRAIK
369	1719	Α	3165	365	12	GYTSQGRWIDIERGPLTANTESLIIENNFNALP GYIRKIE+I+IYKKN+INFGGVGLLNIVKISILS/K IYRFDAIPVKILTRFFINLDKLILKFVLKTKIAK NRIKTFYIMRRKKLGDSS
370	1720	Α.	3170	393	42	GASISPSAVIDGVEGLKPMQEQEAQEAGPCLD  *HMAPEQWVAPR\RLLFRLIFSVLHALIIAAAA QSSAEEDEDPRN*GQSSEDQAPNQNGLIVIVH RVHVPLGAAATVPVHRSHFPR
371	1721	A	3173	770	510	GNGGCGLSQIPPSHLGAFSRGSLLSRG\DPRGP PPHPVIFFVFVVE\QGFTVLARMVSIS*PCDPP ALASQSAGITGVSHLARPQNLYF
372	1722	A	3180	381	76	RVLHHDNVPAHSSPQKREISQEFQLEIRHLP*S PDLAPSGCFLFLNLKNIFK\GTHFSLVDNVKK TVSTWLH/SQNAQFYKDRLNGWYHCLQKCL QHY*AYVEK
373	1723	A	3181	410	14101	RREVAGPEGKGLLLASAHTMLTPPLLLLPLL SALVAAAIDAPKTCSPKQFACRDQITCISKGW RCDGERDCPDGSDEAPEICPQSKAQRCQPNE HNCLGTELCVPMSRLCNGVQDCMDGSDEGP HCRELQGNCSRLGCQHHCVPTLDGPTCYCNS SFQLQADGKTCKDFDECSVYGTCSQLCTNTD GSFICGCVEGYLLQPDNRSCKAKNEPVDRPP VLLIANSQNILATYLSGAQVSTITPTSTRQTTA MDFSYANETVCWVHVGDSAAQTQLKCARM PGLKGFVDEHTINISLSLHHVEQMAIDWLTGN FYFVDDIDDRIFVCNRNGDTCVTLLDLELYNP KGIALDPAMGKVFFTDYGQIPKVERCDMDG QNRTKLVDSKIVFPHGITLDLVSRLVYWADA YLDYIEVVDYEGKGRQTIIQGILIEHLYGLTVF ENYLYATNSDNANAQQKTSVIRVNRFNSTEY QVVTRVDKGGALHIYHQRRQPRVRSHACEN DQYGKPGGCSDICLLANSHKARTCRCRSGFS LGSDGKSCKKPEHELFLVYGKGRPGIRGMD MGAKVPDEHMIPIENLMNPRALDFHAETGFI YFADTTSYLIGRQKIDGTERETILKDGIHNVE GVAVDWMGDNLYWTDDGPKKTISVARLEK AAQTRKTLIEGKMTHPRAIVVDPLNGWMYW TDWEEDPKDSRRGRLERAWMDGSHRDIFVT SKTVLWPNGLSLDIPAGRLYWVDAFYDRIETI
	<u> </u>	1				LLNGTDRKIVYEGPELNHAFGLCHHGNYLFW TEYRSGSVYRLERGVGGAPPTVTLLRSERPPI

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wu	VΙ	וכו	100	

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ł	peptide	,	/=possible nucleotide deletion, \=possible
		·	1	sequence		nucleotide insertion
<u> </u>			<del> </del>	<u> </u>		PEIRIMYDAQHQQVGSNKCRVNNAGCSSLCL
1	ļ		ļ			ATPGSRQCACAEDQVLDADGVTCLANPSYVP
						PPOCOPGEFACANSRCIQERWKCDGDNDCLD
		ŀ				NSDEAPALCHOHTCPSDRFKCENNRCIPNRW
	ļ	1	1	1		LCDGDNDCGNSEDESNATCSARTCPPNQFSC
			ŀ	İ	į	ASGRCIPISWTCDLDDDCGDRSDESASCAYPT
				ļ		CFPLTQFTCNNGRCININWRCDNDNDCGDNS
ł	ł	1	ł			DEAGCSHSCSSTOFKCNSGRCIPEHWTCDGD
			1			NDCGDYSDETHANCTNQATRPPGGCHTDEF
					ļ	OCRLDGLCIPLRWRCDGDTDCMDSSDEKSCE
	ł	ł	ł		1	GVTHVCDPSVKFGCKDSARCISKAWVCDGD
1	Ì			l .		NDCEDNSDEENCESLACRPPSHPCANNTSVC
	İ					LPPDKLCDGNDDCGDGSDEGELCDQCSLNN
1	1	1	ì	ł		GGCSHNCSVAPGEGIVCSCPLGMELGPDNHT
	1	1		•		COIQSYCAKHLKCSQKCDQNKFSVKCSCYEG
1				1	ļ	WVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLH
1		{	ł	l		KGDYSVLVPGLRNTIALDFHLSQSALYWTDV
1	l	1.				VEDKIYRGKLLDNGALTSFEVVIQYGLATPEG
				ļ		LAVDWIAGNIYWVESNLDQIEVAKLDGTLRT
{	İ	ì	1	i		TLLAGDIEHPRAIALDPRDGILFWTDWDASLP
		1				RIEAASMSGAGRRTVHRETGSGGWPNGLTV
		İ				DYLEKRILWIDARSDAIYSARYDGSGHMEVL
ľ	1	1		1	1	RGHEFLSHPFAVTLYGGEVYWTDWRTNTLA
1	1.	1		i		KANKWTGHNVTVVQRTNTQPFDLQVYHPSR
		}		ŀ		OPMAPNPCEANGGOGPCSHLCLINYNRTVSC
ľ		ľ	Ì	i	1	ACPHLMKLHKDNTTCYEFKKFLLYARQMEIR
		ŀ			[	GVDLDAPYYNYIISFTVPDIDNVTVLDYDARE
		1	1	ļ	1	QRVYWSDVRTQAIKRAFINGTGVETVVSADL
		}				PNAHGLAVDWVSRNLFWTSYDTNKKQINVA
ł				1	1	RLDGSFKNAVVQGLEQPHGLVVHPLRGKLY
l	1	1		1		WTDGDNISMANMDGSNRTLLFSGQKGPVGL
1		1				AIDFPESKLYWISSGNHTINRCNLDGSGLEVID
			ļ	1		AMRSQLGKATALAIMGDKLWWADQVSEKM
j		]	J			GTCSKADGSGSVVLRNSTTLVMHMKVYDESI
1						QLDHKGTNPCSVNNGDCSQLCLPTSETTRSC
	i	ì				MCTAGYSLRSGQQACEGVGSFLLYSVHEGIR
]	1	ļ	1			GIPLDPNDKSDALVPVSGTSLAVGIDFHAEND
1.			1	1	1	TIYWVDMGLSTISRAKRDQTWREDVVTNGIG
1		1	1	i	1	RVEGIAVDWIAGNIYWTDQGFDVIEVARLNG
1		1	1		1	SFRYVVISQGLDKPRAITVHPEKGYLFWTEW
		]		1	1	GQYPRIERSRLDGTERVVLVNVSISWPNGISV
	ĺ		1			DYQDGKLYWCDARTDKIERIDLETGENREVV
1	1	1	1	ļ	1	LSSNNMDMFSVSVFEDFIYWSDRTHANGSIK
,	1		1	1	1	RGSKDNATDSVPLRTGIGVQLKDIKVFNRDR
		1.	1	1		QKGTNVCAVANGGCQQLCLYRGRGQRACA
	1	1	1			CAHGMLAEDGASCREYAGYLLYSERTILKSI
1	1	1	1	1		HLSDERNLNAPVQPFEDPEHMKNVIALAFDY
1	1		1	1	1	RAGTSPGTPNRIFFSDIHFGNIQQINDDGSRRIT
		1	1	į	i.	IVENVGSVEGLAYHRGWDTLYWTSYTTSTIT
1						RHTVDQTRPGAFERETVITMSGDDHPRAFVL
	1		1			DECQNLMFWTNWNEQHPSIMRAALSGANVL
1		i	1	{		TLIEKDIRTPNGLAIDHRAEKLYFSDATLDKIE
		1	1		1	RCEYDGSHRYVILKSEPVHPFGLAVYGEHIF
	1					WTDWVRRAVQRANKHVGSNMKLLRVDIPQ
1	1	1	1	ľ	!	QPMGIIAVANDTNSCELSPCRINNGGCQDLCL
	1		i	l	i	LTHOGHVNCSCRGGRILQDDLTCRAVNSSCR
	1	-	1			AQDEFECANGECINFSLTCDGVPHCKDKSDE
1	1	1	1	1	Ì	KPSYCNSRRCKKTFRQCSNGRCVSNMLWCN
			1	1		GADDCGDG\$DEIPCNKTACGVGEFRCRDGTC
	1	1		1	!	IGNSSRCNQFVDCEDASDEMNCSATDCSSYF
	<del></del>		<del></del>	<del></del>		<u> </u>

CGDYSDERDCPGVKRPRCPLNYFACPSGRCM MSWTCDKEDDCEHGEDETHCNKFCSEAQPF CQNHRCISKQWLCDGSDDCGDGSDEAAHCI GKTCGPSSFSCPGTHVCVPERWLCDGDKDC DGADESIAAGCLYNSTCDDREFMCQNRQCII KHFVCDHDRDCADGSDESPECEYPTCGPSEI RCANGRCLSSRQWECDGENDCHDQSDEAPF NPHCTSPEHKCNASSQFLCSSGRCVAEALLC GQDDCGDSSDERGCHINECLSRKLSGCSQDC EDLKIGFKCRCRPGFRLKDDGRTCADVDECE TTFPCSQRCINTHGSYKCLCVEGYAPRGGDF HSCKAVTDEEPFLIFANRYYLRKLNLDGSNY TLLKQGLNNAVALDFDYREQMIYWTDVTTC GSMIRRMHLNGSNVQVLHRTGLSNPPGLAV DWVGGNLYWCDKGRDTIEVSKLNGAYRTV VSSGLREPRALVVDVQNGYLYWTDWGDHS IGRIGMDGSSRSVIVDTKITWPNGLTLDYVTT RIYWADAREDYIEFASLDGSNRHVVLSQDIP IFALTLFEDYVYWTDWETKSINRAHKTTGTN KTLLISTLHRPMDLHVFHALRQPDVPNHPCK VNNGGCSNLCLLSPGGHKCACPTNFYLGSI GRTCVSNCTASQFVCKNDKCIPFWKCDTE DDCGDHSDEPPDCPEFKCRPGQFQCSTGICTI PAFICDGDNDCQDNSDEANCDIHVCLPSQFK	SEC NO: nucl eotic seq- uenc	i- pept de seq- uenc	of hod	SEQ ID NO: im USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion	
VTCAPNOFQCSITKRCIPRVWVCDRDNDCVI GSDEPANCTQMTCGVDEFRCKDSGRCIPARV KCDGEDDCGDGSDEFKEECDEFTCEPYQFRC KNNRCVPGRWQCDYDNDCGDNSDEESCTPI PCSESEFSCANGRCIAGRWKCDGHDCADG DEKDCTPRCDMDQFQCKSGHCIPLRWRCDA DADCMDGSDEEACGTOVRTCPL.DEFQCNNT LCKPLAWKCDGEDDCGDNSDENPEECARFV CPPNRPFRCKNDRVCL.WIGRQCDGTDNCGD GTDEEDCEPPTAHTTHCKDKEFLCRNQRCI SSSLRCNMTDDCGDGSSEEDCSIDPKLTSCA' NASICGDEARCVRTEKAAYCACRSGFHTVPC QPGCQDINECLRFGTCSQLCNNTKGGHLCSC ARNFMKTHNTCKAEGSEYQVL.V1ADDNEIRS LFPGHPHSAYEQAFQGDESVRIDAMDVHVK. GRVYWTNWHTGTISYRSLPPAAPPTTSNRHR RQIDRGVTHLNISGLKMPRGIAIDWVAGNVY WTDSGRDVIEVAQMKGENRKTLISGMIDEPE AIVVDPLRGTMYWSDWGNHPKIETAAMDGT LRETLVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSKRGLSHPFSIDV FEDYIYGVTYINNRVFKHIKFGHSPLVNLTGG LSHASDVVLYHQHKQPEVTNPCDRKKCEWL CLLSPSGPVCTCPNGKRLDNGTCVPVYSPTPP PDAPRPGTCNLQCFNGGSCFLNARRQPKCRC QPRYTGDKCELDQCWEHCRNGGTCAASPSG MPTCRCPTGFTGPKCTQQVCAGYCANNSTCT VNQGNQPQCRCLPGFLGDRCQYRQCSGYCE NFGTCQMAADGSRQCRCTAYFEGSRCEVNK CSRCLEGACVVNKQSGDVTCNCTDGRVAPS							NFGTCQMAADGSRQCRCTAYFEGSRCEVNK CSRCLEGACVVNKQSGDVTCNCTDGRVAPS CLTCVGHCSNGGSCTMNSKMMPECQCPPHM TGPRCEEHVFSQQQPGHIASILIPLLLLLLLVL VAGVVFWYKRRYQGAKGFQHORMTNGAM	

# WO 01/57188

SEQ ID	SEQ ID	Met	CEO	Predicted	Predicted end	LA-l-sall-sall-sall-sall-sall-sall-sall-s
NO: of	NO: of	hod	SEQ ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide	nou	in in	nucleotide	location	F=Phenylalanine, O=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ĺ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	ľ	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ	j	1		peptide		/=possible nucleotide deletion, \=possible
ŀ				sequence		nucleotide insertion
			<del>                                     </del>			DPDKPTNFTNPVYATLYMGGHGSRHSLASTD
ĺ	į	İ	İ	İ	ĺ	EKRELLGRGPEDEIGDPLA
374	1724	A	3187	191	1815	CLELASAGKIPEESKALSLLAPAPTMTSLMPG
ŀ		İ			1	AGLLPIPTPNPLTTLGVSLSSLGAIPAAALDPNI
						ATLGEIPOPPLMGNVDPSKIDEIRRTVYVGNL
1	l	]	ļ	}	ļ	NSQTTTADQLLEFFKQVGEVKFVRMAGDET
				[		QPTRFAFVEFADQNSVPRALAFNGVMFGDRP
	1		Ì			LKINHSNNAIVKPPEMTPQAAAKELEEVMKR
			1		j	VREAQSFISAAIEPGWLHSTSLCNDFLGCF*RR
		1	Î	1	1	RMYRE*APCTICGTFHLCLIINWDL*LF*AYTA
						K*FFPPRVWKEQ*KKRR\RSRSHTRSKSRSSSK
					İ	SHSRRKRSQSKHRSRSHNRSRSRQKDRRRSK
	1	ļ		l	}	SPHKKRSKSRERRKSRSRSHSRDKRKDTREKI
	,	-				KEKERVKEKDREKEREREKEREKERGKN
			1			KDRDKEREKDREKDKEKDREREREKEHEKD
			1			RDKEKEKEQDKEKEREKDRSKEIDEKRKKDK
ĺ		Í				KSRTPPRSYNASRRSRSSSRERRRRRSRSSSRS
			1	. '	·	PRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
'	}		1		·	HISERRERERSTSMRKSSNDRDGKEKLEKNST
375	1725	A	3192	415	101	S AUGGUOTE AN OFFICINITY TOPOLOGO AND COMPANY OF THE AUGG
313	1723	A	3192	415	ÍOI	AHSSHQTRAILQEFQWDIIRHPPL\SPNLALSG
						F\FPNLKKSLRGTHFSSVKK\TTLTWLNSQDP WF/FFYP*SPDLQIPSSFRNGLNDWYHHSQKC
						PDLDGAYVKK
376	1726	A	3199	931	418	GV*WCDLGSPQPPPPGFKQFCLGRSSSWDYR
370	1,20	l ^	31//	331	410	HVPPHPANFVFLLETGFLHAGQAGL\GDPPAS
						ASQSAGITGVSHTWPKNHLIFYACLVIRSKRI
					,	K K
377	1727	A	3201	274	1285	KTGYTSRGSPLSPQSSIDSELSTSELEDDSISM
			520.		1203	GYKLQDLTDVQIMARLQEESLRQDYASTSAS
		ĺ				VSRHSSSVSLSSGKKGTCSDQEYDQYSLEDEE
						EFDHLPPPQPRLPRCSPFQRGIPHSQTFSSIREC
1			i i			RRSPSSQYFPSNNYQQQQYYSPQAQTPDQQP
						NRTNGDK/PPKKYA*PSPDAKYNCH**QH\SSP
						VTVRNSQSFDSSLHGAGNGISRIQSCIPSPGQL
						QHRVHSVGHFPVSIRQPLKATAYVSPTVQGSS
						NMPLSNGLQLYSNTGIPTPNKAAASGIMGRS
						ALPRPSLAINGSNLPRSKIAQPVRSFLQPPKPL
						SSLSTLRDGNWRDGCY
378	1728	A	3202	112	1789	VPGVTESRPSVLRGDHLFALLSSETHQEDPIT
						YKGFVHKV\ELDRVKLSFSMSLLSRFVGWG*
						PFKVNFY/TFNRQPLRV\QHRALELTGRWLLW
						PMLFP\VAPRDVPLLPSDVKLKLYDRSLESNP
						EQLQAMRHIVTGTTRPAPYIIFGPPGTGKTVT
1			(			LVEAIKQVVKHLPKAHILACAPSNSGADLLC
]						QRLRVHLPSSIYRLLAPSRDIRMVPEDIKPCCN
			1			WDAKKGEYVFPAKKKLQEYRVLITTLITAGR
				İ		LVSAQFPIDHFTHIFIDEAGHCMEPESLVAIAG
						LMEVKETGDPGGQLVLAGDPRQLGPVLRSPL
						TQKHGLGYSLLERLLTYNSLYKKGPDGYDPQ
						FITKLLRNYRSHPTILDIPNQLYYEGELQACA
						DVVDRERFCRWAG\LPRQGFPIIFHGVMGKD
						EREGNSPSFFNPEEAATVTSYLKLLLAPSSKK
						GKARLSPRSVGVISPYRKQVEKIRYCITKLDR
				]		ELRGLDDIKDLKVTCCSTVTPCLPCAPTCPLP
						ETSSSFHSSPRPRPTPAALNRARALPEPLTPGD
						SNLRVWDGIRKPACLTNTSCHS
379	1729	Α	3206	432	130	PKAAPSVXLWFPPFL*GSFKPTKGHTXCVXIK
1			1 1	ļ		*LSTREAXDSXPGRQIAXXRQGGKVETTTAL

·	T 44-2	1 5 6	T 252			
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleoude	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN 09/496	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq- uence	uence	1	914	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		residue of	Sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			-	peptide	sequence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<del> </del>	<del> </del>	<del> </del>	sequence		XKQSNNKGTRASSYXEPDAXEQWKFPHKKL
	1	1				OLPGXTHE
380	1730	A	3207	187	507	GGTGHPHPARPPLSGVGGCQCSHSKPWTAGS
300	1,30	11	3207	107	307	PEQRDHPAPHKQIEAGQGLPGPQAWGG*KGP
ļ					ļ	AXLLPGPGGGPGPVASLEARAQASSGVTPNG
		1		1	1	GGRTYPYPTFSSGE
381	1731	A	3225	i	840	GTRPGHLPAPSDGFCV/HL*SIPSWGSF*GESL/
				-		EMOLITSLGLOEPDIARNVLELIYAOTLVWIGI
		1		1		FFCPLLPFIQMIMLFIMFYSKNISLMMNFOPPS
		1	1	ŀ		KAWRASQMMTFFIFLLFFPSFTGVLCTLAITI
			ł	ļ		WRLKPSADCGPFRGLPLFIHSIYSWIDTLSTRP
		1		1		GYLWVVWIYRNLIGSVHFFFILTLIVLIITYLY
İ				1		WQITEGRKIMIRLLHEQIINEGKDKMFLIEKLI
		1		ł		KLQDMEKKANPSSLVLERREVEQQGFLHLGE
			]	j		HDGSLDLRSRRSVQEGNPRA
. 382	1732	A	3238	256	38	LLMIKVSSTCFSCHLHHHHHHHHHHHHQGHNS
	-	ľ				LFFSLKSSSNSSTLPVYLSYNIILVFSKCLVFDF
[	Ï	l		ĺ		LFSNACL
383	1733	A	3241	1542	343	KGAPSFVRLYQYPNFAGPHAALANKSFPKAD
						KVTMLWNKKATAVLVIASTDVDKTGASYYG
	Ì	1			]	EQTLHYLATNGESAVVQLPKNGPIYDVVWNS
		1	-	[		SSTEFCAVYGFMPAKATIFNLKCDPVFDFGTG
		Ī				PRNAAYYSPHGHILVLAGFGNLILQI*AD/IMK
		l				VWNVKNYKLISKPVASDSTYFAWCPDGEHIL
٠.	)	1		}		TATCAPRLRVNNGYKIWHYTGSILHKYDVPS
1				1		NAELWQVSWQPFLDGIFPAKTITYQAVPSEVP
		1				NEEPKVATAYRPPALRNKPITNSKLHEEEPPQ
		1				NMKPQSGNDKPLSKTALKNQRKHEAKKAAK
ļ	1	1		1	}	QEARSDKSPDLAPTPAPQSTPRNTVSQSISGDP
						EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK
		<u> </u>				NQLEKIQKETALLQELEDLELGI
384	1734	A	3242	3	678	IRSPAARSPOLETPTCLLFVIAAIAAVFVDSAIP
						RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP
						LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS
	1	1		l		ASLVRATVRAVSKRKLQPTRAALTLTPSAVN
		ļ	1			KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL
		ļ		1		EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL
				•	-	GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES
205	1505	<b></b>	2010	1000		FNI
385	1735	A	3243	3190	664	VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL
		1				KEEEILPEPGSETPTVASEALAELLHGALLRR
		1				GPEMGYLPGPPLGPEGGEEETTTTITTTTVTT
	ł	]		ŀ	ĺ	TVTSPVLCNNNISEGEGYVESPDLGSPVSRTL
	ļ	l				GLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELL
		1	Ì	}		VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT
			1	-	1	NRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFP
		1				PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG
	1	1				EETLICLNGTRPSWNGETPSCMASCGGTIHNA
	]	ļ	]	j		TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRRL
		1			·	HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS
					[	DMDDVPERGLISDAQSLYVELLSETPANPLLL
			1			SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG
	1	ļ	1	}		ALATFSCLPGYALEPPGPPNAIECVDPTEPHW
	1			1		NDTEPACKAMCGGELSEPAGVVLSPDWPQS
		1	j	1	l	YSPGQDCVWGVHVQEEKRILLQVEILNVREG
	[	1	[	[		DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS
	ļ	1 .	1			GPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPR
	1	•				NDTCPELPPPEWGWRTASHGDLIRGTVLTYQ
L	L	1	<u>i</u>	L	l	CEPGYELLGSDILTCQWDLSWSAAPPACQKI

	T		<del></del>			
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
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eotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	İ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Ghutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	ł	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			Ì	peptide	<u> </u>	/=possible nucleotide deletion, \=possible
L		1		sequence		nucleotide insertion
						MTCADPGEIANGHRTASDAGFPVGSHVQYRC
1	1	1		1	1	LPGYSLEGAAMLTCYSRDTGTPKWSDRVPKC
		ł	Ì	1		ALKYEPCLNPGVPENGYQTLYKHHYQAGESL
1	1	1		1	1	RFFCYEGFELIGEVTITCVPGHPSQWTSQPPLC
1		l	1			KVTQTTDPSRQLEGGNLALAILLPLGLVIVLG
	1		1			SGVYIYYTKLQGKSLFGFSGSHSYSPITVESDF
	]	]	j	1	<u> </u>	SNPLYEAGDTREYEVSI
386	1736	A	3250	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDT
300	1,,,,	1 **	3230	312	3204	RKLLMTWALEVAVVMKKSETYAPLFCLPSF
]	1	}		1		
			[	1		HKFCKGLLADTLVEDVNICLQACSSLHALSSS
1	ļ	ļ	}		j	LPDDLLQRCVDVCRVQLVHRGTCIRQAFGKL
1				1		LKSIPLGVFLSNNNHTEIQEISLALRSHMSKAP
1			1	1	Į	SNTFHPQDFSD/VISFILYGNSHRTGKDNWLE
	] .	]		]	]	RLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
		1		l .	<b>l</b> .	AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIR
,	1	1				SLAGHTLNPDQDVSQWTTADNDEGHGNNQL
	l			1		RLVLLLQYLENLEKLMYNAYEGCANALTSPP
İ	·	1	1			KVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLA
			1	İ		GQPAVTVRHGFDLLTEMKTTSLSQGNELEVSI
	ŀ		1	l	'	MMVVEALCELHCPEAIQGIAVWSSSIVGKHL
1		1	1	Ì		LWINSVAQQAEGRFEKASVEYQEHLCAMTG
				İ		VDCCISSFDKSVLTLASAGCKSASLKHCLNGE
				ŀ		SRKSVLSKPTDSSPEVINYLGNKACECYISTA
1	ł		1			DWAAVQEWQNAIHDLKKSTSSTSLNLKADF
1						NYIKSLSSFESGKFVECTEQLELLPGENINLLA
İ				1		GGSKEKIDMKKLLRNM
387	1737	A	3255	380	76	MDIFLYNCKYQVQTEI*NSIQHIMA\SKKLSRF
· ·						LKYVHNL*AENYKTLMK*INEDLNKQRDVPY
1			1			S*TARLNKMSIPTKTIFRFKAIYIKIPATYFIET
			1 .			NMQ
388	1738	A	3260	685	428	PQWLGLQVYALPPANFVFFVEMRSTILAQTG
				1.000		FELLDSSDLPASASKSAGITCMSHHARTLSLK
1			]			*WPFCLSATQEKFC*PASEGVAW
389	1739	A	3269	1	332	LDGYHTPIYMLNRIIRLPAAL*IISDOTGHALTI
309	1/39	^	3209	1	332	
		ŀ				LTRLETQMINADYQNKLTLDYLLTTDREVYE
İ			1		,	PFNLTNYCLHIHNQRLGAYDLG*V*Q/KLAHV
700	1540	<u> </u>	2070			PVQV*HGFDPEAMFR
390	1740	Α	3270	2	372	GRCHDQNKGKS\DGPDAQAEACGGESTYQEL
1.						LVNQNPIGQPLACRRLTRKIYEGIKKAVKPNH
ļ .		l				SPRGVKKVHKFVNKGEKGIMVLAGDTLGIGV
						YCLLPCMC*DRKLTYAHIPSTTDLGAGAGY
391	1741	Α	3273	1	187	FFQEMLDIMKAISDMMGKCTYPVLKEDAPRQ
	1		1			HVETFFQ\EELTRSQEGMKLGENFLMFAMPP
-			[ [			DDSKESKGK*FFQEMLDIMKAISDMMGKCTY
1						PVLKEDAPRQHVETFFQVGINQKSRGHEVRR
		1				KFPDVCHAPR
392	1742	Ā	3281	901	521	FFFGDGVSPCRQAGV*WHDLDSLQNLPPGFK
				- • •		RFSYLSLPSSW\DYRHVLPRQANFCIF/M*RRG
	]	l	1			FTMLARMVSIS*PRDLPALASQSAGITGVSHH
1		1				
393	1743	Ā	3283	205	3	APPOMDFTFALLCFALKGCLPRQKEGGTLNLI
353	1/43	Α.	3483	385	ا	RNRSVVPEFVLLGLSAGPQTQTLLFVLFVVIC
		}				LLTVMGNLLLLVVINADSCLHTPMYFFLGQL
1						SFLDLCHSSVTAPKLLENLLSEKKTISVEGCM
1						A*VFFVFATGGTESSLLAVMAYDRYVAIRTR
						G
394	1744	Α	3284	575	1054	CTKCKADCDTCFNKNFCTKCKSGFYLHLGKC
						LDNCPEGLEANNHTMECVSIVHCEVSEWNP
	1					WSPCTKKGKTCGFKRGTETRVREIIQHPSAKG
1	[				i i	NLCPPTNETRKCTVQRKKCQKGERGKKGRE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine O=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valline, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, I=possible nucleotide deletion, \=possible nucleotide insertion  RKRKKPNKGESKEAIPDSKSLESSKEIPEQREN KQQQ
395	1745	A	3286	1	340	RVLYVPSMGFCILVAHGWQKISTKSVFKKLS WICLSMVILTHSLKTFHRNWDWESEYTLFMS ALKVNKNNAKLWNNVGHALENEKNFERAL KYFLQATHVQPDDIGAHMNVGR
396	1746	Α	3293	1	172	GFRAVVMTVKTEAAKGTLTYSRMRGMVAIL IAFMKQRRMGLNDFIQKIANNSYACKQ
397	1747	A	3295	12	401	AEPACGASSCTPPSLRSSSSQSVGPLRPGRPL WSEACAFL*AAAPQGPASPCCGLPSGFPRVW AQCCPPGGALRFPEGLGSVLSPRRCPQVSRGS GLSAVPQEVPSGFLGPGLRACPQEAPSRFLRA GLT
398	1748	A	3300	1912	2768	KQRRWQNIQRKGPKRYIVIAGNSQSHQPMIFS MLRKLPKVTCRDVLPEIRAICIEEIGCWMQSY STSFLTDSYLKYIGWTLHDKHREVRVKCVKA LKGLYGNRDLTARLELFTGRFKDWMVSMIV DREYSVAVEAVRLLILILKNMEGVLMDVDCE SVYPIV*ASN*GLASAVGEFLYWKLFYPECEI RTMGGREQRQSPGAQRTFFQLLLSFFVESKSH SVTQAGVQWQFSAHRDLCLPGSSNSHVSASR VAGIAGAHRHTWLIYVFFSWRQGFAVLAGL VSNS
399	1749	A	3301	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSE SPPPITDSWAPFISLTHHVLSQSQSPLSSNCWI CLSTHTQ*FTALPADLLTWTQSNVSLHISYLAI PFLADSFLKPVIL*PGNSAKHLSFKLSSLSMVS GRAVALLHLIASGLTSIQTNTASSKPPIWGY\L STQTSFISPPPLCLSRTYPNFAHATMVGQVPQ SLCGLIFTL/RTPCRPSILHPNYKIISTSAWQKV LCFSGSPTHTSLHLTTGSSFLSPHPIPGFPAAN SALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGS N/RLTVDKDNFFLSPKPNSLHQLPSQ\TPYQAL TGAALAGSYPIWENENTLSWLPTFTYNFCLST PSLFFLCDTN*YLCLPANWSGTCTLVFQAPTI NILPPNQTILISVEASISSSPIRNKWALHLITLLT GLGITAALGTGIAGITTSITSYQTLFTTLSNTVE DMHTSITSLQRQLDFLVGVILQNWRVLDLLT TEKGGTCIYLQEECCFCVNESGIVHIAVRLH DRAAEL*HQVADSWWQGSSLLRWIPWVAPF LGPLIFLFLLLMIGPCIFNLVSRFISQRLNCFIQ ASMQKHIDNIFHLCHV*YQSLRGNHSEAPEPR P
400	1750	A	3303	2	453	THWRHSSGVPGSTTARRRRELEIATSDNQE YYNRLCQEVTNRERNDQKMLADLDDLNRTK KYLEERLIELLRDKDALWQKSDALEFQQKLS AEERWLGDTEANHCLDCKREFSWMVRRHHC RICGRIFCYYCCNNYVLSKHGGKKERCC
401	1751	A	3304	l	626	MAPQHSSLDDKVPQQASTVCFEFQDILQHSQ CTEHKDSLWGPGARSQPFGAHNTRLSPDSCP EKIVLRALKDSRAGMPEQDKDPGVQENPDD QRRVPQGTGDAPSAFRPLWDNGGLSPFVSRP GPLERDLHAQRSEVTYNQRSQSSWMSSFPKR NAFVSPYSSMGQAQP/GLPKTNPIGESCCWEG LSLSTQILG*QKPSKYIPSLCKR
402	1752	A	3305	1678	172	MELPSGPGPERLFDSHRLPGDCFLLLVLLLYA PYGFCLLVLRLFLGIHVFLVSCALPDSVLRRF VVRTMCAVLGLVARQEDSGLRDHSVRVLISN HVTPFDHNIVNLLTTCSTVSESEAESATGRFP

SEQ ID	SEQID	Met	SEQ	Predicted	Dradicted and	Amino cold comment / 11 1 C C
NO: of		hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A-Alanine C-Cysteine,
nucl-	peptide		in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, P=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	иепсе	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	j	1	]	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		Į.	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/=possible nucleotide deletion, \=possible
	ł	İ		sequence		nucleotide insertion
					<del></del>	GAQLKAPLSPLAFRMEDTEALPLTPILYPTCO
i		i	i	i	i	FFFFIFLNIFLLAFSSPGSQPLLNSPPSFVCWSR
		•			ł	GFMEMNGRGELVESLKRFCASTRLPPTPLLLF
		ł				PEEFATNGREGLLRFSSWPFSIQDVVQPLTLQ
1	1	1	1	i		VQRTLVSVTVSDASWVSELL\WSLFVPFTVY
-		1				QVRWLRPVHRQLGEANEEFALRVQQ\LVAKE
ŀ		1	1			LG\QTGTRLTPA\DKAEHMKRQRHPR\LRPQS
		1				AQSSFPPSPWVLSS/SDVQTGOTLGFREFKESF
	İ	1				CPHVAIGVFIPERPWPKTGCCKTLTIHLILL*G
		İ				GPVSFSCPE\DIHPRGT*VPTQQASGLPSFPSYG
	İ	1			1	PARGGVL*HPSAQQPLTFA\KSS\WARAGRAL
400		<u> </u>				QERKQ\ALYEYARRRFTERRAPGGLD
403	1753	Α	3307	44	447	DPSPSLLAVALGLRAGERTRSGPGSSSPSGGIS
		1				GGASAGLASSPECACGRSHFTCAVSALGECT
1		1				CIPAQWQCDGDNDCGDHSDEDGCILPTCSPL
						DFHCDNGKCIRRSWVCDSDNDCEDDSDEQD
404	1754	A	2211	400		CPPRECEED
404	1/34	A	3311	409	1	PRHGWGRRVLGRDRPRLQKVKKSVKAIYIPG
	1					QDHVQNEEIYARVLDKFGSNFLSRDNADLGT
1						AFVKFSTLTK*LSALLKNLLQGLSRNVIFTLDS
1	1	1	1			LLKGDLKGVKGDLKKPFDKAWKDYETKFAK
405	1755	Ā	3322	12	450	IEKEKREREWR
105	1733	^	3322	12	458	AAVPVENPWDDPRVRPRVRIFTWEDCIAGQA
	}	İ			-	KVLCNDSYGVTIDWSPKGAFIRLTSQSVGNG
		ľ	1 1			HPASKENDOMVDTIKNTIKVPIIWTYGDMVE
				į		PRPQMIRPAVGAKHKELWKILMALKKIK\IWE GKYTKPSQYNPNYMLELAHNDSVW
406	1756	A	3324	1	426	LSMLSTISTEHRLSVLWPIWYCCHCPTHLSAV
1			]	•	420	MCVLLWALSLLQSILEWMFCSFLFSDVDSDN
						WCQILDFLTAVWLIFLI\LVLCGFTLVLLVRIIC
			l i			GSQKMPLTRLYVTILLTGLVFLFCSLPLSIQ*F
L	Li		1 1	i		LLYWIEKDLDDL
407	1757	A	3328	213	1841	SGDLSPAELMMLTIGDVIKQLIEAHEQGKDID
				.		LNKVKTKTAAKYGLSAQPRLVDIIAAVPPQY
			<u> </u>		l	RKVLMPKLKAKPIRTASGIAVVAVMCKPHRC
		l			1	PHISFTGNICVYCPGGPDSDFEYSTOSYTGYEP
						TSMRAIRARYDPFLQTRHRIEQLKOLGHSVD
						KVEFIVMGGTFMALPEEYRDYFIRNLHDALS
1	1 1				j	GHTSNNIYEAVKYSERSLTKCIGITIETRPDYC
						MKRHLSDMLTYGCTRLEIGVQSVYEDVARD
				1		TNRGHTVKAVCESFHLAKDSGFKVVAHMMP
İ	1			. 1	1	DLPNVGLERDIEQFTEFFENPAFRPDGLKLYP
1	1		}		}	TLVIRGTGLYELWKSGRYKSYSPSDLVELVA
		1		Ì	1	RILALVPPWTRVYRVQRDIPMPLVSSGVEHG
	]	- 1		ļ	}	NLRELALARMKDLGIQCRDVRTREVGIOEIH
		1		1	l	HKVRPYQVELVRRDYVANGGWETFLSYEDP
	]			j	i	DQDILIGLLRLRKCSEETFRFELGGGVSIVREL
			- [	1	l	HVYGSVVPVSSRDPTKFQHQGFGMLLMEEA
		- 1	j	ĺ	ļ	ERIAREEHGSGKIAVISGVGTRNYYRKIGYRL
408	1758	A	2225	<del>,                                    </del>	467	QGPYMVKMLK
700	1/36	A	3335	3	467	ALASPRAAGIRHELTSTMAAGKNKRLTKGGK
		ľ	- 1			KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG
	1			ļ	- 1	LKGRVFEESLADLQND\TDGYLLRVI*VAFTT
		1				ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPLH
409	1759	<del>,</del>	2220	<del>,                                    </del>	1000	DDFARKVKMLKKPKFELRKLMELHGEGSS
703	1139	A	3338	7	1252	PRWRNSARDEILLSFPQNYYIQWLNGSLIHGL
		- [	į			WNLASLFSNLCLFVLMPFAFFFLESEGFAGLK
		ľ	Ì	1		KGIRARILETLGMLLLLALLILGIVWVASALID
	<b></b>					NDAASMESLYDLWEFYLPYLYSCISLMGCLL

SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	i	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	•	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	İ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		Į		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	İ		peptide		/-possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
					j	LLLCTPVGL\SRMFTVMGQLLVKPTILEDLDE
	ł	ł	1		Ì	QIYIITLEEEALQRPTKWAVFIRW/KYNIMELE
						QELENVKTLKTKLERRKKASAWERNLVYPA
	İ	İ			]	VMVLLLIETSISVLLVACNILCLLVDETAMPK GTRGPGIGNASLSTFGFVGAALEIILIFYLMVS
		1		1	}	SVVGFYSLRFFGNFTPKKDDTTMTKIIGNCVS
	1		[			ILVLSSALPVMSRTLGITRFDLLGDFGRFNWL
						GNFYIVLSYNLLFAIVTTLCLVRKFTSAVREE
	]			1		LFKALGLHKLHLPNTSRDSETAKPSVNGHQK
	}	Į.	ļ			1 .
170	<del> </del>	<u> </u>	2000	l	1422	AL COMPONA SPINDENCON/COSTOMATICALL
410	1760	A	3339	127	1433	GSHRFSLASPLDPEVGPYCDTPTMRTLFNLL WLALACSPVHTTLSKSDAKKAASKTLLEKSQ
		[		1	ļ	
	]	1	[	1	1	FSDKPVQDRGLVVTDLKAESVVLEHRSYCSA
İ			1	1	1	KARDRHFAGDVLGYVTPWNSHGYDVTKVFG SKFTQISPVWLQLKRRGREMFEVTGLHDVDQ
ļ	}		1	l		GWMRAVRKHAKGL\P*CLGSCLRTGLTMISG/
					1	YVLDSEDEIEELSKTVVQVAKNQHFDGFVVE
					İ	VWNQI.I.SQKRVGLIHMLTHLAEALHQARLL
	1			l		ALLVIPPAITPGTDQLGMFTHKEFEQLAPVLD
l	ł	l	ľ	f ·	į.	GFSLMTYDYSTAHQPGPNAPLSWVRACVQV
l	1	l			į	LDPKSKWRSKILLGLNFYGMDYATSKDAREP
1	1		i			VVGARYIQTLKDHRPRMVWDSQVSEHFFEY
	1		ŀ		<u>}</u>	KKSRSGRHVVFYPTLKSLQVRLELARELGVG
i	1	1				VSIWELGQGLDYFYDLL*VGIAASAVDVFFSK
			i			PWSE
411	1761	A	3342	74	2701	VATRKLAKGFTOFAKMTEGTKKTSKKFKFFK
411	1/01	] ^	3342	/*	2/01	FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF
	ŀ					EATODDMVTVPKSPPAYARSSDMYSHMGTM
		1	1			
1		1	1	1		
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV
1						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY
					-	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESPDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS
					-	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQAHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHYALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASFVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIKKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKKLRLDLLERFHTMSIML
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHG\RKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGVRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESPDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGYRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGVRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV
						PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGYRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG
412	1762		3347		898	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIKPEVPTGDVEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESSPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGYRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL
412	1762	A	3347	1	898	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIKPEVPTGDVEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGYRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL
412	1762	A	3347		898	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASFVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGYRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL  IDRAAECRTKFLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI
412	1762	A	3347	1	898	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESPDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLUGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL  IDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL
412	1762	A	3347	1	898	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESPDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL  IDRAAECRTKPIPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHILLPDRDNDKSLRQFRYTFQACL*ELL KRLCNRTALMFVAVAGLTFFALSFGFYYEYG
412	1762	A	3347		898	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGYRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL  TDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL KRLCNRTALMFVAVAGLTFFALSFGFYYEYG WEFLEHTYFYHLTRRDIRHNFSPYFYMLYLT
412	1762	A	3347		898	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESPDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL  IDRAAECRTKPIPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHILLPDRDNDKSLRQFRYTFQACL*ELL KRLCNRTALMFVAVAGLTFFALSFGFYYEYG

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SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1 100	in NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	İ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	-1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ł	ł	l	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ		ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ		peptide	1	/=possible nucleotide deletion, \=possible
			<u> </u>	sequence		nucleotide insertion
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413	1763	A	3361	3	474	SHYKEEPLTERIKYD
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	1					PIVGIVAGLVLLGAVVTGAVVSAVMCRKKNS
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414	1764	A	3363	1488	453	HQILELKKKILKTYNPDYDEDLVQEASSEDVL
						GVHMVDKDTERDIEMKRQLRRLRELHLYST
					]	WKKYQEAMKTSLGVPQRERDEGSLGKPLCP
		1	[		Ì	PEILSETLPGSVKKRVCFPSEDHLEEFIAEHLP
						EASNQSLLTVAHADAGTQTNGDLEDLEEHGP
		1	1			GQTVSEEATEVHMMEGDPDTLAELLIRDVLQ
						ELSSYNGEEE\DPEEVKTSLGVPQRGDLEDLE EHVPGQTVSEEATGVHMMQVDPATLAKSDL
l	ļ	l				EDLEEHVPEQTVSEEATGVHMMQVDPATLACSDL
		l				KQLEDSTITGSHQQMSASPSSAPAEEATEKTK
	1					VEEEVKTRKPKKKTRKPSKKSRWNVLKCWD
		<u>L</u> .				IFNIF
415	1765	A	3369	431	315	IPWSWVGRLSVRKMSILF*LTYNYNAILNKTP
416	1266		3000	40		PSFSPSL
410	1766	A	3373	42	651	RQEKMGLGEIGASGVLRSMLKERKKQNMKG
		·				NGNVTLTPLLPAVQCGCHLQPAGRSPLPSSHS
						APGLCSPLHPLQPQQEASTCPSGTLQGREKAA
						PGQGRPLCSLWAGGAGA\PGERGAEGRGPSD QAPDPKSGPWLFPPGLGAPAEVRLHNVPHNL
						RRPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG
						PKPQCSLPSQVPGDTH
417	1767	A	3382	2	2061	EAQDPRACGPDAGGRFAARDAPGNSLRPPPS
						SPP/GWPGQLRLLPRVPGSELRCGKPERGRLP
						ASPPGKIRGWPPGISKRPGLGGRSFPPGFAPRT
						WRPEARGPSVQSLPPIFSPQSAQTTAR*RPGAP
						KNAGRCGGA\RGPRLSLGPPPGPPPAPALPAR
						ASAGAGAAAAALAVGGVRGAGGARGTGGY
					j	GHCSGR/PTGRTGPGPQGPGPPMPARPR*AS\S
			i i	·		TRGSRRGPGSRPARAAAAPRAGDHGRRPVRV HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP
				İ		R\GPGWDCALLPSPGPRSPRAVGCAEPEIWDP
						SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY
						PLKGPGLPPPWGPRTQTGHVIITVQPSGSCIEH
			1		ļ	SKSLD/RGPWGAPPWGPSSSGLCSPKLATAGP
						PQSWGLCQIGRRRGLGGPGLKRGET/GLL*GC
						SMDHANRTKGPGVPTSNRCFSHIPG\GDGCSD
						HSSCEGHPDLHAGREMPAAPGLSELERVRFT
l						VGCGGLASGISSASVSGLSPNRAGGPGQGDW
			[			EMYPVSWQTQESGGQG/SPKTGR*VGMLQA
					ļ	GAGSLQGGTGDGVWGLWEDGP/RG*DSPLPS
j						GTGTEP*TPTTSIPFFPQPSGVYPSRATLLPMPS
						Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA KGIGQLSEIPLLNVETAFWSMWVTYFRK
418	1768	Α	3398	304	2121	EEEEEEDEDDDDNNEEEEFECYPPGMKVQV
-		••			2161	RYGRGKNQKMYEASIKDSDVEGGEVLYLVH
1						YCGWNVRYDEWIKADKIVRPADKNVPKIKH
İ						RKKIKNKLDKEKDKDEKYSPKNCKPPALGPN
					Ì	PPFQTNPISWKWYPKLDLTDAKNSDTAHIKSI
1	1					EITSILNGLQASESSAEDSEQEDERGAQDMDN
						NGKEESKIDHLTNNRNDLISKEEQNSSSLLEE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion NKVHADLVISKPVSKSPERLRKDIEVLSEDTD YEEDEVTKRKDVKKDTTDKSSKPQIKRGKR RYCNTEECLKTGSPGKKEEKAKNKESLCMEN SSNSSSDEDEEETKAKMTPTKK YNGLEEKRK SLRTTGFYSGFSEVAEKRIKLLNNSDERLQNS RAKDRKDVWSSIQGQWPKKTLKELFSDSDTE
410	1000		3399	206	463	AAASPPHPAPEEGVAEESLQTVAEEESCSPSV ELEKPPPVNVDSKPIEEKTVEVNDRKAEFPSS GSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSS VTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGE LQDLQSERE*LASRF*CQCELKQ**SARTRTS* KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK QQKEGK ORECLSIHIGQAGIQIGDACWELYCLEHGIQP
419	1769	A	3399	206	403	NGVVLDTQQDQLENAKMEHTNASFDTFFCE
420	1770	A	3408	1010	685	TRAGKHVPRALFVDLEPTVIDGIR  RRLSFFF*IWSSVLVTQARVQWRDLGSPQPLP PGFKRFSCLSLPSSWDYRHPSPRPVNF/HVFLV VMGFHHVGQAGLELLTSGDLPALASQSARIT GVNHCAOPRGHFH
421	1771	A	3409	355	1326	ADSNLIESCWQELGLGPWGGDWRVEQVGAS ASLRFPREVCSIRFLFTAVSLLSLFLSAFWLGL LYLVSPLENEPKEMLTLSEYHERVRSQGQQL QQLQAELDKLHKEVSTVRAANSERVAKLVF QRLNEDFVRKPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPPTVILEPHVFP GNCWAFEGDQGQVVIQLPGRVQLSDITLQHP PPSVEHTGGANSAPRDFAVFFLLSFFTHQGLQ VYDETEVSLGKFTFDVEKSEIQTFHLQNDPPA AFPKVKIQILSNWGHPRFTCLYRVRAHGVRT SEGAEGSAQGPH
422	1772	A	3412	2	421	EFDAQPSIGALVVFKRP*ATTGSDPGPKRGMN YLVSCSMRSPESGKGEPGTARDYTPMGRPPP PVPSVSPGPLPGSLAIAPHSPEPHPWEQQPPRG QARSPPGGWLGSAT/RVRRPHNHP/RGH/HSP VDTAGAPASPGPDVCE
423	1773	A	3420	91	706	DAQRAIYSSVGPAVSLRQRQQDGAVKESGR/ RGGVRSFSRAAAAMAPIKVGDAIPAVEVFEG EPGNKVNLAELFKGKKGVLFGVPGAFTPGCS KTHLPGFVEQAEALKAKGVQVVACLSVNDA FVTGEWGRAHKAEGKVRLLADPTGAFGKET DLLLDDSLVSIFGNRRLKRFSMVVQDGIVKA LNVEPDGTGLTCSLAPNIISQL
424	1774	A	3421	4	7688	RQVTRVGTRVLGSTTAAVFLSVEDDNDNAPQ FSEKRYVVQVREDVTPGAPVLRVTASDRDKG SNAVVHYSIMSGNARGQFYLDAQTGALDVV SPLDYETTKEYTLRVRAQDGGRPPLSNVSGL VTVQVLDINDNAPIFVSTPFQATVLESVPLGY LVLHVQAIDADAGDNARLEYRLAGVGHDFP FTINNGTGWISVAAELDREEVDFYSFGVEAR DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQSGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPQFRIDADTGAVTTQA ELDYEDQVSYTLAITARDNGIPQKSDTTYLEI LVNDVNDNAPQFLRDSYQGSVYEDVPPFTSV LQISATDRDSGLNGRVFYTFQGGDDGDGDFI

SEQ ID	SEOID	1 17.2	LARA		18	
NO: of		Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
1	peptide	ł	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	İ	1		peptide		/=possible nucleotide deletion, \=possible
	<del> </del>	ļ		sequence		nucleotide insertion
Į	•	ļ .	ļ			VESTSGIVRTLRRLDRENVAQYVLRAYAVDK
1	1	!				GMPPARTPMEVTVTVLDVNDNPPVFEQDEFD
		l				VFVEENSPIGLAVARVTATDPDEGTNAQIMY
1		Ī				QIVEGNIPEVFQLDIFSGELTALVDLDYEDRPE
		1	]		l	YVLVIQATSAPLVSRATVHVRLLDRNDNPPV
İ		Ì				LGNFEILFNNYVTNRSSSFPGGAIGRVPAHDP
	i .					DISDSLTYSFERGNELSLVLLNASTGELKLSR
						ALDNNRPLEAIMSVLVSDGVHSVTAQCALRV
	]					TIITDEMLTHSITLRLEDMSPERFLSPLLGLFIQ
1						AVAATLATPPDHVVVFNVQRDTDAPGGHILN
						VSLSVGQPPGPGGGPPFLPSEDLQERLYLNRS
				i		LLTAISAQRVLPFDDNICLREPCENYMRCVSV
1	1					LRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGF
1						TGDYCETEVDLCYSRPCGPHGRCRSREGGYT
						CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT
						CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP
						AHSFITFRGLRQRFHFTLALSFATKERDGLLL
1	1 1					YNGRFNEKHDFVALEVIQEQVQLTFSAGEST
						TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG
i						QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS
ļ			1	1		VLGNYSCAA\QGTQGGSKKSLDLTGPLLLGG
	<u> </u>		- 1	i		VPDLPESFPVRMRQFVGCMRNLQVDSRHIDM
	1					ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC
		- 1	- 1			VNQWDAFSCECPLGFGGKSCAQEMANPQHF
	} }		i		}	LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD
			1	1		GVLLQAITRGRSTITLQLREGHVMLSVEGTGL
1				i		QASSLRLEPGRANDGDWHHAQLALGAIGGP
			1			GHAILSFDYGQQRAEGNLGPRLHGLHLSNITY
			1	1	Ĭ	GGIPGPAGGVARGFRGCLQGVRVSDTPEGVN
		ŀ	ĺ	ĺ		SLDPSHGESINVEQGCSLPDPCDSNPCPANSY CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC
		ŀ				EHQSVCTRKPSAPHGYTCECPPNYLGPYCET
i i		i			ł	RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC
] [					İ	NKTSGECHCKENHYRPPGSPTCLLCDCYPTG
	1	ŀ				SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF
					ł	AEVTTNGCEVNYDSCPRAIEAGIWWPRTRFG
		[	ĺ		1	LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF
	1	1	ŀ	1	İ	NCTSITFSELKGFAERLQRNESGLDSGRSQQL
.	[	l	ŀ	1	ļ	ALLENATQHTAGYFGSDVKVAYQLATRLL
		i	ŀ			AHESTORGFGLSATODVHFTENLLRVGSALL
	1	j	ļ	1	1	DTANKRHWELIQQTEGGTAWLLQHYEAYAS
	- 1	- 1	- 1	1	ſ	ALAQNMRHTYLSPFTIVTPNIVISVVRLDKGN
[		- 1				FAGAKLPRYEALRGEOPPDLETTVILPESVFR
	İ	1		ĺ		ETPPVVRPAGPGEAQEPEELARRQRRHPELSQ
[	1	- 1	- 1	- 1	ľ	GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK
	- [	- 1		1		RPIINTPVVSISVHDDEELLPRALDKPVTVQFR
		i				LLETEERTKPICVFWNHSILVSGTGGWSARGC
		- 1	1			EVVFRNESHVSCQCNHMTSFAVLMDVSRRE
		1	[	1		NGEILPLKTLTYVALGVTLAALLLTFFFLTLL
		1	1	ļ		RILRSNQHGIRRNLTAALGLAQLVFLLGINQA
			İ	İ		DLPFACTVIAILLHFLYLCTFSWALLEALHLY
	Ī	- 1	ł	.	ł	RALTEVRDVNTGPMRFYYMLGWGVPAFITG
		- 1				LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP
		- 1	1		į	VAFAVSMSVFLYTLAARASCAAOROGFEKKG
			1			PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL
	1	1		ľ	i	FHYLFATCNCIQGPFIFLSYVVLSKEVRKALK
				1		LACSRKPSPDPALTTKSTLTSSYNCPSPYADG
'				l		RLYQP\YGDSAGSLHSTSRSGKSQPSYIPFLLR
	1					EESALNPG\QGPPGLGGIPGR/LCFLGRFKDQQ
				1		H\DS*TRDFDSDLSLEDDQSGSYASTHSSDSEE

600.00	1 050 10				CW TO THE	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ļ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						EEEEEEEAAFPGEQGWDSLLGPGAERLPLHS
l	ì	į			1	TPKDGGPGPGKAPWPGDFGTTAKESSGNGAP
	ŀ					EERLRENGDALSREGSLGPLPGSSAQPHKGIL
1	Í		}	ļ.	į	KKKCLPTISEKSSLLRLPLEQCTGSSRGSSASE
		Ì				GSRGGPPSRPPPRQSLQEQLNGVMPIAMSIKA
1	}	ŀ	ł		ł ·	GTVDEDSSGSEFLFFNFLH
425	1775	A	3429	155	1417	GEPAVQSCDCGCTQRSCPWLLVAPGLLSSSSS
123	1.75	^^	7.5	1.55	* ' * '	RAASVREAEDAPLQPASIHPVSQGSRGPEGSL
	Ì			ļ		GSAECLPGDPLGARRATRAHSPVPGPPPSLPA
		1	1	į		AGTAVKRGLQPG*GA/GATSTPGTGAATGGL
						CGPAWAAPSAVGPCCCCPSISTTPSQMRSARP
	1	j	j	}	ł	SLGCLPSWAS\PGTEHPPGPQGPGPS*DLCSV*
l			1	<b>!</b>		
1	1		1		1	KREFQRGPWAGMVILHRISAADPARAPGPDS
1		-		1	1	NLQSALQQPATGCSEPAAVYSPPIGLWGA**P
			J	J	J	EYG*PQHSLPG*TAPADR*P\AGIKDRVYSNSI
ĺ	ſ					YELLENGQRAGTCVLEYATPLQTLFAMSQYS
	1					QAGFSREDRLEQAKLFCRTLEDILADAPESQN
	.[				1	NCRLIAYQEPADDSSFSLSQEVLRHLRQEEKE
1	1	1	ĺ		ŀ	EVTVGSLKTSAVPSTSTMSQEPELLISGMEKP
·	ì	ł	ł	}	1	LPLRTDFS
426	1776	A	3431	1662	369	AIWWLSWLQHDLLPTPTQVAIDFTASNGDPR
	j	ł	1			SSQSLHCLSPRQPNHYLQALRAVGGICQDYD/
	1		į	1		SVGESGAGGNRQGGLAQRIPQLFLLPSDKRFP
1				Ì		AFGFGARIPPNFEVG*MRGKEGDGGRVSQAE
1			1		1	KAGPHCSRLALTG\SHDFAINFDPENPECEGK
1	ł	ľ	1	1	ĺ	RGDFHLPRLPADTLHTGAQTPLPRAQLPVPST
İ				1		HPRPVFI\EISGVIASYRRCLPQIQLYGPTNVAP
		ļ				IINRVAEPAQREQSTGQATKYSVLLVLTDGV
ļ		1			1	VSDMAETRTAIVRASRLPMSIIIVGVGNADFS
1		ł	1	1	į	DMRLLDGDDGPLRCPRGVPAARDIVQFVPFR
		ļ		]		DFKDVSPPGPFRLKDSSASHPPKSDLRLPPFD
				1		VLLRTREPSWPP*SPTSPSDDPASPTLPLTPNHI
1		1				TVPTL\AAPSALAKCVLAEVPRQVVEYYASQ
ĺ				<u> </u>		GISPGAPRPCTLATTPSPSP
105	1000	<del>                                     </del>	7776	170	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW
427	1777	A	3446	. 79	9/48	
1	1	İ	1	į		GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA
1	1			1		ASRPEASGDCRAGRETAMATLEKLMKAFESL
		1		1		KSFQQQQQQQQQQQQQQQQQQQQQPPPP
]	1	]	J	1	1	PPPPPPPQLPQPPPQAQPLLPQPQPPPPPPPPP
		1		1		GPAVAEEPLHRPKKELSATKKDRVNHCLTIC
					1	ENIVAQSVRNSPEFQKLLGIAMELFLLCSDDA
1	1		1	1		ESDVRMVADECLNKVIKALMDSNLPRLQLEL
1		1		1	1	YKEIKKNGAPRSLRAALWRFAELAHLVRPQK
1		1		1	}	CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP
1		1		ļ		KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI
				1		RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG
1	1	1	1			LLVPVEDEHSTLLILGVLLTLRYLVPLLQQQV
	1	1	1	1		KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL
	ļ	1	j	ì		TLHHTOHODHNVVTGALELLQQLFRTPPPEL
1		1	]	1		LQTLTAVGGIGQLTAAKEESGGRSRSGSIVELI
		1	1			AGGGSSCSPVLSRKQKGKVLLGEEEALEDDS
					1	
			1		1	T ESRSDVSSSALTASVKDBISGBLAASSGVSTPG
						ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGHDUTEOPRSOHTLOADSVDLASCDLTSS
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIKGDIGQSTDDDS
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GTLICSILSRSRPHVGDWMGTIRTLTGNTFSL ADCIPLLRKTLKDESSVTCKLACTAVRNCVM SLCSSSYSELGLQLIIDVLTLRNSSYWLVRTEL LETLAEIDFRLVSFLEAKAENLHRGAHHYTGL LKLQERVLNNVVIHLLGDEDPRVRHVAAASL IRLVPKLFYKCDQQADPVVAVARDQSSVYL KLLMHETQPFSIFSVSTITRIYRGYNLLPSITD VTMENNLSRVIAAVSHELITSTTRALTFGCCE ALCLLSTAFPVCIWSLGWHCGVPPLSASDESR KSCTVGMATMILTLLSSAWFPLDLSAHQDAL ILAGNLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLONSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAHNHIRLFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYIEVGGPRESEAIIPNIFF FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLLRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILPMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFBPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSFFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTFKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRVEMLLAANLQSSMAQLPMEEINRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMLOKYGULHIFKS GMFRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW ABVQQTFKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRVEMLLAANLQSSMAQLPMEEINRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PVYSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVILLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHHHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERTNTTPKAISEEBEEPVDPTTQNPKYI TAACEMVAEMVESLQSVLALGHKNSGVPA FLITPLLRNIISISARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYR NTLGWTSRTQFETWATLLGV

SEQ ID NO: of nucl- ectide seq- uence	SEQ ID NO: of, peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL
						LELYSRWILPSSSARRTPAILISEVVRSLLVVS DLFTERNQFELMYVTLTELRRVHPSEDEILAQ YLVPATCKAAAVLGMDKAVAEPVSRLLESTL RSSHLPSRVGALHGILYVLECDLLDDTAKQLI PVISDYLLSNLKGIAHCVNIHSQQHVLVMCAT AFYLIENYPLDVGPEFSASIIQMCGVMLSGSE ESTPSIIYHCALRGLERLLLSEQLSRLDAESLV KLSVDRVNVHSPHRAMAALGLMLTCMYTG KEKVSPGRTSDPNPAAPDSESVIVAMERVSVL FDRIRKGFFCEARVVARILPQFLDDFFPPQDIM NKVIGEFLSNQQPYPQFMATVVYKVFQTLHS TGQSSMVRDWVMLSLSNFTQRAPVAMATWS LSCFFVSASTSPWVAAILPHVISRMGKLEQVD VNLFCLVATDFYRHQIEEELDRRAFQSVLEV VAAPGSPYHRLLTCLRNVHKVTTC
428	1778	A	3449	3	430	NSRPSPSAALVEVLLRSGSTFPHTVSGGWAA WGPWSSCSRDCELGFRVRKRTCTNPEPRNGG LPCVGDAAEYQDCNPQACPVRGAWSCWTS WSPCSASCGGGHYQRTRSCTSPAPSPGEDICL GLHTEEALCATQACPEGWS
429	1779	A	3464	583	3	DALDRRYLERCHPAAGGWVGEGE*ALCQKT/ RFSGVLEPPLPSLKDGGRFPAWT*RSCSKSLR AAFTSQFFPSRRSRASPGSAP\GNGQNLTEQHP CPGSCDPQVLSASWM*VEHRSKFRPPP*NSTI PPES\RS*QGGTVQTGQHSSGREAGSWRARGR NAGRR*KGGGKIGTKQGAVRARKECRGEMA SGETDSE
430	1780	A	3473	2802		FRMRIFLHCPWNQQMWKIWNLLETSLESCKA HLSIQKLLKER\Q\QLPVFKHRDSIVETLKRHR VVVVAGET\GSGKSTQVPHFLLEDLLLNEWE ASKCNIVCTQPRRISAVSLANRVCDELGCENG PGGRNSLCGYQIRMESRACESTRLLYCTTGV LLRKLQEDGLLSNVS/HMFIVDEVHERSVQS DFLLIILKEILQKRSDLHILILMSATVDSEKFST YFTHCPILRISGRSYPVEVFHLEDIIEETGFVLE KDSEYCQKFLEEEEEVTINVTSKAGGIKKYQE YIPVQTGAHADLNPFYQKYSSRTQHAILYMN PHKINLDLILELLAYLDKSPQFRNIEGAVLIFL PGLAHIQQLYDLLSNDRRFYSERYKVIALHSI LSTQDQAAAFTLPPPGVRKIVLATNIAETGITI PDVVFVIDTGRTKENKYHESSQMSSLVETFVS KASALQRQGRAGRVRDGFCFRMYTRERFEG FMDYSVPEILRVPLEELCLHIMKCNLGSPEDF LSKALDPPQLQVISNAMNLLRKIGACELNEPK LTPLGQHLAALPVNVKIGKMLIFGAIFGCLDP VATLAAVMTEKSPFTTPIGRKDEADLAKSAL AMADSDHLTIYNAYLGWKKARQEGGYRSEI TYCRRNFLNRTSLLTLEDVKQELIKLVKAAGF SSSTTSTSWEGNRASQTLSFQEIALLKAVLVA GLYDNVGKIIYTKSVDVTEKLACIVETAQGK AQVHPSSVNRDLQTHGWLLYQEKIRYARVY LRETTLITPFPVLLFGGDIEVQHRERLLSIDGW IYFQAPVKIAVIFKQLRVLIDSVLRKKLENPK MSLENDKILQITELIKTENN
431	1781	A	3474	1	-	FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ PCPPAPAPSRPRSLGSLGQRVPAALATAAQEL PATLGGDGGKPALTAGEAALPGLHRSGVPAA AARC*PCT/SRPT*STLSPTQAAWWCRPSRRQ QRGEASTGGASGRRCGSCFQV

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	_	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ŀ	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	1	/=possible nucleotide deletion, \-possible
422	1782	<del></del>	2.470	sequence		nucleotide insertion
432	1/82	A	3478	416	23	OLRRLTLPNFKTY/YSS*IIEIAWH**KNMQID
i				1		QWFRRESPEIDLCKYS*LSFDKEAKAIK/WKE
		l	}	l		CSLFNKWC/YKNWM/LHVQKKRI*VQTLHPS QKLK\SKWIKDLNVECRITKLLDQEYPGDLGY
	j					SRALNSGSR
433	1783	A	3504	1876	552	CLAPCSPQPEKNGMQPLLLLLPPLLYQQLLHS
1				10.0	552	SLGAPGESTLLVRTSKLLVGLGLQLLVWLLL
1		}	1			QTRSLLALQLHLTSSAPLLAAPTAVCSCSRCS
						APRSRCVARPAARTGLPTPAPASSPAPAASPA
			Ì			PAASPAPAESTA\PQPLILLPKP/PPAPGAPPPRP
	1					GAPPPRPAASPSPAASPAPPAASPVLTASPPLP
		ļ				AASPSPAASPAPPAASPVLTASPPLPAASPSPA
		l				ASPAPPAASPVLTASPPLPAASPALAASPVHT
		1				ASPPVHVASPPVHTASPPVHVASPPVHTASPP
1.						VHVASPPVHTASPHVHVASPPVHVASPPVHV
		i				ASPPVHTASPPVHVASPPVHTASPHVHVASPP
		ļ	ŀ			VHTASPPVHVASPPVHVASPPVHVAYPPVHV
		Ì				ASPPVHVASPPVHVASPPVSCSGDSTSDCFPP
434	1784	Ā	3516	142	590	QPGAVFPHSLAPSLGGWSHLVAALP GGVNRPRSETEQVKTPVLISSWDYRHPPPRPA
	1701	ļ <sup>(*</sup>	33.0	172	350	SFFVFLV*TGF\TALARMVLISWPCDLPTSASQ
						SAGITGVRHHA\RLLYFEQESHSVTQAGW\VQ
						WHNLGSLQPLSLEDRLSPGVLGCSALCRSGV
					•	RTKFGINMVTSRERGTTRLPKEG
435	1785	A	3529	1	3161	MSLVRAALEALDELDLFGVKGGPQSVIHVLA
						DEVQHCQSILNSLLPRASTSKEVDASLLSVVS
						FPAFAVEDSQLVELTKQEIITKLQGRYGCCRF
						LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC
						EWPLFWTYFILDGVFSGNAEQVQEYKEALEA
			[ [			VLIKGKNGVPLLPELYSVPPDRVDEEYQNPHT
,						VDRVPMGKLPHMWGQSLYILGSLMAEGFLA
			1			PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTIL
	i					KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF
						LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK
				i		LYDIRKTIFTFTPQFIDQQQFYLALDNKMIVE
						MLRTDLSYLCSRWRMTGOPTTTFPISHSMLDE
ĺ						DGTSLNSSILAALRKMQDGYFGGARVOTGKL
						SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN
,	}					YDYLESGNWMNDYDSTSHARCGDEVARYL
						DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT
					l	TCDLMSLVTKAKELHVQNVHMYLPTKLFQA
					Į	SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ
			]		I	SGEVDFKALVLQLKETSSLQEQADILYMLYT
						MKGPDWNTELYNERSATVRELLTELYGKVG EIRHWGLIRYISGILRKKVEALDEACTDLLSH
	}			J		QKHLTVGLPPEPREKTISAPLPYEALTOLIDEA
						SEGDMSISILTQEIMVYLAMYMRTQPGLFAE
	l				i	MFRLRIGLIIOVMATELAHSLRCSAEEATEGL
,	j			ļ	J	MNLSPSAMKNLLHHILSGKEFGVERSVRPTD
[	į	•				SNVSPAISIHEIGAVGATKTERTGIMQLKSEIK
	į					QSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW
	1					QRRRRLDGALNRVPVGFYQKVWKVLQKCH
	1		ŀ		i	GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL
	i		ľ			NRVPQPEYRQLLVEAIL\VLTMLADIEI\HSIGS
						IIAVEKIVHIANDLFLQEQKTLGADDTMLAKD
	ļ					PASGICTLLYDSAPSGRFGTMTYLSKAAATY
436	1706		2546	72	202	VQEFLPHSICAMQ
+30	1786	A	3546	73	393	CP*LTWELLEVKKAEVLQDSLDGRYSTPSSCL
1						EQPDSCRPYGRSFYALEEKHVIFSLDVGETDN

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  KGKGKTIRGI*TFKGRKGGTYQREHDANPLA
437	1787	A	3554	5157	2939	PXSARSCWMRKG  AVRAEPGLEELSSGLRAHSPSATTVCEPEAQG SASGCRYAAHPHWGLGGAAAAGGSWEPQPP RPVCEPAGRGKPHPPAAPRSPLLPGSRRRPHA AQPGARARTSPPPASARNMAARPAATLAWSL LLLSSALLREGCRARFVAERDSEDDGEEPVVF PESPLQSPTVLVAVLARNAAHTLPHFLGCLER LDYPKSRMAIWAATDHNVDNTTEIFREWLK NVQRLYHYVEWRPMDEPESYPDEIGPKHWP TSRFAHVMKLRQAALRTAREKWSDYILFIDV DNFLTNPQTLNLLIAENKTIVAPMLESRGLYS NIFWCGITPKGFYKRTPDYVQIREWKRTGCFP VPMVHSTFLIDLRKEASDKLTFYPPHQDYTW TFDDIIVFAFSSRQAGIQMYLCNREHYGYLPIP LKPHQTLQEDIENLIHVQIEAMIDRPPMEPSQ YVSVVPKYPDKMGFDEIFMINLKRRKGQGGD RWLRTLYEQEIEVKIVEAVDGKALNTSQLKA LNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSV WKEVIDRELEKTLVIEDDVRFEHQFKKKLMK LMDNIDQAQLDWELIYIGRKRMQVKEPEKA VPNVANLVEADYSYWTLGYVISLEGAQKLV GANPFGKMLPVDEFLPVMYNKHPVABYKEY YESRDLKAFSAEPLLIYPTHYTGQPGYLSDTE TSTIWDNETVATDWDRTHAWKSRKQSRIYSN AKNTEALPPPTSLDTVPSRDEL
438	1788	A	3563	130	527	IFFNSSSLFCRVFCLFLRWSFTLVAQARVQ*C NLSSLQPLPPGFK*FSCLSPPRS*DYRRPPPRPA NFLYF**RQGFTVLGQAGLELLT/S/GDPPTSA SQSAGITGVSHRAWPVHAISTHISLVKTRPSLT TLG
439	1789	A	3565	446	1834	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSY GQPSLQDELKDNTTVFTRILDRLLDGYDNRL RPGLGERVTEVKTDIFVTSFGPVSDHDMEYTI DVFFRQSWKDERLKFKGPMTVLRLNNLMAS KIWTPDTFFHNGKKSVAHNMTMPNKLLRITE DGTLLYTMRLTVR\AECPMAFGRDFPMD\AH ACPLKFGSYAYTRAEVVYEWTREPARSVVV AEDGSRLNQYDLLGQTVDSGIVQSSTGEYVV MTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSF WLNRESVPARTVFGVTTVLTMTTLSISARNSL PKVAYATAMDWFIAVCYAFVFSALIEFATVN YFTKRGYAWDGKSVVPEKPKKVKDPLIKKN NTYAPTATSYTPNLARGDPGLATIAKSATIEP KEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLL FGIFNLVWATYLNREPQLKAPTPPLL
440	1790	A	3568	1	350	STSSCFPAAAAAIMREIVHLQAGQCGNQIGAK FWEVISDEHGIDPTGTYHGDSDLQLERINVYY NEATGEAPVPSPTALRGPRGPCLG*RPPVPAG GKYVPRAVLVDMEPGTMDSV
441	1791	A	3569		1751	FVAVAGAVSGEPLVHWCTQQLRKTFGLDVS EEIIQYVLSIESAEEIREYVTDLLQGNEGKKGQ FIEELITKWQKNDQELISDPLQQCFKKDEILDG QKSGDHLKRGRKKGRNRQEVPAFTEPDTTAE VKTPFDLAKAQENSNSVKKKTKFVNLYTREG QDRLAVLLPGRHPCDCLGQKHKLINNCLICG RIVCEQEGSGPCLFCGTLVCTHEEQDILRGDS NKSQKLLKKLMSGVENSGKVDISTKDLLPH QELRIKSGLEKAIKHKDKLLEFDRTSIRRTQVI

1	CDC 70	000 m	1 1/-4	Larc	1 6 . a	1 8 (***	
	SEQ ID NO: of	SEQ ID NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	nucl-	peptide	noa	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, B=Glutamic Acid,
	eotide	seq-		USSN	location		F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	uence		09/496	correspondi	corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine,
-	uence	uonoc		914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Ì	donoo		1	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
		1	ŀ	1	peptide	sequence	/=possible nucleotide deletion, \=possible
		1			sequence		nucleotide insertion
- !			<del></del>		Doguesto	<del> </del>	DDESDYFASDSNQWLSKLERETLQKREEBLK
						İ	ELRHASRLSKKVTIDFAGRKILEEENSLAEYH
			ł	1			SRLDETIQAIANGTLNQPLTKLDRSSEEPLGVL
- 1						•	VNPNMYQSPPQWVDHTGAASQKKAFRSSGF
I			1		İ		GLEFNSFQHQLRIQDQEFQEGFDGGWCLSVH
1			ŀ			1	QPWASLLVRGIKRVEGRSWYTPHRGRLWIAA
- 1							TAKKPSPQEVSELQATYRLLRGKDVEFPNDY
- [							PSGCLLGCVDLIDCLSQKQFKEQFPDISQESDS
١							PFVFICKNPQEMVVKFPIKGNPKIWKLDSKIH
ı							QGAKKGLMKQNKAV
	442	1792	Α	3576	1	2019	MPRSHTGERLCEGKEGSQCAENFSPNLSVTK
							KTAGVKPYECTICGKAFMRLSSLTRHMRSHT
1			١,				AIRANEKPYKCKEC\GRAFSLSQILSK\IIERSH
-							TGEKPYKCKQCGKTFIYHQPFQRHERTHIGEK
١							PYECKQCGKALSCSSSLRVHERIHTGEKPYEC
١							KQCGKAFSCSSSIRVHERTHTGEKPYACK\EC
-[							GKAFIS\TTSVLTHMITHNGDRPYKCKECGKA
							FIFPSFLRVHERIHTGEKPYKCKQCGKAFRWS
1							TSIQIHERIHTGEKPYKCKECGKSFSARPAFRV
١		· l					HVRVHTGEKPYKCKECGKAFSRISYFRIHERT
1							HTGEKPYECKKCGKTFNYPLDLKIHKRNHTG
1						Ì	EKPYECKECAKTFISLENFRRHMITHTGDGPY
ı							KCRDCGKVFIFPSALRTHERTHTGEKPYECKQ
١			Ì				CGKAFSCSSYIRIHKRTHTGEK\PYECKECGK
						. !	AFIYPTSFQGHMRMHTGEKPYKCKECGKAFS
1							LHSSFR\RHTRIHNYEKPLEC*Q\CGKAFSVSTS
1							LKKPMRNAQSDRKLY/KCEK*EKVFNSNRCF QSCENSH*REKSCQCK*YRKRDTR*FMYSQV
							PHNHVSVSNGPYR/CGSPIRLYNT*NISINRNL
1							VAVVTP*CSTLFKCLWCWCKRAALSVV*/IVO
							DSGRGRWLTPVIPALWEAKAGGSRGQEIKTIL
1							ANTVKPHLY
ſ	443	1793	A	3578	287	114	DFYERKFEQFIEGHKQIVNKWRDLLCSWKRK
L				·			LSIIKKSVLQNNL*FSAASMRFQKVFF
Γ	444	1794	A	3582	3335	1909	HLFFSLFLAAMAMTGSTPCSSMSNHTKERVT
			. 1	i			MTKVTLENFYSNLIAQHEEREMRQKKLEKV
1					-		MEEEGLKDEEKRLRRSAHARKETEFLRLKRT
1						:	RLGLEDFESLKVIGRGAFGEVRLVQKKDTGH
				i		:	VYAMKILRKADMLEKEQVGHIRAERDILVEA
	-		ļ	l			DSLWVVKMFYSFQDKLNLYLIMEFLPGGDM
1	İ			1		:	MTLLMKKDTLTEEETQFYIAETVLAIDSIHQL
			1			•	GFIHRDIKPDNLLLDSKGHVKLSDFGLCTGLK
			1	İ		1	KAHRTEFYRNLNHSLPSDFTFQNMNSKRKAE
1	ļ	.					TWKRNRRQLAFSTVGTPDYIAPEVFMQTGYN
		Ì	j	ŀ	1	i	KLCDWWSLGVIMYEMLIGYPPFCSETPQETY
	ļ				Į	!	KKVMNWKETLTFPPEVPISEKAKDLILRFCCE
1			İ	ļ	Ī	,	WEHRIGAPGVEEIKSNSFFEGVDWEHIRERPA
	ļ	ļ	ŀ		1		AISIEIKSIDDTSNFDEFPESDILKPTVATSNHPE
	l	1			İ	:	TDYKNKDWVFINYTYKRFEGLTARGAIPSYM
H	445	1795	A	3584	$\overline{}$		RAAK PTROJEKBEAVSELOOLIBANDEAHOVILERB
		.,,,	^	2204	•	107	RTRGIEKRFAYSFLQQLIRYVDEAHQYILEFD GGSRGKGEHFPYEQEIKFFAKVVLPLIDOYFK
	-	i			1	;	NHRLYFLSAASRPLCSGGHASNKEKEMVTSL
1	l	Ī	İ		1		
	ļ		J		l		FCKLGVLVRHRISLFGNDATSIVNCLHILGQT
					j		LDARTVMKTGLESVKSALRAFLDNAAEDLE KTMENI KOGOFTHTPNOPKGVTOINVTTVA
			İ				KTMENLKQGQFTHTRNQPKGVTQIINYTTVA LLPMLSSLFEHIGQHQFGEDLILEDVQVSCYRI
	1	İ		1	1		LTSLYALGTSKSIYVERQRSALGECLAAFAGA
						i	FPVAFLETHLDKHNIYSIYNTKSSRERAALSLP
1			ı		ļ		TNVEDVCPNIPSLEKLMEEIVELAESGIRYTO
_						;	

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	i l	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		)	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	İ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}			peptide		/=possible nucleotide deletion, \=possible
	l			sequence		nucleotide insertion
					i	MPHVMEVILPMLCSYMSRWWEHGPENNPER
i	ĺ			ŀ		AEMCCTALNSEHMNTLLGNILKIIYNNLGIDE
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ADAAEVPGTRGHSQQEAAMPHIPEDEEPPGE PQAAQSPAGQQEPTAGVSCSPTPTIVLTGDA TSPEGETDKNLANRVHSPHKRLSHRHLKVST ASLTSVDPAGHIIDLVNDQLPDISISEEDKKKN LALLEEAKLVSERFLTRRGRKSRSSPGDSPSA VSPNLSPSASPTSSRSNSLTVPTPPEGDEADVS SPHPGEPNVPKGLADRKQNDQRKVSQGRLAP RPPPVEKSKEIAIEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE		450	1800	A	3620	1	2676	
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TSPEGETDKNLANRVHSPHKRLSHRHLKVST ASLTSVDPAGHIIDLVNDQLPDISISEEDKKKN LALLEAKLVSERFLTRRGRKSRSSPGDSPSA VSPNLSPSASPTSSRSNSLTVPTPPEGDEADVS SPHPGEPNVPKGLADRKQNDQRKVSQGRLAP RPPPVFKSKEIAIEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE				1	-	i		POAAOSPAGOOGPPTAGVSCSPTPTIVI.TGDA
ASLTSVDPAGHIIDLVNDQLPDISISEEDKKKN LALLEEAKLVSERFLTRRGKSRSSPGDSPSA VSPNLSFSASTTSSRSNSLTVPTPEGDBADVS SPHPGBPNVPKGLADRKQNDQRKVSQGRLAP RPPPVFKSKEIAIEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGFAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKBVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE	1	j		- 1	1			TSPEGETDKNLANRVHSPHKRI SHRHI KVST
LALLEEAKLVSERFLTRRGRKSRSSPGDSPSA VSPNLSPSASPTSSRSNSLTVPTPPEGDEADVS SPHPGEPNVPKGLADRKQNDQRKVSQGRLAP RPPPVEKSKEIAIEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKBVENVPVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE				- 1	[	1	- [	ASLTSVDPAGHIIDI VNDOI PDIGIGEEDKUKNI
VSPNLSPSASPTSSRSNSLTVPTPPEGDEADVS SPHPGEPNVPKGLADRKQNDQRKVSQGRLAP RPPPVEKSLAIEQKENFDPI_QYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE				- 1	1	-	1	LALLEFAKI VSERFI TROCDE POR DISISERDIKANI
SPHPGEPNVPKGLADRKQNDQRKVSQGRLAP RPPPVEKSKEIAIEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLBSRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE				-		1	1	VSPNI SPSA SPTSSR SNSI TVDTDDEADE ADVO
RPPPVEKSKEIAIEQKENFDPLQYPETTPKGLA PVTNSSGKMALNSPQPGPVESELGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE	1		ŀ	- 1	1	ļ	1	SPHEGENAPKOI VEDROMODENTOCOM TO
PVTNSSGKMALNSPQPGPVESÈLGKQLLKTG WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE	١		1		1	I		DDDDVEKCKET VEOKENEDDI COMPANDICOLA
WEGSPLPRSPTQDAAGVGPPASQGRGPAGEP MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEKKFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE		1		}		İ	ł	DUTNICOCUMAL NODODODODODO CONTROLO CONT
MGPEAGSKAELPPTVSRPPLLRGLSWDSGPEE PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKBVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE		1	1	- 1	ı	I	1	
PGPRLQKVLAKLPLAEEEKRFAGKAGGKLAK APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE	ĺ	1		l	- 1	ŀ	l	
APGLKDFQIQVQPVRMQKLTKLREEHILMRN QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE			i	1	j	ļ	4	MOTEAGSKAELPTIVSRPPLLRGLSWDSGPER
QNLVGLKLPDLSEAAEQEKGLPSELSPAIEEE ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE	1	ļ	İ	J	J	ļ	]	PURLUK YLAKLPLAEEEKRFAGKAGGKLAK
ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE	l	į	ļ	i	ļ	1	İ	
LTEKEVENVFVQLSSAFRNDSYTLESRINQAE RERNLTEENTEKELENFKASITSSASLWHHCE		İ	1		l	j	ł	UNLYGLKLPDLSEAAEQEKGLPSELSPAIEEE
RERNLTEENTEKELENFKASITSSASLWHICE	1	ļ	ł	i	ŀ	Į.	1	ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPP
RERNLTEENTEKELENFKASITSSASLWHHCE HRETYQKLLEDIAVLHRLAARLSSRAEVVGA	l	- 1		- 1	ł		1	
HRETYQKLLEDIAVLHRLAARLSSRAEVVGA	1	ļ	1				]	RERNLTEENTEKELENFKASITSSASLWHHCE
	L							HRETYQKLLEDIAVLHRLAARLSSRAEVVGA

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  VRQEKRMSKATEVMMQYVENLKRTYEKDH AELMEFKKLANQNSSRSCGPSEDGVLRTARS MSLTLGKNMPRRRVSVAVVPKFNALNLPGQ TPSSSIPSLPALSESPNGKGSLPVTSALPALLE NGKTNGDPDCEASAPALTISCLEELSQETKA RMEEEAYSKGFQEGLKKTKELQDLKEEEEEQ KSESPEEPEEVEETEEEEKDPRSSKLEELVHFL QVMYPKLCQHWQVIWMMAAVMLVLTVVL GLYNSYNSCAEQADGPLGRSTCSAAQKDSW WSSGLQHEQPTEQ
451	1801	A	3623	504	198	QLIQHQTVHTGRKLYECKECGKAFNQGSTLI RHQRIHTGEKPYECKVCGKAFRVSSQLKQHQ RIHTGERPYQCKELKGRGAEMLAVLAVKEQ NRTPVNYGK
452	1802	A	3628	2	195	MTCLHSAKAFHY*SSCSFSCEEGFALIGPEVV QCTALGVWTAPAPVCIAVQCQHLEALNEGT MG*DYPFTAFAYGSSCKYECHTVYRVRGLD MLHSRGCYLWNGHFTT*EAISCEPLERPCH*S V*CSFSCEEGFALIGPEVVQCTALGVWTAPAP VCIAVQCQHLEALNEGTMG
453	1803	A	3637	662	142	IQAKGLGIWHVPNKSPMQHWR\KGSLLRYRT DTGFLQTLGHNLLGIYQKYPVKYGEGKCWT DNGPVIPVVYDFGDAQKTASYYSPYGQREFT AGFVQFRVFNNERAANALCAGMRVTGCNTE HHCIGGGGYFPEASPQQCGDFSGFDWSGYGT \HVGYSSSREITE\AAVLLFYR
454	1804	A	3641	1	362	TOVHPAMLGLDELGRSGCGHCTQADLRFGD AAGRDPGQDNDRNTAEPAFPPPPRVMAAAA ALRAPAQSSVTFEDVAVNFSLEEWSLLNEAQ GCLYHDVMLETLTLISSLGKVLILNCDLS
455	1805	A	3646	2	414	AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT
456	1806	A	3656	396	8 .	QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F
457	1807	A	3660	14	1961	SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMYLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS VVLSPGQKNKAGMSQCDMHPEMVSLCQENF LMDNAYFCEADAKKCIPVAPHIKVESHIQP\S LNQEDIYITTESLT\TAAGSP\GTGEHVPGSEM

## WO 01/57188

OPO ID	CEO TO	11-4	Lopo	Deading 1	Danding 1 1	[A-b9]
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	noa	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ucisco	(	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uottoo		ł	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l	1	}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	acquaiio	/=possible nucleotide deletion, \=possible
	,	ì		sequence		nucleotide insertion
	<del> </del>	<del> </del>	<del>                                     </del>	1 - 1		PVPDVTSIHIVQSPQCLILNATALPLPDKEFLS
	1		1	1		SCGYVSTDQLNKIMP
458	1808	A	3663	154	462	TRAPASGRSGAGLALSANAPDSGGHPGATEG
		ł	1	1		PAGSLAHASGSARGTWRVRGRGSHGWERTV
		j	j			GAGGCANPVPALHSCASAPRGTGRVSALGPK
	ĺ	1	1	1		TGSSPLSSPKG
459	1809	A	3664	902	135	LOKYNTSMALFDFVLHNSTGEIRYTTEDDVIQ
		Ì				SQNALGKYNTSMALFESNSFEKTILESPYYVD
		1	1	ļ		LNQTLFVQVSLHTSDPNLVVFLDTCRASPTSD
						FASPTYDLIKSGCSRDETCK\VYPLFGHYGRF
				1		QFNAFKFLRSMSSVYLQCKVLICDSSDHQSRC
		(		1		WQGCVSRSKRDISSYKWKTDSIIGPIRLKRDR
		1	1	1		SAINGNSGFQHETHAEETPNQPFNSVHLFSFM
		1	]			VLALNVVTVATITVRHFVNQRADYQ\YQKLQ
		<u> </u>	L			NY
460	1810	A	3670	850	557	LGILMSPQVEAGEI*ALLTPPPGCMQFSPLTL/P
			l	l		K*WVSPGLTP/PPPEVPSVFLVEPGLPHAGQA
		1	į.			GLDLL\TSGDPPASTSQSARTTDVSHRAQPLAI
		ļ.,	1451		4004	S
461	1811	A	3671	2472	2099	IGVLAFETGSCSVTRLYCIGIIMPHCSLDLAGS\
		1				TSAFRIAGTTSVHHHPQLTFFFFWIETGSHCV
						VQTGL*LLALSNPPALASQIAGISGMSHRAWP
462	1812	A	3672	394	110	GLVLYSLEFSLLCASQSLIMLFTCYNE
402	1012	A	30/2	394	110	VKPVNGESKRD*GADTQTCEGEADEQLQT\N
	}	1	1	1		CYYD/STKSFFYISCG*K\RKPTWAENRRLNA KMFGIPLHSNSDPWGYEEREVIGFHRSRVSRG
						HGS
463	1813	A	3673	348	1	QRNPFSAGHPQRPPTSGSQSELLAQPRLRPGR
100	1015	1 **	30,3	340	'	KSSFSRDQDVW*SQAVPKRQ*QRNPFSAGHP
			1			QRPPTSGSQSELLAQPRLRPGRKSSFSRDQDV
	1.	1	}	1		WPGQKPRPSQQQHQMCASPTLGQRSPFALEP
		ì	ŀ			VPAYHGGRDPFASARPSPVGIPKPRAAPAGG
						GWRRIRPKSSTK
464	1814	A	3676	2253	320	PVIQRCSQPYGFSLLISFFLKCVSETSQQPPSR
			1			KVFQLLPSFPTLTRSKSHESQLGNRIDDVSSM
				Ì		RFDLSHGSPOMVRRDIGLSVTHRFSTKSWLS
			j			QVCHVCQKSMIFGVKCKHCRLKCHNKCTKE
						APACRISFLPLTRLRRTESVPSDINNPVDRAAE
			İ	[		PHFGTLPKALTKKEHPPAMNHLDSSSNPSSTT
	i	l		1		FSTPSSPAPFPTSSNPSSATTPP\NPSP\GQR\DSR
	1	1 .				I TO I TO STATE I DOI TO STATE I THI SE TO SECOND
				1		FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR
	-	•				FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGR WGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \GISGVVP\EGRRENQLKLSHDWLCYLAPEIVR
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \GISGVVP\EGRRENQLKL\SHDWLCYLAPEIVR EMTPGKDEDQLPFSKAADVYAFGTVWYELQ
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \(\text{GISGVVP\EGRRENQLKL\SHDWLCYLAPEIVR}\) EMTPGKDEDQLPFSKAADVYAFGTVWYELQ ARDWPLKNQAAEASIWQIGSGEGMKRVLTS
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \GISGVVP\EGRRENQLKL\SHDWLCYLAPEIVR EMTPGKDEDQLPFSKAADVYAFGTVWYELQ
						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \(\text{GISGVVP\EGRRENQLKL\SHDWLCYLAPEIVR}\) EMTPGKDEDQLPFSKAADVYAFGTVWYELQ ARDWPLKNQAAEASIWQIGSGEGMKRVLTS
,						FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDNKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \GISGVVP\BGRRENQLKLSHDWLCYLAPEIVR EMTPGKDEDQLPFSKAADVYAFGTVWYELQ ARDWPLKNQAAEASIWQIGSGEGMKRVLTS V\$LGKEV\$ENLSACWAFDLQERPS\FSLLMD
465	1815	A	3679	8	803	FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \GISGVVP\EGRRENQLKLSHDWLCYLAPEIVR EMTPGKDEDQLPFSKAADVYAFGTVWYELQ ARDWPLKNQAAEASIWQIGSGEGMKRVLTS V\$LGKEVSENLSACWAFDLQERPS\FSLLMD MLEKLPKLNRRLSHPGHF*KSADINSSKVVPR
465	1815	A	3679	8	803	FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \(\text{GISGVVP\(\text{BGRENQLKLSHDWLCYLAPEIVR\)}\) EMTPGKDEDQLPFS\(\text{AADVYAFGTVWYELQ\) ARDWPLKNQ\(\text{AAEASIWQIGSGEGMKRVLTS\) VSLGKEVSENLSACWAFDL\(\text{QERPS\(\text{FSLIMD\)}\) MLEKLPKLNRRLS\(EIPGHF\*KSADINSSKVVPR\) FERFGLGVLESSNPKM
465	1815	A	3679	8	803	FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGR WGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \GISGVVP\EGRRENQLKLSHDWLCYLAPEIVR EMTPGKDEDQLPFSKAADVYAFGTVWYELQ ARDWPLKNQAAEASIWQIGSGEGMKRVLTS VSLGKEVSENLSACWAFDLQERPS\FSLLMD MLEKLPKLNRRLSHPGHF*KSADINSSKVVPR FERFGLGVLESSNPKM IPSPAWWNSTWADTFSLLLALAVALYLGYY WACVLQTHRAFCASNTEDLETVVNHIKHRYP QAPLLAVGISFGGILVLNHLAQARQAAGLVA
465	1815	A	3679	8	803	FNFPSC/AYFIHHR\Q\QFIFPDISAFAHAAPLPE AADGTRLDDQPKADVLEAHEAEAEEPEAGK SEAEDDEDEVDDLPSSRRPWRGPISRKASQTS VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR WHGEVAIRLLEMDGHNQDHLKLFKKEVMN YRQTRHENVVLFMGACMNPPHLAIITSFCKG RTLHSFVRDPKTSLDINKTRQIAQEIIKGMGY LHAKGIVHKDLKSRNVFYDNG\KVVITDFGLF \(\text{\text{GISGVVP\certs}}\text{\text{CISGVVP\certs}}\t

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			İ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=1 yrosine, X=Unknown, *=Stop codon,
1		ľ		peptide	•	/=possible nucleotide deletion, \=possible
<b></b>				sequence		nucleotide insertion FGYODCVTYYKAASPRTKIDAIRIPVLYLSAA
1			ļ			DDPFSTVCALPKQAAQHSPYVALLITARGGHI
ſ						GFLEGLLPWQHWYMSKLLHQYAKAIFQDPE
						GLPDLRALLPSEDRNS
466	1816	Α	3684	3	307	SSQYIVQSKTKIFL*AAREKQ/RHTCRRFSIRLS
1	1					ANISSQTGEARGQWPSVFKVLKEKKLSTKKS
1		İ				FGQK*GR\RKTFPDKQK/LREFDTTRPTIQEML
467	1017		3687	2465	027	TGVLQG
407	1817	A	308/	2465	837	ELPTPLIAAHQLYNYVADHASSYHMKPLRMA RPGGPEHNEYALVSAWHSSGSYLDSEGLRHQ
[			•			DDFDVSLLVCHCAAPFEEQGEAERHVLRLQF
			1			FVVLTSORELFPRLTADMRRFRKPPRLPPEPE
		ſ	1			APGSSAGSPGEASGLILAPGPAPLFPPLAAEVG
			1			MARARLAQLVRLAGGHCRRDTLWKRLFLLE
			1	·		PPGPDRLRLGGRLALAELEELLEAVHAKSIGD
		<b>!</b>			!	IDPQLDCFLSMTVSWYQSLIKVLLSRFPQSCR
	}	Ì	İ			HFQSPDLGTQYLVVLNQKFTDCFVLVFLDSH LGKTSLTVVFREPFPVQPQDSESPPAQLVSTY
					ļ.	HHLESVINTACFTLWTRLL*GSGLDH*MSLFL
	}	1	ł	i		ESWAYQIACQRQD*PALLGPRASQTLSDTKG
	1	~	İ			FVTMS*GSAAPAWQQEPPSPNTHSH*PIQDSR
		Ì			·	ESGQPRGPLGPFWGTPFGPPGRVSGVHTGWQ
						TPPRAPLPESCPL\PLTTVSHLCPLSLRVFTSHL
				_		DITAGHSHRDDTWVPIPALPLKHLRPPSSPFA
1		ì	l	·		LGPWVSHPLMRWVQKLSHLHSNPGTGFSMG GKQQRN
468	1818	A	3691	960	499	OTCRKDKRAIYPHFQNE*MNEIKAI*SGTGGI
1 700	1010	1 ^	3071	500	177	OCFHSONDSAFFFFLFLLETEFCSAA/TYOWH
	[	Ì				DFLSMQPPPPGFKQFTCLSLLSSWNYRR\PPPF
1		1				PGNF\*FLVKTGFPHVGQTGFELLTSSDLAPLA
	<u> </u>					SQNGGITGMSPCAWPFFFFFFGLC
469	1819	A	3714	4747	495	MAYSWQTDPNPNESHEKQYEHQEFLFVNQP
1			1	ł	1	HSSSQVSLGFDQIVDEISGKIPHYESEIDENTFF VPTAPKWDSTGHSLNEAHQISLNEFTSKSREL
		ĺ		-		SWHQVSKAPAIGFSPSVLPKPQNTNKECSWG
		l				SPIGKHHGADDSRFSILAPSFTSLDKINLEKEL
		1	1	1		ENENHNYHIGFESSIPPTNSSFSSDFMPKEENK
1	1		l		1	RSGHVNIVEPSLMLLKGSLQPGMWESTWQK
				į		NIESIGCSIQLVEVPQSSNTSLASFCNKVKKIR
		1	l	Ì	}	ERYHAADVNFNSGKIWSTTTAFPYQLFSKTK
		1	1	ł	1	FNIHIFIDNSTQPLHFMPCANYLVKDLIAEILH FCTNDOLLPKDHILSVWGSEEFLONDHCLGS
			1			HKMFQKDKSVIQLHLQKSREAPGKLSRKHEE
1		1	1	1	{	DHSQFYLNQLLEFMHIWKVSRQCLLTLIRKY
		1		<b>{</b>		DFHLKYLLKTQENVYNIIEEVKKICSVLGCVE
1		ł	1	ł		TKQITDAVNELSLILQRKGENFYQSSETSAKG
						LIEKVTTELSTSIYQLINVYCNSFYADFQPVNV
		ł	1	l	1	PRCTSYLNPGLPSHLSFTVYAAHNIPETWVHR
	1	1		i		INFPLEIKSLPRESMLTVKLFGIACATNNANLL
	}	1			{	AWTCLPLFPKEKSILGSMLFSMTLQSEPPVEM ITPGVWDVSQPSPVTLQIDFPATGWEYMKPD
1		ł	1	l	ł	SEENRSNLEEPLKECIKHIARLSQKQTPLLLSE
			1		ļ	EKKRYLWFYRFYCNNENCSLPLVLGSAPGW
1	!	l	1	{	}	DERTVSEMHTILRRWTFSQPLEALGLLTSSFP
1.				]	Į	DQEIRKVAVQQLDNLLNDELLEYLPQLVQAV
1	1	1	1	}	}	KFEWNLESPLVQLLLHRSLQSIQVAHRLYWL
			1	1	ļ	LKNAENEAYFKSWYQKLLAALQFCAGKALN
		}				DEFSKEQKLIKILGDIGERVKSASDHQRQEVL KKEIGRLEEFFQDVNTCHLPLNPALCIKGIDH
			}			DACSYFTSNALPLKITFINANLMGKNISIIFKA
L	L		L	L	l	PUCO II. I DIVILLI LIZI I TIMMINLINIONI NIGHTAN

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GDDLRQDMLVLQLIQVMDNIWLQEGLDMQ MIIYRCLSTGKDQRLVQMVPDAVTLAKIHRH SGLIGPLKENTIKKWFSQHNHLKADYEKALR NFFYSCAGWCVVTFILGVCDRHNDNIMLTKS GHMPHIDFGKFLGHAQTTGGIKRDRAPFIFTS EM\(\text{EYFITEGG\(\text{KNPQHFQDFV\(\text{ELCRAYNIIR}\)}\) KHSQLLL\NLL\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
470	1820	A	3718	430	75	SHGSISII.NLHQGCVFLPSLPAQGLRCYRCLA VLEGASCSVVSCPFLDGVCVSQKVSV/CWQ*/ CPWGARAEGRLSAVVDSQISCCKGDLCNAV VLAAGSPWALCVQLLLSLGSVFLWALL
471	1821	A	3723	891	494	LRQSL/NSVPQAGVQWRDSSLQAPPPRFTPLS CLSLPSSWDYRRLPPCLANFLYF**RRGFTML ARMVLIS*PRDPPASASQ\STEITGGSHRAQHP TDSRDHSERSVKKSHEVISELRMKVIKCKVAF SKNPI
472	1822	Α	3734	443	251	GFIET*NFCVSKDTSKKLS/RLPTKWKNVFAN *ISDKGLVSRICQELLRHLDAEQVSSTAGLSL
473	1823	A	3746	3	500	THASGGARSGAGWAGRGVRAGTEAGRGOIF LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV KFAENRAK
474	1824	A	3753	2	5262	RPLFAREGGIYAVLVCMQEYKTSVLVQQAG LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ MTREIFASIDSATRPGSESLLLTVPAAVILMLN TEGCSSAARNGLLLNILLCNHHTLGDQIITQ ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL QQETOPFILLLRTLDAPGPNKTLLLSVLRVIT RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE IVQELTCFLHRLASMHKDYAVVLCCLGAKEI LSKVLDKHSAQLLLGCELRDLVTECEKYAQL YSNLTSSILAGCIQMVLGQEDHERTHQPINIP FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN PHRASKLTDHNPKTYWESNGSTGSHYITLHM HRGVLVRQLTLLLVASEDSSYMPARVVVFGG DSTSCIGTELNTVNVMPSASRVILLENLNRFW PIIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL GKTCWEALVSPLVQNITSPDAEGVSALGWLL DQYLEQRETSRNPLSRAASFASRVRRLCHLL VHVEPPPGPSPEPSTRPFSKNSKGRDRSPAPSP VLPSSSLRNITQCWLSVVQEQVSRFLAAAWR APDFVPRYCKLYEHLORAGSELFGPRAAFML

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of	hod	ID NO:		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
1	1	nou		beginning		
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ĺ		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	ł	1	ł	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	]		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ì	1			peptide	,	/-possible nucleotide deletion, \-possible
				sequence	,	nucleotide insertion
	<del></del>			Soquence		ALRSGFSGALLQQSFLTAAHMSEQFARYIDQ
1	İ					ALASOFSOALLQQSFL I AARIVISEQFAK I IDQ
i	ł					QIQGGLIGGAPGVEMLGQLQRHLEPIMVLSG
1						LELATTFEHFYQHYMADRLLSFGSSWLEGAV
	'			,		LEQIGLCFPNRLPQLMLQSLSTSEELQRQFHLF
1						QLQRLDKLFLEQEDEEEKRL*EEEEEEEEA
	<b>}</b> ·					EKELFIEDPSPAISILVLSPRCWPVSPLCYLYHP
				l		RKCLPTEFCDALDRFSSFYSQSQNHPVLDMG
ĺ	ĺ					PHRRLQWTWLGRAELQFGKQILHVSTVQMW
						LLLKFNQTEEVSVETLLKDSDLSPELLLQALV
1						PLTSGNGPLTLHEGQDFPHGGVLRLHEPGPQ
1				,		RSGEALWLIPPQAYLNVEKDEGRTLEQKRNL
					'	LSCLLVRILKAHGEKGLHIDOLVCLVLEAWO
j						
[						KGPNPPGTLGHTVAGGVACTSTDVLSCILHLL
				1		GQGYVKRRDDRPQILMYAAPEPMGPCRGQA
						DVPFCGSQSETSKPSPEAVATLASLQLPAGRT
1	·			1		MSPQEVEGLMKQTVRQVQETLNLEPDVAQH
						LLAHSHWGAEQLLQSYSEDPEPLLLAAGLCV
)	!					HQAQAVPVRPDHCPVCVSPLGCDDDLPSLCC
						MHYCCKSCWNEYLTTRIEQNLVLNCTCPIAD
		. 1				CPAQPTGAFIRAIVSSPEVISKYEKALLRGYVE
						SCSNLTWCTNPQGCDRILCRQGLGCGTTCSK
1						CGWASCFNCSFPEAHYPASCGHMSQWVDDG
<b>!</b>	1					· ·
						GYYDGMSVEAQSKHLAKLISKRCPSCQAPIE
1						KNEGCLHMTCAKCNHGFCWRCLKSWKPNH
						KDYYNCSAMVSKAARQEKRFQDYNERCTFH
1			i			HQAREFAVNLRNRVSAIHEVPPPRSFTFLNDA
				,		CQGLEQARKVLAYACVYSFYSQDAEYMDVV
1				:		EQQTENLELHTNALQILLEETLLRCRDLASSL
1					·	RLLRADCLSTGMELLRRIQERLLAILQHSAQD
						FRVGLQSPSVEAWEAKGPNMPGSQPQASSGP
						EAEEEEDDEDDVPEWQQDEFDEELDNDSFS
						YDESENLDQETFFFGDEEEDEDEAYD
475	1825	A	3754	1093	96	GTSRNQHSPKTHA*RSS/WPQPPPLFLPPLQPQ
1 '''	1025	_^^	3/34	1075	/0	ATGRRRRTRTQQRTAALLTDGTTKTGAAW
1						SRRPSLCWPSRTTGAPGAK*AVLVRSATPTTN
1						PPNPQSPTGAAGKLRAPGNRAG/SEPSSQEPPP
						DGTR\RPASITGVAQSPATRATPSLPCLHVPAP
1 1						SRGQTLGVRTTGRASRLTVDRSRLSWPGRSA
				·		RSGGGRWRPNAPRGRWPRAP*SWEPGSWTE
						PWRWPFPAAESPPHRCIYCTNHVSPAGPARPS
1				]		HVYIIRATINSISHPLCRAQSSPWEAAGVWRR
1						PAQPAPTSDVNINLLRKPRVKRHDLIYQFLGN
1						TLWEEGRORPPETLOPAR
476	1826	A	3758	901	521	FFFGNGVSPCPOAGV*WHDLDSLONLPPGFK
'''			3,30	-0.	221	RFSYLSLPSSW\DYRHVPPRQANFCIF/M*RRG
]						
[						FTMLARMVSIS*PRDLPALASQSAGITGVSHH
L.	1005					APPQMDFTFALLCFAPKGCLPRQKEGGTLNLI
477	1827	A	3761	843	575	GVISAHCNLRL/CHLPGSSNSPASASQVAGTIG
j						ARTTPS*IFVFLVETGFHHVSQDGLDLL/NFVI
						RPRRPLKVLGLQACTRARLPSPLKEL
478	1828	Α	3763	267	1240	HLLSFHLWSASLDCLEQLSQERHVKGMLLGP
1	*					PPVNESTKPSPSPWKLTPPMCSIPPVFPPKSGS
1 1						PTTSWS/PSGHSKLEVERAOTGPFCLHIYCP*P
1						GVTDNTTSLLHYIPFPRL\SGLVCFPAH*FPSY
		'				
						WTOHSFASQAWLRQVPEVSKHLQCPSAESLL
[						TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG
1						PDEHPQDTDARDADGEAREREP/RRPSFAA*P
į l		l			1	VWGQP\ESPLPEASSAPPGPTLGTLPEVETIRA
j ļ				,		CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE
i						QTPIITQSTNGPLPSPCHHEHPLSSVEGEAPPA

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide insertion
479	1829	A	3766	2	2152	YSPIRLLEVCVPLPKIFIKRQAPLKVSLLQDLK DFFQKVSQVYVAIDERLASLKTDTFSKTREEK MEDIFAQKEMEEGEFKNWIEKMQARLMSSS VDTPQQLQSVFESLIAKKQSLCEVLQAWNNR LQDLFQQEKGRKRPSVPPSPGRLRQGEESKIS AMDASPRNISPGLQNGEKEDRFLTTLSSQSST SSTHLQLPTPPEVMSEQSVGGPPELDTASSSE DVFDGHLLGSTDSQVKEKSTMKAIFANLLPG NSYNPIPFPFDDKHYLMYEHERVPIAVCEKE PSSIIAFALSCKEYRNALEELSKATQWNSAEE GLPTNSTSDSRPKSSSPIRLPEMSGGQTNRTTE TEPQPTKKASGMLSFFRGTAGKSPDLSSQKRE TLRGADSAYYQVGQTGKEGTENQGVEPQDE VDGGDTQKKQLINPHVELQFSDANAKFYCRL YYAGEFHKMREVILDSSEDFIRSLSHSSPWQ ARGGKSGAAFYATEDDRFILKQMPRLEVQSF LDFAPHYFNYITNAVQQKRPTALAKILGVYRI GYKNSQNNTEKKLDLLVMENLFYGRKMAQ VFDLKGSLRNRNVKTDTGKESCDVVLLDENL LKMVRDNPLYIRSHSKAVLRTSIHSDSHFLSS HLIIDYSLLVGRDDTSNELVVGIIDYIRTFTWD KKLEMVVKSTGILGGQG*MPTVVSPELYRTR FCEAMDNYFLMVPDHCTGLGLNC
480	1830	A	3777	251	3	QGCGSAGTLIHY**ECKMVQLLWKTV*QFLI KLNIKDPAITLDVYPNEVKNYVRTKTYTQMF I/ANFIMAKSWKQPTHPSVRT
481	1831	A	3779	333	3	EAAIRQPEPNILDVNQIFKDLAMIIHDQGDLID SIEANAESSEVLVERAPGQLQRPA\YYQKKSR KKMCLVVLVQTAIILICERIM*VVYTTKWSPPI VLPVSCFQGQKFN
482	1832	A	3780	2	371	TGGRQGKNDHTSITEKPSRDFNRHLITQNI*M PNQDMKSSSNSLJIRKVQIKPTILYHHIFTRKA KMKTTDKTKYR*GFKAITTLJHCSQDCKLQ*S /L*ENHFMIFPKAEQHITYDTTIPFLR
483	1833	A	3787	43	448	LMKDLSPYVMETHYILNRLNER/RSMWRHIIG KLPNTKDQEKILKAIRGRREVIQGS/RQQYRR PAAFSAAEKARRLWCS/VFNIERRNL/CEYPTK LSFNIKGEMTFSDKTEFTTNRPSLKMLLKDRI QEEGKMF*KEKCFKRKE
484	1834	A	3798	1	727	FFFFETESRSVAQAGVQWCNLGSLQALPPGF\ SHSPASASRVAGTTGTRH*ARLIFYIFSRDGVS PC*PGWS*SPDLVIRPPRLPKCWDYRREPPRP A*FFVFLVE\QGFTMLARMVSIS*PQ/CDLPAS VSQNAGITGVSHCAWPCLHFCFFGFFFEMESC SVAQAEVQWHDLRSLQAPPPGFTPFSCLSLPG SWDYRRPPPRPANF\CIFSRDGVSPC*PGWSRS PDLVIRPPRPPKVLGLQA
485	1835	A	3802	1	239	FFFFEMECLTVSQAGVQWYNLHSLQPLPPGF KQFSC\LSLPSSWD*RVPTSRPAKF/CVIF*DGV SHCQPGWSAVVQPPLH
486	1836	A	3811	378	98	RYD*SSQSENIP\QKEFLLKYP*CTATLGMRN MSIMKKKSIFSAEFYKVSLPSLLL\HLLAIEWG FHIEIQLTIHQHPLNYELESDFVHIVEYM
487	1837	A	3814	771	320	FDPDWTRAAGIRHEKKPKALAYRRENSPGDL PPPPLPPPEEEASWAL/GAEGSRQHVLPGAGA QWGEESGPGRAPGSPAGAPPR*RGLAP\NSRP SFLSRGQGTSTCSTAGSNSSRGSSSSRGSRGPG RSRSRSQSRSQSQRPGQKRREEPR

- COCO 170	L OFF O TO	137.	(dec	18.0	1 ==	
SEQ ID	SEQ ID NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of		hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1		Į.	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	İ		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
٠,	i			peptide		/-possible nucleotide deletion, \-possible
	ļ			sequence		nucleotide insertion
488	1838	Α	3818	1	781	FRACLLELIPYAPTLSWTACPPAMAGPRGLLP
ĺ	ŀ	1	ľ	1		LCLLAFCLAGFSFVRGQVLFKGCDVKTTFVT
		1	1		i	HVPCTSCAAIKKQTCPSGWLRELPDQITQDCR
l	ł		İ		ļ	YEVQLGGSMVSMSGCRRKCRKQVVQKACCP
İ	1				l	GYWGSRCHECPGGAETPCNGHGTCLDGMDR
i	1	i	1	ĺ	ľ	NGTCVCQENFRGSACQECQDPNRFGPDCQSV
1	1	l				CSCVHGVCNHGPRGDGSCLCFAGYTGPHCD
İ			Ì		ł	QELPVWQELGFPQNNPRLRKAPNCKCLPG*H
	ĺ	[		ļ		RNGLIATPNPCRP
489	1839	A	3822	934	669	FFFSEMESRSVTRLECSGAISAHLRLLGSSNSP
1	l .				1	ASAS*VAGTIGACHHAQLIFVFLVETGFHHVG
{	1	1	1	(		QDGLDLLNLMIHPPRPPKVLGFQA
490	1840	$\Lambda$	3825	79	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW
				1		GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA
I						ASRPEASODCRAGRETAMATLEKLMKAFESL
ľ	1	ĺ				KSFQQQQQQQQQQQQQQQQQQQPPPP
	1					PPPPPPPQLPQPPPQAQPLLPQPQPPPPPPPPPPPPPPP
1	1					GPAVAEEPLHRPKKELSATKKDRVNHCLTIC
İ	1					ENIVAQSVRNSPEFQKLLGIAMELFLLCSDDA
ŀ	į į					ESDVRMVADECLNKVIKALMDSNLPRLOLEL
			1			YKEIKKNGAPRSLRAALWRFAELAHLVRPOK
	1		ŀ			CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP
İ	1			<i>'</i>	·	KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI
						RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG
į	1					LLVPVEDEHSTLLILGVLLTLRYLVPLLQQQV
ĺ	1					KDTSLKGSFGVTRKEMEVSPSAEOLVOVYEL
[						TLHHTQHQDHNVVTGALELLQQLFRTPPPEL
						LOTLTAVGGIGQLTAAKEESGGRSRSGSIVELI
	1					AGGGSSCSPVLSRKQKGKVLLGEBEALEDDS
İ	1					ESRSDVSSSALTASVKDEISGELAASSGVSTPG
						SAGHDIITEQPRSQHTLQADSVDLASCDLTSS
İ	1					ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG
					:	TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD
						GTDNQYLGLQIGQPQDEDEEATGILPDEASEA
	1					FRNSSMALOQAHLLKNMSHCROPSDSSVDKF
						VLRDEATEPGDQENKPCRIKGDIGQSTDDDS
						APLVHCVRLLSASFLLTGGKNVLVPDRDVRV
						SVKALALSCVGAAVALHPESFFSKLYKVPLD
				1		TTEYPEEOYVSDILNYIDHODPOVRGATAILC
						GTLICSILSRSRFHVGDWMGTIRTLTGNTFSL
						ADCIPLLRKTLKDESSVTCKLACTAVRNCVM
				1		SLCSSSYSELGLQLIIDVLTLRNSSYWLVRTEL
						LETLAEIDFRLVSFLEAKAENLHRGAHHYTGL
	1			-		LKLQERVLNNVVIHLLGDEDPRVRHVAAASL
				İ		
						IRLVPKLFYKCDQGQADPVVAVARDQSSVYL
	1					KLLMHETQPPSHFSVSTITRIYRGYNLLPSITD
					i	VTMENNLSRVIAAVSHELITSTTRALTFGCCE
						ALCLLSTAFFVCIWSLGWHCGVPPLSASDESR
	(					KSCTVGMATMILTLLSSAWFPLDLSAHQDAL
				İ		ILAGNLLAASAPKSLRSSWASEEEANPAATK
						QEEVWPALGDRALVPMVEQLFSHLLKVINIC
	]					AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK
						GKEKEPGEQASVPLSPKKGSEASAASRQSDTS
						GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA
						NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL
						ATLQDIGKCVEEILGYLKSCFSREPMMATVC
	}					VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA
						QRLGSSSVRPGLYHYCFMAPYTHFTQALADA
						SLRNMVQAEQENDTSGWFDVLQKVSTQLKT
						NLTSVTKNRADKNAIHNHIRLFEPLVIKALKQ

SSQ ID   Mot   hot   hot   hot   multiple   poptide cottode   sequence   poptide cottode   sequence   poptide cottode   sequence	[ 000 TO	CEO TO	1/4	1 880	Dundicted	Dundint - 1 1	Amino acid sequence (A=Alanine C=Cysteine,
nuciotóde sequence vence							
Sociation   194			поа				
Sequence			ĺ				
Serior   S		-			-		
antino acid residue of peptide sequence  T-Throatins, W-Typtophan, Y-Typton, W-Tynton, W-Typtophan, Y-Typton, W-Typtophan, P-possible nucleotide detection, W-possible nucleotide nestertion  TTTTT/CVQLGEQYLDLI_ACI_VQLRVIYYCLL DSDQVFIGFVLK.VGEVIEVGCPRESEAITPNITGE PTVLLSYERYHSKQIGFPEIQLCDGIMASGR KAVTHAIPALQPIVHILI_VLRGTNKADAGKE LETQLGEVVXMILLIQPHQULE_VLRQMEIL VQLQ CHEKNEDKWKRLSRQIADIILEMIAKQOMHI DSHEALGVIAT_HEBLAPSEXEYDWILLEMIA  DSHEALGVIAT_HEBLAPSEXEYDWILLEMIA VTPNTMASVSTVQLWISGILALRVLISGSTED IN_SRIQELSSPYLISCTVINIRLRGDGSTSILE EHSEGKQRN.PEETFSRTLQ.VGILLEDIVT KQLKVEMSEQQHTYYCQELGTLAMCHIFIES GMFRRTIAAATALFRSDCGGSSTYTLDSI.NLR ARSMITHFIAL_VLLWCQILLLVHNITDYRWW AEVQOTFKRRISLSTKLLSFQMSGEEEDSDLA AKLGMCNEEVSTRRGALLIFCPOVCONLINDS HLTWLINNHQDLISLSHEPFVQDFISA-VHRNS AASGLFQAGNGKENLSTPTWIKKTLQCLEEGI HLSQSGAVLTLVVDRLLCTPSRVLARMVDIL ACRRVEMLLAANLQSSMAQLMEELTNICQPS LQSSGLAQRRQRLYSLLDRERLSTMQDSI.SPS PPVSSHPLGDGMVSLETVSPKDWYVHVK SQCWTRSDSALLEGASLVWRTPAEDMAAPM MMSEPNSLLAAANLQSSMAQLMEELTNICQPS LQSSGLAQRRQRLYSLLDRERLSTMQDSI.SPS PPVSSHPLGDGMVSLETVSPKDWYVHVK SQCWTRSDSALLEGASLVWRTPAEDMAAPM MMSEPNSLLAACSLSCAGGASLAEA ARSUTLARVSGTVQQUPAVHHIVGQPELPAEP AARWSKLNDLFGDAALVOSLTAARLQFGL UVVSKLESHLHLPPEKKENDVXFVVATLEAL SWHLIBEQFILSDLQAGLDCCCLALQFGL WSVVSSTERVTHAGSLIVCVHFILEAVAVQP EQLLSPRRTINTKAASBESEBVDNTTQNFKV1 TAACCBWAZBWYBELGVSLALQFGL WSVVSSTERVTHAGSLIVCVHFILEAVAVQP EQLSPRRTINTKAASBESEBVDNTTQNFKV1 TAACCBWAZBWYBELGVSLAUCHKNNGVPA FILTILRINIISLARLPLVNSVTRVPPLVWKLG WSKKGGGGFATAFBEVFEELGKEVEFEFFFY RITLGWTSKTGFEETWAATLGGVLYQVXCGLUCCCLALQFGL WSKKGGGGFATAFBEVFEELGCAGASLEVE LEUGAMAVSKENDATAHLTQCANSLSLVSSAG VKLGQVSBFSVVSLLVVS DCFTERRQFELMYYTLTELRRVPFSDEBLAQ YLVPATCKAAAVGAMBAAVGAMSLAVAGNASLVASSV UFDRJRKGFFCGARVAVARLPQRDDFFDQ DDARNVGGFELSTRONQPYSGRAVSRLCSGOFL LEUGAMAVSKENDATAHLTQCRDDFFPQ DDARNVGGFELSTRONQPYYDRAVFSILLORGHL VKSLSCFPQAATSSPFYTSLANGALGHAUTVYKVFCI LHSTQSSMYRDWVABLSSNFTGARVAMA TYPSSLSCFPQAATSSPFYTAALSHAWALGHAUTVMYX VLJDRJRKGFFCGARVAAAA TYPSSLSCFPQAATSSPFYTAALGGLRCHLLISEGUSSUADBELD VKSLSCFPQAATSSPFYTSLANGALFVYRLVEGT LHSTQSSMYRDWYMLSSTSAQTTE HHYDRO		ценсе					
residue of peptide sequence  V=Tyrosine, X=Usanown, **Sisp codon, peptide sequence  V=Tyrosine, X=Usanown, **Sisp codon, peptide sequence  V=Tyrosine, X=Usanown, **Sisp codon, peptide sequence  V=Tyrosine, X=Vsanown, **Sisp codon, peptide sequence  V=Tyrosine, X=Vsanown, **Sisp codon, peptide sequence  RAYTHAIPALQPIYHBLPVLRGTPKADAGKE  LETOKEYVVSMLRILDYHVJUSEMETLVLQ  CHKENEDKWKRLSRQIADIII PMI.AKQQMHI  DSREALGVLNTLFELLAPSSLRYVDMLIRSMF  VTNYTMANSVSTQUMISGILARUVSIQSTED  INLSNIGLSFSPYLISCI VINRLINGDOSTSILE  EHSEGRQINTPLPETTSRRILQVOILLEUNTIT  KQIKVVEMSEQQHTYYCQELGTLIMCLHIFKS  GMFREITAATULRVOILLUTHITVRW  ARWQITYKRISLSSTKLLSSYNGSEGEDSDIA  AKLGMCNEUVRRGALLIFCDYVCQNLOHDSE  HLTWLINNHODISLSHEEPTVQFUSGEGEDSDIA  ARGAITGARGSRCSINLSTPTMLKKTLQLEGI  HLSQSGAVLTLYVDRLLCTPSRVLARWVDIL  ACREVEMILAANLQSSKAQLIFCDYVCQNLOHDSE  HLTWLINNHODISLSHEEPTVQFUSALARWVDIL  ACREVEMILAANLQSSKAQLIFCDYVCQNLAMBE  SQSGAVATISLALGCALVINGTEDSDATAWN  MISEPINISLAPCLSLGMSEISGGQKSALFEA  ARWYLARVSLALGCALVINGTEDSDATAWN  MISEPINISLAPCLSLGMSEISGGQKSALFEA  ARWYLARVSLALGCALVINGTEDDMATAWN  MISEPINISLAPCLSLGMSEISGGQKSALFEA  ARWYLARVSTRYTHACSLIVCYHHYQFEDPLAPF  ARWYLARVSLANDLFQDAALVQSLFTLARALQY  LVVVSKLPSHLEPEKERDIVKVVVATELAL  SWHLHBGPISLDLQAGLDCCCLALQFGI,  WSVVSSTEVTHACSLIVCYHYLGELAVAVQP  EQLISPERITITYRKAISEEEEVDPPTTOPKYN  TAACEMVARWFELOSVALGHKRNGVYPA  FLIPILANNISLARLPLVNSYTRYPPLVWKLG  WSPKPGGGFGTAPFEPVERLQFKRYFOTPK  RITLGWTSRTQPEELMYVTLTELRAVVPQELPAPF  RITLGWTSRTQPEELMYVTLTELRAVVPGELEGMS  YKKGQVSIBSVALGALVSLANGANSKENALATHULTQAVD  PYSISSPATTGALISHEKLLLQNFERLGSMS  YKKGQVSIBSVALGALVSLANGANSKENALACHATCANT  GESSPFEDITFRTONIAVAQUATSLVSLANT  VPYAGRAVSCLEOQPRINERKALDLINGREEE  ADAPASSEPTSIVNSKRHAAQVDIISCSQFL  LELYSRWLPSSARRTPALLISGUSSDFLANGANISGS  EESTISMYTCHARGANAVARDATSLVATSLVS  LELYSRAVERSSARRTPALLISGUSSDFLANGANA  TWISLSCFTYSASTEWALDLINGRAPTVANGAL  VLYPATCKAAAVAGMDKAAVARDYSRLLSRULL  RSHLPPRVGALHGVLYVLECDLDDTTAKQL  PYSISPATISMSVALDRINGANATSLVATSLV  GESTPESITISHTALRANGANATSLVATSLV  UNDREKKFPCBARVAARLPOFLDDFPRV  DIBRIKVIGETSROQPYPGMATVYKVROT  LHSTGQSSPFEDITERSAGQNV  AMATTYNTERC	uence		ļ	914			
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FLVLLSYERYHSKQIGERKIIQLCOGIMASGK RAVTHAIRACQPYNDLFURGTNKANAGKE LETQKSYVVSMLIR.IQYHQVLEMPIL.VIQQ CHEKDERGWKRLSKQIADIT.PML AKQANI DSHEALGYLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASYSTVQLWISGILAILRYLSQSTED WLSRIQELSSPSYLIACTVINIRLGGIDSTSIC FUNSKQIELSTSSYLIACTVINIRLGGIDSTSIC WLSRIQELSSTSYLIACTVINIRLGGIDSTSIC RQLXVEMSEQQHTFYCQELGTLLMCLHIPTS GMFRRTAAATRIFRSDCGGSFYTLDSLNLR ARSMITTIPALVILWCQILLVNHTDYRW AEVQQTPKRHSLSSTKLLSPQMSGEEDSDLA AKLGMCNREURSGALLFODVCQNLDSD HLTVLIVNHQDLISLSHEPPVQDFISAVHRISS HLTVLIVNHQDLISLSSHEPPVQDFISAVHRISS HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRAVEMILAANLQSSMAQLPMELNRIQEY LQSSGLAQRHQRLYSLDRFRLSTMQDSLSYS PPVSSHPLDODGHYNLSTVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNIPADDMYNAW MNSEFNISLLAPCLSLGMSEISGGCKSALFEA AREVITLARVSTVQQLPAVHHVQPELPAL ANYSKLNDLFGDAALYQSLFTLARALAQY LVVVSKLFSSALLEGAELVNIPAVDRAWAW MNSEFNISLLAPCLSLGMSEISGGCKSALFEA AREVITLARVSTVQQLPAVHHVQPELPAL SWHLHEOGIPLSLDLQAGLDCCCLALQLFQI WSVSTSTESTVYHACSKLYCYHFILERAVAQPG EQLLSFERRITNFRAISEEBEEVDPTQNFRKYI TAACEMWARWYSLQSVLYCHFILERAVAQPG EQLLSFERRITNFRAISEEBEEVDPTQNFRKYI TAACEMWARWYSLQSVLYCHFILERAVAQPG EQLLSFERRITNFRAISEEBEEVDPTQNFRKYI RTAACFMYAVSCLOQFRRICALGHFRNSQHVI WTYNAGFFYANGLEACHFICHTYPH COLLADA- FLIPLIRMIISLABLQNVSKERINATHHLYQAWD FYRYSGFYTHACSKLYCYCHFILERAVAQPG EQSESPFEEDTERTQNVLAVQATISTVLSAMT VPYAGRYAVSCLOQFRRKLKALDTFEGRK LSIRGGVEGEIQAMVSKERINATHHLYQAWD FYRYSGFYTTAGLISTERCHARQAVISTEGEEE ADAPATSSFYTTYNCSKLYLQOPERLESTL RSSHLPSKYCALGHVRNSCHALQNVXSLLVAQ LUFTERNYFTAGLISTERCHARQAVISTEGEEEE ADAPATSSFYTTYNTSKLYLCQNPERLESTL RSSHLPSKYCALGHVNYSCRLVVSLLVAQ LIFTERNYFTSCHERKRAQAVDISCSGCGEEEEE ADAPATSSFYTTYNTSKRIKRAQAVDISCOGGMAG-039 EESTFISTYHTACALGUPEPRICECTE ADAPATSSFYTTYNTSKRIKRAQAVDISCOGGMAG-039 EESTFISTYHTACALGUPEPRICECTE ADAPATSSFYTTYNTSKRIKRAQAVDISCOGGMAG-039 EESTFISTYHTACALGUPEPRICECTE ADAPATSSFYTTYNTSKRIKRAQAVDISCOGGMAG-039 EESTFISTYHTACALGUPEPRICECTE ADAPATSSFYTTYNTSKRIKRAQAVDISCOGGMAG-039 EESTFISTYHTACALGUPEPRICECTE ADAPATSSFYTTYNTSKRIKRAATALLSEVADWALDOJLDABLU- VALPACARPORE HITTOTT GKEKVSPEGREENTYNTAATALLSEVADWALDOJLDABLU- VALPACARPORE HITTOTT GKEKVSPEGREENTYNTAATAL	1			1	ļ	1	
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LEVVAAPGSPYHRLLTCLRNVHKVTTC   491   1841   A   3826   469   302   SNPPASASRVAGITGVHQHAWLIFVFLVEMEF   HHVGQAVLKLLISGDLPVSASQSA   492   1842   A   3836   392   88   VAPSPMIMPDLYFYRDPEEIEKEE*AAAEK\EE   FQSEWTAVV/P/EFTATQSEVADWFKDMQVP   SVPIQQFPTEDWST*PTMNDWSATSTAQTTE							I·
491   1841   A   3826   469   302   SNPPASASRVAGITGVHQHAWLIFVFLVEMEF   HHVGQAVLKLLISGDLPVSASQSA   492   1842   A   3836   392   88   VAPSPMIMPDLYFYRDPEEIEKEE*AAAEK\EE   FQSEWTAVV/P/EFTATQSEVADWFKDMQVP   SVPIQQFPTEDWSI*PTMNDWSATSTAQTTE							
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SVPIQQFPTEDWST*PTMNDWSATSTAQTTE	492	1842	A	3836	392	88	
WVRITTEWP						}	
	L						

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	J	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
i		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	İ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	I	1	i	peptide	i	/=possible nucleotide deletion, \=possible
L				sequence		nucleotide insertion
493	1843	Α	3838	19	380	TPSDMNRAFETDTQSIGEKNRSPSEPDYFERK
1	ľ	}			1	KFKRS*EKAHIRYKIDQPEDIPLK\EFLCKHSK
	ļ			}		CTATLSMRNMSLMKKKCSFSEEF\LAFFPSLL
						VCHLLAIKLGFYIBIHLTTFNNTF
494	1844	A	3845	2	352	FFFLRRSL/DSVAQAEAQWL\ELGLLQAPPPGF
1	1	ľ	1		1	KPISLP\GLPSSWDYGRPPPCPANFCIF/M*RRG
	j		1			FTVLARMVLIS*PCDPPTLASQGTAITGMSYH
			1			ARPQDIDFLYAHQGRCWFRLL
495	1845	Α	3847	1774	40	DIFFRRAKEGMGQDEAQFSVEMPLTGKAYL
1	1					WADKYRPRKPRFFNRVHTGFEWNKYNQTHY
ł		]	1		l	DFDNPPPKIVQGYKFNIFYPDLIDKRSTPEYFL
						EACADNKDFAILRFHAGPPYEDIAFKIVNREW
1						EYSHRHGFRCQFANGIFQLWFHFKRYRYRR*
j .		j	j		]	RPWGTAGRCPRGHSKGASVKLVVTPGPLSGL
			1		·	QGRGFTSHLRPHLSFARPQFPPI*KGGHH*AC
<u>}</u>		1	1 .			HGELRRHWDRLA*GPDATEGALGASFEHEG
		ŀ				GQQPPADLTVQADTLHRPSARLGGAHRACPK
1		1				RRPHRVLWRWARGAWAWRCQAREKQETQG
ŀ	1	1				QPCHITGHPLGREAEPAAAGAAPALAHRPPF
		1	1			ARTGSTE\PGPCWRPIRHCRRDPLWTPTLC\RD
1						WPPTHPVLAGGVHFPAAG/IGGCVEVPVSVN
1			1			VMGTKSH*AVLPPPPSTGPGGQGLPEGWGLE
1		}	]	ĺ		KGEGLPPGIPPPGLLTGPW\SMRPVTPSFAHIR
1		}		i		TVAPSHSPFSGQEGRGPHGCHSPGR\SGP\AGR
						LVLQHPTGTSPTEAKRKVPPGPPEGHPTSPVT
						SPRPPTAPPRHPASSGNSSVCFSKKTCRWEKK
496	1846	A	3849	830	442	SFVLMELAYWQDRMFF AKSPLPLG*IQWR/NLGSLKLRLPGFK*FTCLG
490	1040	, A	3049	830	442	LLSSWDYRSLPPRPVNFCILVELGFHHVDQAG
į.	1	İ				LKLLTSSALPALASQSAEITGMSHRIWPLPLLR
]		ļ	]	! :		RPPVIRIRAPPQRLPFNLITSLKALSPNMATF
497	1847	A	3859	2	393	ALRKTRDGIARTGAQPAASWKGTNNYPWR
**′	107/	^ _	3037	_	373	LEMAGRPGSQEQSKDRGTGSLPPPSQRPLGPS
	ł	!	1		}	PEGAGPSPPPPGIPRGGGSSSSEGP/POLLFVPR
İ	Ĭ	İ				RFPAPKKGLPSDTPHSKAPPTPHLILGGEDSO
	1					VPIL
498	1848	A	3860	253	634	KNASTVYSSQGDPKSFFFLLRWSLALVAQAG
170	1070	11	2300	200	337	EQ*RDLSSLQPPPPGFK*FSCLSLPSSWD\YRCP
		l	1			LPCLANIN*FLVETGFHHVGQADLKLLTSGDP
}	l	]	1		1	PTSASESAGITGVSHRAWPRIHFLYWKTFFL
499	1849	A	3863	423	263	·APSOISVAFLYAA/DKLFEKEI*KKIPFIIAS/DKI
'''	1.0.5	( **	1 2003	123	1 ~~~	KIGINLTKEVKYLYTENYITLMKEIK/DTDKW
-	1		1			KDILY*WIGKINI*KMSTPPKAIYRFNAIPTKIP
1		1	1			MTFFTEIEKSIIKFIWNIIKKPPNTQSNIEQKE*S
	1	[		1		FCSILLWVFGGFLWFHMNFMIDFSISVKNVIGI
		1	1			LVGIALNL
500	1850	A	3865	2	15246	LPRGCLWCLQRSPTPARPQPSRPARSPLPLFP
~~~ .	1000	l ''	3003	~	1 *****	DLRPWASDLDIMGDAEGEDEVQFLRTDDEV
}	1	}	1	1	}	VLOCSATVLKEOLKLCLAAEGFGNRLCFLEP
Į.	l					TSNAONYPPDLAICCFVLEOSLSVRALOEML
		1	1		l	ANTVEAGVESSQGGGHRTLLYGHAILLRHAH
J		}	J		j	SRMYLSCLTTSRSMTDKLAFDVGLQEDATGE
1		1	}			ACWWTMHPASKORSEGEKVRVGDDIILVSVS
1	1	1	1	1	}	SERYLHLSTASGELQVDASFMQTLWNMNPIC
	1	1			}	SRCEEGFVTGGHVLRLFIIGHMDECLTISPADS
1	1			İ	1	DDQRRLVYYEGGAVCTHARSLWRLEPLRIS
			1			WSGSHLRWGQPLRVRHVTTGQYLALTEDQG
		1		ļ	l	LVVVDASKAHTKATSFCFRISKEKLDVAPKR
	]	1	1		)	DVEGMGPPEIKYGESLCFVQHVASGLWLTYA
	•		<del></del>	·	<del></del>	

NO. of nucl- coide as a part of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice coide seq- unice							
Sequence   USSN   corresponding   blast amino acid residue of peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   pe							
uence    1946   1946   20   20   20   20   20   20   20   2		,					
uence  914 ag to first amino seid of pepidid residue of pepidid residue of pepidid sequence  Possible nucloside deletion, "possible nucloside insertion  APPSPALALE, VONDING, NOPIGE, LOBERT TROOGESQA, ARMHISTNOI, VNOPIGE, LOSES OKKPRGOPPO AT ALPIEOVILS, UDLIN TEPPS BEDLOHEEK, SKLRSLENROSLEPOEGMIS, SMV LINCIDRIN YTTAAHFABFAGERAABSWIGH WILLIELLASSGILEVI, YCVLIESEPULNITIGENIT KSIISLICK, SKRAN, SKLRSLENROSLEVI, CVLIESEPULNITIGENIT KSIISLICK, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SKRAN, SK							
anino acid residue of peptide sequence  T-Threanine, Ye-Valine, W-Tryptophan, Yelynosine, X-Unknown, **Silop coden, Apossible nucleotide deletion, \=possible nucleotide insertion  APPRALELGYLEKEAM HOGERHADALSE.  TROQEESQAARMIHSTNGLYNOFIKSLOSES GKPROSDPJAGILAFIGOTUSLQULITY-FEPS EDLQHIEKQSKLRSR.RNRQSLRQEEGMLSMV LNCDRINVYTAAHPABFAGEAALSWKEI  NILDELLASELIKONRSNCALETINLDWINVS KLDRLEASSILEVLYLVUESESPULNIQOPHI KSISLLDKHGRNHKVLDVLCSLCVCNGVAV RSNQOLITENLDGRELLQUTNLINYVTSISRN IFVGRAAGGTTQYSKWYFEVMODEVTPEITAQ ATTELROVENLOW GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV GDDLYSYGFDGLHLWTOHNARVSTSGOHL LAPEDVISCOLISTYSTISTRANGEOFOGOVGNOV DONKH.HPCLOPHSLEPERNYNLOMSGETL KTILLALGCHWADEKAEDVIVEDVISCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYCOLORYC							
residue of peptide sequence   Popsible nucloside deletion, Prossible nucloside deletion, Prossible nucloside insertion  APPSPALAEL CRYLKEK AND EPGERIMDOLISE. TRCQGESQA ARMHISTNOI, VNOFIKSL DESS OKPRIGOPPO FLA PILEGUE NIS QUALIFIEDES OKPRIGOPPO FLA PILEGUE NIS QUALIFIEDES OKPRIGOPPO FLA PILEGUE NIS QUALIFIEDES OKPRIGOPPO FLA PILEGUE NIS QUALIFIEDES OKPRIGOPPO FLA PILEGUE NIS QUALIFIEDES OKPRIGOPPO FLA PILEGUE NIS QUALIFIEDES OKPRIGOPPO FLA PILEGUE NIS QUALIFIEDES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORIS OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORIS OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIGORES OKPRIG							
peptide sequence    APDEKALELGYLKKKAMLEGEGIRADDALSE   TROQUEESCAARMINISTICALYOPICKUS CONTROL   TROQUEESCAARMISTICALYOPICKUS COLINIVERPS   GEPEGSOPPACITAL PILGYULS CQUALIFYERPS   BELOHEEKQSKLESLRARGEAGEAASWEI   VILLYELLASLIRONSINGALFSTEOMISMY   LINCDRLIVYTTAARIFAGEAGEAASWEI   VILLYELLASLIRONSINGALFSTEOMISMY   KISISLLOKIGRINIKYLDYLCSLCVCNOVAN   RESINDLITTEALPREAGUEAAASWEI   VILLYELLASLIRONSINGALFSTEOMISMY   KISISLLOKIGRINIKYLDYLCSLCVCNOVAN   RESINDLITTEALPREAGUEAAASWEI   VILLYELLASLIRONSINGALFSTENDWINGENIT   KISISLLOKIGRINIKYLDYLCSLCVCNOVAN   RESINDLITTEALPREAGUEAAASWEI   VILLYELLASLIRONSINGALFSTENDWINGENIT   KISISLLOKIGRINIKYLDYLCSLCVCNOVAN   RESINDLITTEALPREAGUEAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1				residue of		
sequence   nucloside insertion	į				peptide		
TRCQGESQAARMIISTNGL YNQFESLDSFS GKPRGSOPPAGTALPIEVI SLQDLITYPSS EDILOHEEKOSKLESI.RNRQSLROSEGMI.SMV LNCDRLINVTTAAHEAFAGEAABSWEL VNLLYELLASLIRONRSNCALFSTNLDWLVS KLDRLASSGILEVI YCVLESFEVLNIGENHI KSIISLLDKRGRNIKK.UDVLCSLCV:NOVAV RSNQDLITENLLPGRELLLQTNLINYVTSIRPN IF VGRAGTTOYSK.WYFEWMOPEVTPLTAQ ATHLRYGWALTEGYTTYPSAGEWGOWGOWG ODDLYSYGFDOLHLWTGHVARPYTSFGQWI LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENYDLSCVETLING ROPHLWOFSCLSLDSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LAPEDVISCCLDLSYBISTRINGCPVGOVERSF NLDGLIFFEVYSSAGAVENTLIGGRISTIC LATHLAGGCHVGMADEK ABDNILKTIL PETY MASNOYEVAPAL DLSHWALTHAGTTI.VORTY MASNOYEVAPAL DLSHWALTHAGTTI.VORTY MASNOYEVAPAL DLSHWALTHAGTTI.VORTY MASNOYEVAPAL DLSHWALTHAGTTI.VORTY ORGAWYSFEGAVITIGEMSVOWARFELREDV LVPYRLLDEATKRSRDSL.CQAVARTLLGVGY NIEPPOGEPSQVENGGRICHVANGGOVENTLIGAGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIGGOVENTLIG							nucleotide insertion
GKPGGSOPAGINALPIGOVILSLO, DULIVYEPPS BDLQHERG (SKLERS, IRNS) LAPGEMAS MY LNCIDELNYVITA-AHFAEPAGEBA-ABSWKEI VNLLYELLASLIRONRSNCALFSTNLDWLYS KLORLEASSGILEVLYCVLUESPEVLNIIGENHI KSIISLLDKGRINKKYLDVLCSLCVCNGVAV RSNODLITENLLPGRELLLQTNLLDYLINGENHI KSIISLLDKGRINKKYLDVLCSLCVCNGVAV RSNODLITENLLPGRELLLQTNLLDYLINGENHI KSIISLLDKGRINKKYLDVLCSLCVCNGVAV RSNODLITENLLPGRELLLQTNLLDYLAG ATHLRYGWALTEGYTPYJGAGE WGGOVO GDDLYSYGFDGLHLWTGHVARPYTSFGGHL LAFEDVISCCLLJSYNSISTRINGCYGQGYPFSF NLDGLFFPVYSPSAGVKVRFLLGGRHGEFKF LPPFGVARCHEAVLPRETIL HEPREVRENGE ROPHLVGPSICLSHTDFYPCPVDTVQIVLPPH LEARBELLASINHELWALTREGGWTYGDWLDD DNKRLHPCLYDFISLPEPERNYNL, MSGGTL KTLLAGGHVGMADERAEDNLKKTLLRCTY MMSNOYKFAPLDLSHYRLTRAGGTLYDRLAE MGHNVWARDRVGGGWSYSAVQDIPARNFR LVPYRLLDEATRSNRDSLCQAVRTLLGYGY NIEPPDGEPSQVENGSRCDRVRIFRAKSYTV QSGRWYFEFEAVTTGEMRWOWAPRELRPDV ELGADELAYVNNGHRGQRWHLGSEPFGRPW OPGDVWGCMDLTENTIETINGEVLMSGSS STARREIEGGGFLYCSLGFGGVGHLNLGOD VSSLRFRACIGLGGGEFFFINNGPWTYTPFCLR LTHRTWGSQNSLVERHAMOPPATTPLRCLR GGGAGPGFEVPLEHPHYS VGRVDGTVDTPFCLR LTHRTWGSQNSLVERHERNKKRGFTFT KGGAGGAGGAGGTFQ AGGEAGPARAENBKDATTENKKRGFTFT CTAGATTLAPPGLGFPAEDEARAAEPDPDYS NIRRSAGGWSBARDNKGETTAENKKRGFTFT RTRAGGGAGGAGGARGARDROP PEILNTTTYTYYSVRVRAGGRESCVMARWD PEILNTTTYTYYSVRVRAGGRESCVMARWD PEILNTTTYTYYSVRVRAGGRESCVMARWD PEILNTTTYTYYSVRVRAGGRESCVMARWD PEILNTTTYTYYSVRVRAGGRESCVMARWD PHILVTYTYYSVRVRAGGRESCVMARWD PHILVTYTYYSVRVRAGGRESCVMARWD PHILVTYYSVRVRAGGRESCVMARWD PHILVTYYTYYSVRVRAGGRESCVMARWD PHILVTYYTYYSVRVRAGGRESCVMARWD PHILVTYYTYYSVRVRAGGRESCVMARWD SSKCRSVRVMVWGGFPGCPGKGKNINGMRYSWS MPNHELQVFTRAGGERIC MAWAQCCEPT WARD ALHIPBENRCMDILEISBRLDLQRPHSHTLRL VRAVACLAGNINAALACHTPGAQALLARLE BAHLPGPIRAGYYDLLISHIBSACRSRSRENGE BERGEBEEFTERGEBEEGE EGGLLQMKLPESVRLQMCHLLEYFCDQELQ HRYSLAAFARYVDLLSHIBSACRSRSRENGE EGEEPPEGETHAGRENGEREEGEBEEGE EGEEDLEGGRUNDHAVFYVFTEEFEGEBEEGEBEEGE EGEEDLEGGRUNDHAVFYVFTEEFEGEBEEDEEGEBEDE EKEEDLEETAGRESTENGLUSHMVVRWAGEDE VGVSILKMSILLECLGGRISLLLVOMGPGE EKEPPEEGEBETTLGGRINDNAVFYVFTGLGELLCALRAFGE PEERSAEBSKPRSLGELUSHMVVRWAGEDE VGSPLUNKDSICHNINNKVFYVFTALLECLGGGLDL GGEEPPEGEBETTLGG							APDPKALRLGVLKKKAMLHOEGHMDDALSL
EDLQHEEKOSKLRSLNROSI-FQEEMALSMY LNCIDLANYTTA-HAPEAGGBA-RSSWEI VNLLYELLASLIRONRSNCALFSTNLDWI-VS KLDRLEASSGILEVLYCV-LIESPEVLNIIQENHI KSISLLDKRIGNHKV-LDVLCSL-CV-NOVAV RSNQLITENLI-GRELLLQTNLINYYTSIRPN IFVGRAEGTTQYSK-WFEW-MYDEVYTPFLTAQ ATHLRVOWALTEGYTPYFGAGEGWGGNGV ODDLYSYGFOGLHL WTOHNARPYTSFGOHL LAPEDVISC-CLIS-VPSISFRINGCPV-GGVFESF NLDGI-FPV-VSFSAGVKVEFLLGGRIGEFEK LPPPGVAPCHBA-VL-PREILHLEPKE-VRREGP RGPHLVGPSRCLSHTDFV-PCPVDTVQIV-UPPH LERIREKLASHIELW-ALTRIEQ-GWTY-GPV-RD DNKRLHPCL-VDFHSLEEPER-YNL-QWSGETL KTLLALG-CHVGMADBKAEDDLKKKTL-KT-Y MMSNGYK-PALDL-SHYRLIT-RAQTIL-LYDRLA-B HOHNWADDRVGG-WSYSA-VQDIP-BRRIPER LVPYRLLDBATKRSNDISLC-QAVRTLLGYGY NIEPPD-GPSQ-VENGSC-DRV-RIF-RASKS-YT-V QSGR-WYFEFB-AVTTGE-MR-VW-MSDESG BTAFREIGHG-GR-WH-LGS-BPF-GR-PW QPODV-WG-MIDL-TENTIFTLNGEV-LMSDGS BTAFREIGHG-GR-WH-LGS-BPF-GR-PW QPODV-WG-MIDL-TENTIFTLNGEV-LMSDGS BTAFREIGHG-GR-PW-SUS-BPF-GR-PW QPODV-WG-MIDL-TENTIFTLNGEV-LMSDGS BTAFREIGHG-FR-Y-NG-WH-LSB-PF-GR-PW NER-PG-GR-WH-Y-BFF-GR-PW-H-MS-PF-GR-PW QPODV-WG-MIDL-TENTIFTLNGEV-LMSDGS BTAFREIGHG-FR-Y-NG-WH-LSB-PF-GR-PW QPODV-WG-MIDL-TENTIFTLNGEV-LMSDGS BTAFREIGHG-FR-Y-BR-PH-PW-SR-WD-GT-VDT-PF-CLR LTHRT-WGSONS-LV-WL-RL-SL-Y-PG-HQ-HF-FR CTAGATTL-APPOL-QP-PAEDEAR-AAEPDP-DY-B NLR-SAGG-WS-BA-RAG-BP-DT-YB-F-BR-PH-PW-SR-WD-GT-VDT-PF-CLR LTHRT-WGSONS-LV-WL-RL-SL-SL-Y-PG-HQ-HF-FR CTAGATTL-APPOL-QP-PAEDEAR-AAEPDP-DY-B NLR-SAGG-WS-BA-RAG-BG-TP-Q-AGG-QAR-RAEED-ATTERNKK-RG-FL-FKA- KX-VAMM-TO-PAT-PT-LP-HD-W-VAD-NR-DD PEILL-TTT-Y-Y-Y-SW-Y-R-Q-QEPS-CW-M-GW-Y-PD-Y-HQ-HD-WSFDLS-KW-WY-V-T-Y-HD-W-D-W-D-W-D-PH-D-W-T-W-T-H-IN-WI-T-HL-R-HD-W-W-B-W-R-B-R-B-W-W-H-I-T-R-W-W-R-B-W-R-B-W-W-W-W-R-B-R-B-W-W-H-I-T-R-W-W-R-B-W-R-B-W-W-W-W-R-B-R-B-W-W-H-I-T-W-W-R-B-W-W-W-W-W-R-B-R-B-W-W-H-I-T-W-W-R-B-W-W-W-W-W-W-W-W-R-B-R-B-W-W-H-I-T-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W-W		ļ					TRCQQEESQAARMIHSTNGLYNQFIKSLDSFS
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VNLLYELLASIGNEY LYCULESPEVINIOENHI KSIISLLDKHGRNHKVLDVLCSLCVCNGVAV RSNQDLITENLLPGRELLLQTNLINYYTSIZW IFVGRAEGITTYSK WFEWYMDEVTPLTAQ ATHLRVGWALTENTTPYFOAGEGWGCNGOV GDDLYSYGFOLGHL WTOHNARVTSPGQHL LAPEDVISCCLDLSVPSISFRINGCPVGGVFESF NLDGLFFEVVSFSAGVKVEFLLGGRIGEFKK LPPPGVAPCHBAVLPGERLHLPKEVRREGP ROPHLVOPSRCLSHTDFVPCPVDTVOLVDPH LERIREKLAENHEL WALTREGGVTYGPVEND DNKRLHPCLVDFHSLPEPENYNLQMSGEIL KTLLALGCHVGMADEKAEDDLKKTLKFKY MMSNGYKFAFLDLSHVALTHAGTILVDRIAB HOHNWARDRVGGWSYSAVQDIPARRYPR LVPYRLLDBATKRSNRDSLCQAVRTLLGYGY NEPPDGPSQVENGSCDWKIFFLAGKSYTV QSGRWYFEFAAVTIGEMROWARPELRPDV GPGDVGCMDLTENTIFTLINGEVLMSDSGS ETAFREIEIDDGFLPVCSIGPQQVGHLNLGQD VSSLRFFACGLQEGFEFFAINMGRPVTTWFS KGLQFEPVPLEHPHEVSRVDGTVDTPPCLR LTHRTWGSNSLVEMLIRLSLEVQHQHIPE CTAGATTLAPPQLQPFAEDBARAAEPDPDYS NLRSAGGWSEANKGGTAKEGAFGGTPQ AGGBQPARAENEKDATTEKNKKGFLFKA KKVAMMTOPATTFLIPHDVVADRDD PEILINTTTYYSVRVAGGGPSCVWAGWT PDYYHGHDNSPDLSKVRVTVTTMGDGGNVL HSSLKCSNCYMVWGGDFVSPQQGRISHTDL VIGCLVDLATGLAMTTANOKESNTFFQVERY TLEPPAVTVLFTIGNVINGELKGKINMELSA AMFQSERKNPARQCPPRLEMGMLMPSWSK MPHIFLQVETRAGERIG WAVQCOPETIMM ALHIPERNSCHOLLELSRIDLQRFHSHTILR VRAVCALGNRVAHALCSHVQGLLHALE DAHLPGPRAGVYDLLISHIRSACRSRRSML SEYLVPLTFTRATLTPPROFRSTEGHERHGLE GWGVTTSLRPPHFSPPCFVAALPAGAABAP ARLSPAPILBARDVALGSHTGLE BEGLUMKLPSSVKLVALGSHLARGLYGGDFL GWGVTTSLRPPHFSPPCFVAALPAGAABAP ARLSPAPILBARDKALGSHTGCAVRGGGE EFEREETTGEREGEEGEEGEE EKEEDBEETTGLEKGRAFGEGEEGEE EKEEDBEETTGLEKGRAFGLAVALCGGOPL DWKQLKMIPPEVFTEEBEEEDBEEGGEEGEE EKEEDBEETTGLEKGRAFGLAVALCGGOPL ARLSPAPILBARDKALGSHTGLAUNGGGDE DWKQLKMIPPEVFTEEBEEEDBEEGGEEGEE EKEEDBEETTGLEKGRAFGLAUNGGLAUNGGGE DWKQLKMIPPEVFTEEBEEEDBEEGGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEEGEE EKEEDBEETTGLEKGRAFGLEGEE							
KLDRLEASSGILEVI,YCVLIESPEV,NIICENHI KSISLLDKHGRNHKVLDVLCSLCVCNOVAV RSNQDLTENLLPGRELLLQTNLINYVTSIRPN IFYGRAEGTTQYSKWYFEWMDEVTPFLTAQ ATHLRVGWALTEGYTPYPGAGEGWGNOV GDDLYSYGPOGHHLWTOHVARPYTSPOGHL LAPEDUYSCCIDLSYSSISRINGCPGYGYFESF NLDGLFFPVYSSAGWKVEFLLGGRIGEFKF 1PPGYAPCHENAVLPREINLEPGKYREGP ROPHLVOFPSCLSHTDFYPCPVDTVQIVLPPH LERIREKLAENIHELWALTRIEQGWTYGPVRD DNKRLHPCLVDFHSLEFEERNYHLQWSGZIL KTLLALGGHYGMADEKAEDNLKKTKLPKLTY MMSNGYKPAPLLDSINKLTLATQHTLDYBLAE NGHNWARDRVGQGWSYSAVQDIPARRINFR LYPYRLIDEATKRSNRDSLCQAWTHLDYBLAE NGHNWARDRVGQGWSYSAVQDIPARRINFR LYPYRLIDEATKRSNRDSLCQAWTHLGYGY NIEPPDGEPSQVENGSRCDRXHRAEKSYTV QSGRWYFEFEANTTGBRWGWAPFLRDW QRGDVVOCMDLTSNTIFTLINGEVLMSDSGS ETAFREIEGDGFLYCSLGRGQVGHLN.GQD VSSLRFFALGGLQGFFPFAINMGRPYTTWFS KGLOPGPVPLEIPHFWSNRDGTYDTPFCLR LTHRTWGSONSLVEMLFLRLSLPVQFHQHFR CTAGATTLAPFGLQPFPDEARAAAEPDPDYS NLRSAGGWSEAENKEGTAKEGAACGAPPO AGGEAQPARAPEKDATTEKKKRGFLFKA KKVAMMTQPRATTLIFRLPHDVVPADNRDD FEILINTTTYYSVRVFAGGEPSCVWAGWYT PDYNQHDMSPDLSKRVTVTVTMGDEQGNV HSSLKCSNCYMWWGGDFVSFQQQGRISHTDL VGGLVDLATGLMTFTLANKESNTFFQVPR TLLPFAVFVLPTHQNNTQFELGRQKNIMPLSA AMFQEEKMPPAQCPPLEMGALHAPWSWSR MPNHFLQVETRRAGERLGWAVQCQEFLTMM ALHIPERRCMDLELSBRIDLQRFISHTLRL VRAVCALGNRNVAHALCSHVDQAQLLHALE DAHLPGFLRAGYYDLLISHILSSACRSRRSML SEYIVPLTFETRATLTPPGRSTEGNHEWFIGUF GGGVTTSLEPPHHFSPFCVVALIPAGAGABAP ALLSPAJFVLTFTETRATTPPGRSTEGNHERFIGLF GGGVTTSLEPPHHFSPFCVVALIPAGAGABAP ALLSPAJFVLTFTETRATTPPGRSTEGNHERFIGLF GGGVTTSLEPPHFSSPFCVALIPAGAGABAP ARLSPAJFLARDRAARMGGAGAACH RDPVGASVERGPVPVLLISHTLLWGFGGD DVKQILKMIFPEVFTEEEEEDEEDEEBGEEDEE EKEEDEETAGEKENDEECERGARGERGED EKEEDEETAGEKENDEECERGARGERGED EKEEDEETAGEKENDEECERGEEGDEE EKEEDEETAGEKENDEECERGEEGDEE EKEEDEETAGEKENDEECERGEEGDEE EKEEDEETAGEKENDLANGROUGLIAAC FSMMAAETARRTFFFSSPFQGONMILLGFKGD DPDCDCPCPLERGNCDLLDFHODLLAHGGIGLD GEEEFFEETTLGSKLMSLLEVRLVKKKERG FEEFFASEESKPRSLQELVYRLWYKKKERG PEEFERAEESKPRSLQELVYRLWYRKAGED POUKQILKMIFPEVFTGEFEEDDEEGEEDEEDEE EKEEDEETAGEERGERGERGEBOBE EKEEDEETAGEKENGLLINVQMGPGE BLANGGGRINMNNVYFYQHFPILMRAACHME	1						LNCIDRLNVYTTAAHFAEFAGEEAAESWKEI
KSIISLLDRIIGRNHKVLDVLCS.CVCNGVAW RNOQLITENLI-DGRELLIQTNILINYVISRPN IFVGRAEGITQYSKWYFEVMVDEVTPFLTAQ ATHLRVOWALTEGYTPYFOAGEGWGGNGV GODLYSYGFDGLHL WTGHVARPYTSPGGHL LAPEDVISCCLDLSYPSISFRINGCPVGGVFRSF NLOGLFFFVYSFSAGVKVFFLLGGRIGGFKK LPPGVAPCHBAVLPRERI-HLEPKEYRREGP ROPHL-VOPSRCL-SHTDVPCPVDTVOVIDPH LERIREKLAENHEL WALTRIEQGWTYGPVRD DNKRLHPCLVDFHSLEFERNYNLQNSGETL KILLALGHVGMADBKAEDNLKKTLKTLYT MMSNGYKPAFLDLSHVRLTPAQTIL-VDRLAE HGHNVWADDRVGGGWSYSAVQDIPARRIPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDGPSQVENQSRCDRWTFREAKSYTV QSGRWYFEFAVTTGEMRVOWARPELRPDV ELGADELAYYFNGHRGGRWHLGSEPFGRPW QFGDVVCCMDLTENTUFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSURFFACGLGEGFPAINMGRPYTTVFS KGLPQFEVPLEIPHYEVSRVOGTVDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR CTAGATFLAPFOLQPFAEDBEARAAEPDPDYE NILRRSAGGWSEAENKEGTAKEGARAEPDPDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENKEGTAKEGARAEPDFDYE NILRRSAGGWSEAENCEGEFFERE EEGALGWGEGEGEFFERE EEGALGWGEGGEGEFFERE EEGALGWGEGGGGARAEPTFACHAERT NTHILVYSTRYEGGGEGGGARAEPTFACHAERT NTHILVYSTRYEGGGEGGGGGEGEFFE EEGALGWGEGGGARAEPTFACHAERT NTHILVYSTRYEGGGEGGGGGGGEGFFE EKEGEGEKAPGCGGGARAEPTFACHAERT EEGALGWGCGGARAEPTFACHAERT NTHATATATATTPTTAGGGGGGAA REPPYGASVEFGYPVILLVMGGGGGA EEGEFFEETTLGSRLARMGGAVGGGGEGEFFE EKEGEGEEFFEETTLGGRLARMGLACHAEGGGLD GEGEFFEETTL	ļ						VNLLYELLASLIRGNRSNCALFSTNLDWLVS
RSNQDLITENLLPGRELLLQTNLINYYISRPG IFVGRAGITOYSKWYFEWMYDEVTPPLTAQ ATHLRVGWALTEGYTPYPGAGEGWGGNGV GDDLYSYGFDGLHE WTGWTAFREYTBYPGHELL LAPEDVISCCLDLSVPSISTRINGCPYGGVFRSF NLDGLFFPVYSFSAGVKVRFLLGGRHGEFKF LPPGYAPCHEA VLPRERLHLEFIKEYRREGF RGPHLVGFSKCLSHTDFYPCPVDTVGVLVPPH LERREKLAENHELWALTREGGWTYGPVRD DNKRLHPCLVFFSLDEFERNYALQMSGETL KTLLAGCHVGMAGETL KTLLAGCHVGMAGETL KTLLAGCHVGMADEKAEDNLKKTKLPKTY MMSGYKPAPLDLSHWALTPAGUMTYGPVRD DNKRLHPCLVFFSLDEFENYALQMSGETL KTLLAGCHVGMADEKAEDNLKKTKLPKTY MMSGYKPAPLDLSHWALTPAGVATLLGYGY NEPPPQEPSQVENQSKCDRVRIFAEKSYTV QSGRWYFEFGAVTTGGMKVGWAPTLLGYGY NIEPPPQEPSQVENQSKCDRVRIFAEKSYTV QSGRWYFEFGAVTTGGMKVGWAPTLLGYGY NIEPPPQEPSQVENQSKCDRVRIFAEKSYTV QSGRWYFEFGAVTTGGMKVGWAFLLGYGP QPDVVGCMDLJENTUITLINGSVLMSDSGS ETAFREIBIGDGFLPVCSLGPGGVGHLNLGQD VSSLRFFAICGLQEGFEPFANNQRPVTTWFF KGLPGPFPVBLEHPYFYSVSRVDGTVDTFPCLR LTHRTWGSQNSLVEMLFILSLFVQFHQHFFR CTAGATTLAPPGLGPAEDEARAFDPDTVS NLRRSAGGWSEARGKEGTAKSGAPGGTPQ AGGEAQPARAENEKADATTEKKKRGFLFAA KKVAMMTQPATPTLFRLPHDVVPADNRDD PRILINTITYYSVRVFAGGPSCVWAGWVT PPYHQDMSFDLSKWVVTTWGDEPGGNV HSSLKCSNCYMVWGGDPVSFQQQGRISHTDL VIGCLVDLATGLMTFANGKESTIFQVEN TKLFPAVFVLPTHQNVIQGELGKQKNIMPLSAA AMFQGSKRNAPVLPTHQNVTJPHQNVFSKA AMFQESKNAP AMFGERKNAP AMFGLER GWAVQCQEPLTMM ALHPENRCMDLELSEARDLAFFHSTILL YRAVGALGNINFALSA MFPHELQVTLRFRAGERLGWAVQCQEPLTMM ALHPENRKMDLELSEARGERGLFG GWAVTISLRFPHHFSPPCTVALFAGAABAP ARLSFAFLAGEL GWAVQCQEPLTMM ALHPENRKMDLELSEARGERGLFG GWAVTISLRFPHHFSPPCTVALFAGAABAP ARLSFAFLAGERLGWAVGCORPLTHMM ALHPENRKMDLELSGARGRINGL GWAVTISLRFPHHFSPPCTVALFAGAABAP GWAVTISLRFPHFSPPCTVALFAGAABAP GWAVTISLRFPHFSPFCTVALFAGAABAP GWAVTISLRFPHFSPPCTVALFAGAABAP ARLSFAFLAGERGE GREEPEETTLGSRLMSLLKVRLVKKKFGLF GFGFFFRAGYFOLLDHCHOLLHGIQLD GEGEPFEETTLGSRLMSLLKVRLVKKKFGK FESMTAAETARRTEFRSPFGQINMLLQKKGF GEGEPFEETTLGSRLMSLLKVRLVKKKFGK FESMTAAETARRTEFRSPFGQINMLLQKKGF GEGEPFEETTLGSRLMSLLEKVRLVKKKFGK FEEFSAEESKFRSLGLLVGGRALLVQMGFGDE DVKQILKMIEPEVFTGEGEETTLGGRALLFYLDGGGLA RYPFGSSAEESKFRSLGELVSHMVRWAVGDDF VQSPFLVRAMFSLLERCGGURSLLLVQMGFGDE DVKQILKMIERSSVLLQNCHLLEFYFCOGLI							KLDRLEASSGILEVLYCVLIESPEVLNIIQENHI
IFVGRABGTTQYSKWYFEVM/DEVTPH/AGE ATHLR/VGWALTEGYTYP/AGEGWGGNGV GDDLYSYGFDGLHL WTGHVARRYTSPGQHL LAPEDVISCCLDLSVPSISFRINGCPVGGVFSFF INLDGLFFPVVSSFSTRINGCPVGGVFSFF LPPFGYAPCHEAVLPRERLHLEPIKEYRREGE RGPHLVGPSRCLSHITDFVPCPVTVGIVLPPH LERIREKLARNHELWALTRIEQGWTYGYVLPPH LERIREKLARNHELWALTRIEQGWTYGYVLPDD DNKRLHPCLVDFHSLPEPFERNYNLQMSGETL KITLALGCHVGMADEKAEDNIKKTKLPKTY MMSNGYKPAPLDLSHVALTPAQITLVDRLAG NGHNVWARDRVGGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLQAVRITLGYGY NIEPPPOEPSQVENQGSCDRVLFRAKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELQADELAYVFNOHRGGRWHLGSEPFGRPW QFGDVGGMDLTENTUIFTLNGEVLMSDSGS ETAFREIEIGGFLPVCSLGFGQVGHLNLGQD VSSLRFAKCLGGFEPFANNGRPVTTWFS KGLPOFEPVRLHPHYEVSRVDGTVDTPFCL LTHRRYGSONSLVEMLFLRSLEDVQHOHER CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NIRRSAGGWSEANREKGTAKEGAPGGTYQ AGGEAQPARAENEKDATTEKNKKRGFLFRA KKVAMMTQPATPTLFRLPHDVYPADNRDD PEILLTTTYTYSVRVAGGDPSSCVWAGWVT PPYHQHDMSFDLSKVRVVTVTMGDEQGNI HSSLKSNCYMVWGGDVSFQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TIKLPFAVFVLPTHONVGGELGKQKNIMPLSA AMFQESKNIPAPQCPPRLEMGMLMPVSWSR MPHHFLQVETRRAGERLGWAVQCOPETHMM ALHIPERNCKODIELSBELDLGHPSHTLRL YRAVCALGNNRVARAALCSHVDQAQLLHALE DAHLFOPLRAGYYDLLISHI ESACRSRRSML SEYLVLTTETRATLFPFORSTENGPRHGLP GVGVTTISLRPHHFSPPCTVALIPAGAGABAP ARLSSAPIPLALRAGYPTLLISHI ESACRSRRSML SEYLVLTTETRATLLFPFGRSTENGPRHGLP GVGVTTISLRPHHFSPPCTVALIPAGAGABAP ARLSSAPIPLALRAGYTPLLESBELDLGHPGHFLRL YRAVCALGNNRVARAALCSHVDQAQLLHALE DAHLFOPLRAGYPTLLISHILLSKERLDGHPGHGLP GVGVTTISLRPPHHFSPPCTVALIPAGAGABAP ARLSSAPIPLALRAGYTPLLISHILLSKERLDGHPGHGLP GVGVTTISLRPPHHFSPPCTVALIPAGAGABAP ARLSSAPIPLALRAGYTPLLISHILLSKERLDGHPGHGLP GVGVTTISLRPPHHSPPCTVALIPAGAGABAP ARLSSAPIPLALRAGYTPLEEPEEDEEGEGEBOBE EKEDDEETAQRKEEBERAAEGEKEGG LEEGLLGWALPAGAABAP ARLSSAPIPLALRAGYTLLSHULLSKERLDLAHGQGHA RDPYGASVEPGFVPVLKLVSTLLVMGIFGIDE DVKQILKMIEPSVTPTEEPEEDDEGEEGEBOBE EKEDDEETTAGRKMSILLBKVRLVKKKEKEK PEERSKAEESSYRSLOCHLSHVWAVQCDF VQSPLVRAMFSLLHRQYDGLGGLLRALPRA YTTSPSSVEDTMSLLECLGQURSLLIVQMGFGDG FOREDFSSTURMAGLOGHE FOREDFSSTURMAGLOGHARAUTHARA YTTSPSSVEDTMSLLECLGQURSLLIVQMGFGDF FOREDFSSTURMAGAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA							KSIISLLDKHGRNHKVLDVLCSLCVCNGVAV
ATHLRVGWAİTEGYTPYPGAGEGWGGNOV GDDLSYGERGLHUTOHVARPYTSGQHL LAPEDVISCCLDLSYPSISFRINGCPVQGVFESP NLDGLFPVVSFSAGVKVRFLLGGRHGEFKF LPPGYAPCHEAVLPREZHLEPJEKFYRREGP ROPHLVGPSKCLSHTDFVPCPVDTVQIVLPPH LERIREKLARNIHELWALTREGQGWTYGPVPD DNKRLHPCLVDFHSLPEFERNYNLQMSGETL KTLLALGGHVGMADEKAEDNLKKTKLKTY MMSNGYKPAPLDSHYNLTYNLLYDRLAE NGHNVWARDRVGGGWSYSAVQDIPARRINF LVPYRLDDEATKSKNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENQSRCDRVRIFAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELGADELAYVFNOHRGGRWHLGSEFGRFW QPGDVVGCMIDLTENTUITLINGSVLMSDSGS STAFREIEIGGFLPVCSLGFGQGVENLINGQD VSSLRFFALGGLGGFEPFANNQRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPFCLR LTHRTWGSQNSLVEMLFLRISLTVQFHQHFR CTAGATTLAPFGLQPAEDEAKAAEPPDVV NIRRSAGGWSEARMSEDATTEKNKKRGFTFKA KKVAMMTQPPATPLJRFLPHVVPDDNRDD PEILINTTTYYSVRVFAGQEPSCVWAGWVT PPYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKSNCYMVWGGDVSFQCQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVERP TLAFPAFVLTPHONVGGELGKGKNIMPLSA AMPGGERKNPAPQCPPRLEMMMLMPVSWSR MPNHFLQVETRRAGERLGWAVQCQEPLTMM ALHIPEENRCMDLELSISRLDLGRFISHTLAL YRAVGALGNNRVAHALCSRVDQAQLLHAA ALHIPEENRCMDLELSISRLDLGRFISHTLAL YRAVGALGNNRVAHALCSRVDQAQLLHAA SEVIVLTFETRATLEPFGRSTENGHPRIGGD GVGVTTSLRPPHFSPPCEVAALPAAGAAEP ARLSPAPLEALRDKALRALGRGRAFGFGDHA RDPVGASVERGFFFQFFT SEVIPLTFETRATLEPFGRSTENGHPRIGGD GVGVTTSLRPPHFSPPCEVAALPAAGAAEP ARLSPAPLEALRDKALRALGRAFGRFIGGDHA RDPVGASVERGFFFFTEEFEEDEEDEERGEEDEE EKEEDEEFTAQBKEFEERAAERGERGDE EKEEDEEFTAGRKEFERAAERGERGDHA RDPVGASVERGFFFTEEFEEDEEDEERGEEDEE EKEEDEEFTAGRKEFEERAAERGERGDE GEGEEFEETTLGSRLMSLLEKVRLVKKWGEDF PEERSAEESKPSPVLLVANGLEGOD TDEEDCALFERGERGDE GEGEEFEETTLGSRLMSLLEKVRLVKWKGEDF PEERSAEESKPSRLQCLUSHMLARKGEDF PEERSAEESKPSRLQCLUSHMLARKGEDF PEERSAEESKPSRLGCLUSHMLARKGEDF PEERSAEESKPSRLGCLUSHMLARKGEDF PEERSAEESKPSRLGCLUSHMLARKGEDF PEERSAEESKPSRLGCLUSHMLARKGEDF PEERSAEESKPSRLGCLUSHMLARKGEDF PEERSAEESKPSRLGCLUSHMLARKAREEDF PEERSAEESKPSRLGCLUSHMLARKAREEDF PEERSAEESKPSRLGCLUSHMLARKAREEDF PEERSAEESKPSRLGCLUSHMLARKAREEDF PEERSAEESKPSRCGLUGHSLLIVQMGGDG DVGGLIKMIEPSVTFTEEFEEDEEDEERGEEDEE EKEDDEETTLGGRGGLURHALLOVAGGDD GEEFFEETTLGSRLMSLLEKVRLVKKWREDF PEERSAEESKPSRLGCLUSHMLARKAREEDF PEERSA	ł						RSNQDLITENLLPGRELLLQTNLINYVTSIRPN
GDDLYSYGFOOLH.WTOHWARPYTSPOGUL LAPEDVISCLDLSVPSISFINGCPVQGVPESF NLDGLFPPVVSPSAGVEVRELIGERIGEFEK 1.PPPGYAPCHEAVLPRERLILEPIKEYRREGE RGPHLVGPSRCLSHITDFVCPVDIVQIVLPPH LERIREKLARNIHELWALTRIEQGWTYGYWD DNKRLHPCLVDFHSLPEPERNYNLQMSGEIL KITLALGCHYGMADEKAEDNIKKIKLEKTY MMSNGYKPAPLDLSHWALTPAQTILVDRLAE NGHNWARDRVGGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELQADELAYVFNOHRGGRWHLGSEPGRFW QPGDVVGCMIDLETNITITINGSTMSGSWSSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELQADELAYVFNOHRGGRWHLGSEPGRFW QPGDVVGCMIDLETNITITINGSTMSGSWSSAVGFFACGGOPQ VSSLRFALCGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVYELBPHYFVSRNDGTWINGSPGSFF KGLPQFEPVYELBPHYFVSRNDGTVDTPPCLR LTHRTWGSQNSLVEMLFLR.SLEVQFHOJETF CTAGATFLAPPGLQPFAEDEARAAEPDPDYE NLRSAGGWSEARNGKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPPATPTLFRLPHUVFADNRDD PEILLNTTTYYYSVRYAGQEPSCVWAGWVY PPYHQDMSFDLSKVRVYTVTMOEDGONV HSSLKCSNCYMVWGGDPVSPGQQGRISHTDL VIGCLVDLATGLMTTFANGKESNTFFQDGNVT PSYHQIDMSFDLSKVRVYTVTMOEDGONV HSSLKCSNCYMVWGGDPVSPGQQGRISHTDL VIGCLVDLATGLMTTFANGKESNTFFQUSNYML ALHPEENRCMDLELSRELDLQRFISHTLRL YRAVCALGNNRVAHALCSHVQQDFLTMM ALHPEENRCMDLELSRELDLQRFISHTLRL YRAVCALGNNRVAHALCSHVQQDFLTMM ALHPEENRCMDLELSRELDLQRFISHTLRL YRAVCALGNNRVAHALCSHVQQDFLTMM ALHPEENRCMDLELSREDLORGFRODE GVGVTTSLRFPHIRSPPCTVALLAPAGAABAP ARLSPAPLEALRDKALRM.GBAVRDGGHA RDPVGASVEPGFVPVLKLVSTLLVMGGHGH GVGVTTSLRFPHIRSPPCTVALLAPAGAABAP ARLSPAPLEALRDKALRM.GBAVRDGGHA RDPVGASVEPGFVPVLKLVSTLLVMGGHGDL GGEEPEBETTLGSRLMSLLEKVRLVKKKREEK FERERAAESKRFNENLOGLAHARGARAP ARLSPAPLEALRDKALRM.GBAVRDGGHA RDPVGASVEPGFVPVLKLVSTLLVMGGHGLD GGEEPEPEETTLGSRLMSLLEKVRLVKKKREEK FERERAAESKRFNENLOGLAHARGLOHALDFGOLD GGEEPEPEETTLGSRLMSLLEKVRLVKKKREEK FERERAAESKRFNENLOGLAHARGLOHALDGGLOL GGEEPEPEETTLGSRLMSLLEKVRLVKKKREEK FERERAAESKENNENLOGLAHARGLOHALDGGLOLAHGGLOLD GGEEPEPEETTLAGRRAFLERGERGEBLDVGGLAHAL	1	•			1		IFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQ
LAPEDVISCLIDLSVPSISFRINGCPVQGFPSF NLDGLFFPVVSFSAGVEVARPLIGGENGEFEKE LPPPGY APCHEAVLPRERLHLEJKEYRREGP RGPHLVGPSRCLSHIDFVPCPVDTVQ/LPPH LERIREKLAENHEL WALTRIEGGWTYGPVRD DNRLHFCLVDFHSLPFERNYNLGMSGFL KTLLAIGGHVGMADEKAEDNIKTKLEKTY MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE NGRNVWARDRVGGGWSYSAVQDIPARNPR LVPYRLIDEATKRSNRDSLCQAVRTLLGYGY NIEPPDGEPSQVENQSRCDRVBIFRAEKSYTV QSGRWYFEFEAVTTGEMR WGWAPPELRPDV ELQADELAYVFNGHRGQRWHLGSEPFGRPW QPGDVVGCMDLTSRUTHITINGEVLMSDSGS ETAFREIEIGDGFLPVCSLGFGQVGHLNLGQD VSSLRFFALGGLQEGFEFAINMQRPVTTWFS KGLPGPEPVELEIPHVEVSRYOGTVDTPPCLR LTHRTWGSONSLVEALFLRLSLPVQFHOHFR CTAGATPLAPPOLQPPAEDEARAAEPPDYSE NIRRSAGGWSEAENKEGTAKEGAPGGTPQ AGGEAQPARAENEKDATTERNKKRGFLKFA KKVAMMTOPPATTTIPLRIPHDVVPADNRDD PEILINTTTYYSVRVFAGGEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSPQQGRISHTDL VIGCLVDLATGLIMTFTANGKESNTFFQVERN TKLFPAVFLYFTHGNVIGPELGKQKNIMPLS, AMFOSSEKNPAPOCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERLGWANDLAVSSR MPNHFLQVETRRAGERLGWANDLAVSSR MPNHFLQVETRRAGERLGWANDLAVSSR MPNHFLQVETRRAGERLGWANDLAVSSR MPNHFLQVETRRAGERLGWANDLAVSSR MPNHFLQVETRRAGERLGWANDLAGGLGDHAM ALHIPERNRCMDLELSSRLDLQRFHSHTLRL YRAVCALGNNRVAHALCSHVDQAGLIALBE DAHLPGPTRAGGPTYDLLSHLEGKQKNIMPLS SEVIPLTFETRAITLFPFGRSTENGHPRIGIP GVGYTTSLRPPHISSPPCTAGRACSRRSML SEVIPLTFETRAITLFPFGRSTENGHPRIGIP GVGYTTSLRPPHISSPPCTAGRACSRRSML SEVIPLTFETRAITLFPFGRSTENGHPRIGIP GVGYTTSLRPPHISSPPCTAGRACSRRSML SEVIPLTFETRAITLFPFGRSTENGHPRIGIP GVGYTTSLRPPHISSPPCTAGRACSRRSML SEVIPLTFETRAITLFPFGRSTENGHPRIGIP GVGYTTSLRPPHISSPPCTAGLAGAABAP ARLSPAIPLEALROKALRMLGEAVRDGQHA RDPVGASVEFGPFVLKLAVSTLLVMGIFGDE DVKQILKMIPPEVPTFEEEEEDEEEEGEEDDEE EKEEDEEETAGEKEDEEEEGEEDEE EKEEDEEETAGEKEDEREEEEEEEEDEEE EKEEDEETAGEKEDEREEEEEEEDEEEEGEEDEE EKEEDEETTAGERLAURALLGRAVARAGGER DEECPLPEERINGLLLGVRAWARAGEP VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDITMSLECLLGQURSLLIVQMGPGE EVELMQSIGGINKNNKVYPYPHINLMAALGMHE	]						ATHLRVGWALTEGYTPYPGAGEGWGGNGV
NLDGLFFPVSFSAGWEVRFLLGGRIGEFKF LPPFQYAPCHEAVLPRERLHLEPIKEYRREGP RGPHLVGPSRCLSHTDFVPCEVDTVQIVLPPH LERIREKLAENHIELWALTRIEGGWTJGPVRD DNRKLHFICLVDFHSLPPERSHYNLGMSGETL KTLLALGCHVGMADEKAEDNLKKITKLFKTY MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE NGHNVWARDRVGGGWSYSAVQDIPARRPR LVPYRLLDEATKRSNRDSLCQAVRTLLTQGY NIEPPDQEPSQVENQSRCDRVAFUFAEKSYTV QSGRWYFEFEAVTTOEMRVGWARPELRPDV ELQADELAYVFNGHRGQRWHLGSEPFGRPW QPGDVVGCMIDLTENTUFTLNGEVLMSDSS ETAFREIEIGDGFLPVCSLCPGQVGHLNLGQD VSSLRFAICIG.GGGFEFAMMQRVTTWFS KGLPGFEPVPLEHPHYSYSRVDGTVDTFPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHTR CTAGATTLAPPGLQFFAEBARAEPPDDYE NIRRSAGGWSEAENKEGTAKKAFGGTFQ AGGEAQPARAENEKDATTEKKKRFGTFKA KKVAMMTQPPATPTLPRLPHDVVPADNRDD PHILLNTTTYYSYRVFAGQEPSCVWAGWT PDYHQHDMSFDLSKWRVVTVTMGDEQGNV HSSLCSNCYMVWGGDFVSPQQQGRISHDL VIGCLVDLATGLAMFTANKEKSNTFFQVERN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMMQSBRKNPAPQCPPRLEMQMLMPVSWSR MPNHFLQVETRRAGERIGAWQCOEPLTMM ALHIPEENRCMDLELSBRLDLQRFHSTHLRL YRAVCALGNRVAHAESTNOQALLHALE DAHLPGPLRAGFYDDLLSHLIESACRSRRSML SETVIPLTFETRAHTLFPGRSTENGHPRHGLP GVGYTTSLRPPHISSPCPCVALAFAAGAABAP ARLSPAPLBALROKALRNLGBAVRDGGQHA RDPYGASVEFOFVPVLKLVSTLLVMGIFGGE DVKQLIKMIPPEVFTEEEEEDEEEGEBEDEE EKEEDEET AQEKERDLLDFFTQDLLAHCGJULA FSMTAAETARTREFRSPPQEQINMLLQKKGE  DVKQLIKMIPPEVFTEEEEEDEEEGEBEDEE EKEEDEETTAGEKRARGFLEKEG LEEGLLQMKLLEFVFCOQELL GEEEPFEEETTLGSRLMSLLEKVELVKKKEEK FSMTAAETARRTREFRSPPQEQINMLLQKKOPD VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSVEDTMSLLECLGQRSLLIVQMGPGE ENLMQSIGGINKNNKVFYCHPMLMAALGMHE	1						GDDLYSYGFDGLHLWTGHVARPVTSPGQHL
LPPPGYAPCHEAVLPRERLHLEPJKEYRREGE RGPHLVGPSRCLSHTIDFVPCPVDTVQIVLPPH LERREKLASNIHELWALTRIEGGWTYGPVRD DNRLHPCLVDFHSLPPERNYNLGMSGETL KTLLALGCHVGMADEKAEDDILKKTKLPKTYY MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE NGRNVWARDRVGGWSYSAVQDIPARRPPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDGEPSQVENQSRCDRVRIFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELQADELAYVPNGHRGQRWHLGSEPFGRPW QPGDVVGCMIDLTENTUFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFAICGLQEGFEFADNIQRRVTTWFS KGLPOFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRLSLPVQFHOHTR CTAGATTLAPPGLQPFAEDEARAAEPDDVB NIRRSAGGWSEAENGKEGTAKEAPGPGTV AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPPATPTLPRLPHDDVVPADNRDD PEILINTTTYYSIVSVRAGGEPSCWWAGWYT PDYHQHDMSPDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSPQGQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVERN TKLFFAVFULFTIQNVUQFELGKQKNIMPLSA AMFOSERKINP APQCPPRLEMMPVSWSR MPNHFLQVETRRAGERLGWAVQCQEPLTMM ALHIPEENRCMDLELSBRLDLQRFHSHTIRL YRAVCALGNRVAHALCSHVDQAGLLHALE DAHLPGPLRAGYYDLLISHH.BSACRSRSML SEYIYPLTFETATLT.PPGRSTENGHPPRHGLP GVGVTTSLRPPHHFSPPCTVALLPAGAGAAP ARLSFAPLBALRDKALRNLGEAVBDGQHA RDPVGASVEFOTYVLKLUNGIFGDE DVKQILKMIPPEVTTEEEEEDEDEEEGEEDDEE EKEEDEETTAGSKLMSLEKKEGLILGYFCDQGLA FISHALPBALRDKALRNLGEAVBDGQHA RDPVGASVEFOTYVLKLUNGIFGDE DVKQILKMIPPEVFTEEEEEDEEEEGEEDDEE EKEEDEETTAGSKLMSLEKKURVRKKREK FSMTAAETARRTEFFSRPPGOINMLLQKKOG TDEEDCPLPEERQDLLDFHQDLLAHCGLDG GEEEPFEEETTLGSRLMSLLEKVRUNKKREK FSMTAAETARRTEFFSRPPGOINMLLQKKOG TDEEDCPLPEERGDLLDFHQDLLAHCGLDG GEEEPFEEETTLGSRLMSLLEKVRUNKKKREK PEERSAESSKPRSLQELVSRLWVRWAQGDE VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDITMSLLECLGQURSLLIVQMGPQE ENLMQSIGNIMNNKVFVQHPNLMMALGMAD ENLMQSIGNIMNNKVFVQHPDLMARACHME	1						LAPEDVISCCLDLSVPSISFRINGCPVQGVFESF
RGPHLVGPSRCLSHTIDFVPCPVDTVQIVLPPH LERIREKLAENIHELWALTRIEQGWTYGPVRD DNKRLHPCLVDFHSLPEPERNYNLQMSGETL KTLLALGCHVGMADEKAEDNLKKTKLFKTY MMSNGYKPAPLDLSHVRLTPTLTVDRLAE MGHNVWARDRVGQGWSYSAVQDIPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTILGYGY NIEPPDQEPSQVENQSRCDRVGHRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELGADELAYVRGHRGGRWANGSEPGRPW QPGDVVGCMIDLTENTUFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNGQD VSSLRFFACIGLGGGFEFFARMQRVTTWFS KGLPQFEPVPLEIPHVEVSRVDGTVDTPCLR LTHRTWGSONSLVEMLFLRLSLPVQFHOHFE CTAGATPLAPPOLQPPAEDEARAAEPDPYE NIRRSAGGWSEAENKEGTAKEAGPGGTPQ AGGEAQPARAENEKDATTEKKRGFLFKA KKVAMMTQPPATPTLPRLPHDVVPADNRDD PEILINTTYYYSVRVFAGQEPSCVWAGWYT PPYHQIDMSFDLSKVRVVTYTMGDEQGNV HSSLKCSNCYMVWGGDFVSPQQQERSCUWAGWYT PPYHQIDMSFDLSKVRVVTYTMGDEQGNV HSSLKCSNCYMVWGGDFVSPQQQERSCWWGWYT FLFFARVFUPTHQNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMMLMVSWSR MPNHFLQVETRRAGERLGWAVQCQEPLTMM ALHIPEENRCMDLELSBRLDLQRFHSHTLRL YRAVCALGINRVAHALCSHVDQAQLLHALE DAHLPGPLRAGYYDLLISHLESACRSRRSML SETVPLTFETRAITLFPPGRSTENOHPRRGIP GVGVTTSLRPPHISSPCPCVAALPAAGAAEAP ARLSPAPLBALRDKALRMLGBAVRDGQHA RDPPGASVEFGOFVPVLKLVAMGIFGDE DVKQLKMIEPEVFTEEEEEDEEEEEBEBDEE EKEEDBEET AGBKERGLAEGGHARDPAGAGAAEP ARLSPAPLBALRDKALRMLGBAVRDGQHA RDPPGASVEFGOFVPVLKLVAMGIFGDE DVKQLKMIEPEVFTEEEEEDEBEEEBEBDEE EKEEDBEETTAGSKLMSLEKVBLVKKGEK FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEERGPLLDFHGOLLAHCGIQLD GEEEEPFEETTLGSRLMSLLEKVBLVKKGEK FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEERGPLLDFHGOLLAHCGIQLD GEEEEPFEETTLGSRLMSLLEKVBLVKKGEK PEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSPEEETTLGSRLMSLLEKVBLVKKWEK PEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSPEEETTLGSRLMSLLEKVBLVKWACKGEK PEERSAEESKPRSLQELVSRUVVRWAQCDE PGEERSPEESTTLGSRLMSLLEKVBLVKWACCCE PEERSAEESKPRSLQELVSRUNDLAGGULARLAGGULA PTINSPSVEDTMSLLECLGGRSLLIVVGWAGCE PEERMAGGSHNNNKVYFVPHDLMAALGMUHE	1						NLDGLFFPVVSFSAGVKVRFLLGGRHGEFKF
LERIREKLAENIHELWALTRIEQGWTYGPVRD DNKRLHPCLVDFHSLPEPERNYNLQMSGETL KTLLALGCHVGMADEKAEDNLKKTKLPKTY MMSNOYKPAPLDLSHVRLTPAQTIT.VDRLAE BIGHNVWARDRVGGGWSAV QUDPARRNPR LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENQSRCDRVUFFAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELQADELAYVFNGHRGGRWHLGSEPFGRPW QPGDVVGCMIDLTENTHFILMGVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFFAICGLQEGFEPFAINMGRYTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR CTAGATTLAPPGLQPPAEDEARAAEPDPDYE NLRRSAGGWSEAENGKSATKGCAPGGTPQ AGGEAQPARAENEEDATTEKNKKRGFLFKA KKVAMMTQPPATPTLPRLPHDVVPADNRDD PEILINTTTYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDQGNV HSSLKCSNCYMVWGGDPSPGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFVLPTHQNVLQFELGKKNIMPLSA AMFQSEKNRPAPQCPPFLEMQMLMPYSWSR MPNIFLQVETRRAGERLGWAVQCQEPLTMM ALHIPEENRCMDILELSERLDLQRFHSHTLRL YRAVCALGNNRVAHALGSHVDQAQLHALE DAHLPGFLRAGYYDLLISHHLSAGKRSSMM. SEYIPVLTPETRATLFPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPPCFVAALPAGAAEAP ARLSPAIPLEALROKALRM.GBAVPGGQGH SEYIPVLTPETRATLFPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPPCFVAALPAGAAEAP ARLSPAIPLEALROKALRM.GBAVPGGQGH BDFUYGASVETGEEEEDEEEGEEDDEE EKEEDEETAQEKEDEEKEEEGAEDEDEE EKEEDEETTAGRKMSLLEKVRLVKKHEEK PEEGRALEESKPRSLQELVKKKHEK PSETRLAGERSPRSLLELVRLVKKHEEK PEEGRSALEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLEKGRUSHLIVVKKHEEK PEEGRSALEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLELCQUISLLIVVKKHEEK PEEGRSALEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLELCLQUISLLLIVVRMFPGE ENNLMJOSIGNIMNNKVFYQHFNLMRALGMHE							LPPPGYAPCHEAVLPRERLHLEPIKEYRREGP
DNKRLHPCLVDFHSLPEPERNYNLQMSGETL KTILALGCHVGMADEKAEDNLKHTKLPKTY MMSNOYKPAPLDLSHVRLITPAQITLYDRLAE NGHNVWARDRVGGWSYSAVQDDPARRNPR LVPYRLDATKRSNRDSLCQAVRTLLGYGY NIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV QSGRWYFEFEAVTIGEMRVGWARFLRPDV ELGADELAYVNGHRGGROWHLGSEPFGRPW QPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS ETAFREIRIGDGFLPVCSLGFGQVGHLNLGQD VSSLRFFALGCLGEGEPFAINMQRPVTTWFS KGI-PQFEPVPL EHPHYEVSRVDGTYDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR CTAGATILAPPOLQPPAEDEARAAEPPPDYE NLRRSAAGWSEAENGKEGTAKEGAPGOTPQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPPATPILFRLPHDVVPADNRDD PEILNTTTYYYSVRVFAGQEPSCVWAGWYT PDYYHQHDMSPDLSKVRVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSPQQQRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVERN TKLFPAVFVLYFHQNNVGGLGKGKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MPNIFLQVETRRAGERLGWAVQCGPLTMM ALHTBERNCMDLELSSBLDLQRFHSITLIL YRAVCALGNNRVAHALCSHVDQAGLLEALE DAHLPGPLRAGYYDLLISHLESACRSRRSML SEYTYPLTTETRAITLFPGRSTENGHPAHGLP GVGVTTSLRPPHHSPPCTVAALPAGAABAEP ARLSPAPLEALRDKALRML GBAVRDGGQHA RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVKQILKMIEPSVFTEEEEEDEEEGEEDEE EKEEDEEETAQRKEDFEKEEEBEAEGERGEDEE EKEEDEEETARRETREFRSPQOGNINMLJQKDG TDEEDCYLPEERQDLLDFHQDLLAHCGIQLD GEEEPPEETTILGSRLMSLLEKVRLVKKFEEK PEEERSALESKFRSLOLLEVRLVKKFEEK PEEERSAEESKFRSLOLLSVHMVVRWAQEDF VQSPELVRAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLELCAQUSHLVKKYEEK PEEERSAEESKFRSLOLLSVHMVVRWAQEDF VQSPELVRAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLELKQUSHMVVRWAQEDF VQSPELVRAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLELKQUSHLIVVKKYEEK PEEERSAEESKFRSLOLLVSHMVVRWAQEDF							RGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPH
KTLLAGCHVGMADEKAEDNILKEKIELPKTY MMSNGYKPAPLDLSHVRLTPAQTITLVDRLAE NGHNVWARDRVQGWSYSAVQDIPARRNPR LVPYRLIDEATKRSVRDSLCQAVRTLAGYGY NIEPPOQEPSQVENQSRCDEVRIFRAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELGADELAYVFNOHRGQRWHLGSEPFGRPW QPGDVVGGMDLTENTIUFTLNGEVLMSDSGS ETAFREIEIGGGLPVCSLGPGQVGHLNLGQD VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSQNSLVEMLFLRLSLPVQFHQHTR CTAGATPLAPPOLQPPADEARAAEPDPDVE NLRRSAGGWSEAENGKEGTAKEGAPGDTVQ AGGEAQPARAENEKDATTEKNKKRGFLFKA KKVAMMTQPATPTLAPHDVVPADNRDD PEILINTTTYYYSVRVFAGQEPSCVWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMVWGGDFVSFQQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFVLPTHQNVIQFELGKQKNIMPLSA AMFQSEKKNPAPQCPPLEMQMLMPVSWSR MPNIFLQVETRRAGERLGWAVQCCPLTMM ALHPEENRCMDLELSBRILDLQRFFISTILRL YRAVCALGNNRVAHALCSHVDQAQLLHALE DAHLPGFLRAGYVTOLLISHHLESACRSRSMI. SEYIPVLTPETRATILFPPETSENOHPRHIGLP GVGVTTSLRPPHHSPPCFVAALPAAGAAEAP ARLSPAIPLEALRDKALRMLGSEREGBEDDE EKEEDEETAGEKDEKEEEBEADEGEREDEE EKEEDEETAGEKDEKEEEBEADEGEREDEE EKEEDEETAGEKDEKEEEBEADEGREDEE EKEEDEETAGEKDEKEEEBEADEGREDEE EKEEDEETAGEKDEKEEEBEADEGREDEE EKEEDEETLIGSRLMSLLEKVRLVKKFEEK PEEERSALESSKPRSLQLVJNMLVRWAQEDF VQSPELVRAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLEKQTLJKWKRFEEK PEEERSALESSKPRSLLGLYNMVVRWAQEDF VQSPELVRAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLEKCQUSHLIVVRWAPQEDF VQSPELVRAMFSLLHRQVDGLGELLRALPRA YTISPSSVEDTMSLLECLGQUSSLLIVVQMGPQE ENILMIQSIGNIMNNKVFYQHPNLMRALGMHE							LERIREKLAENIHELWALTRIEQGWTYGPVRD
MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE NGHNVWARDRVQGWSYQDIPARRNPR LVPYRLLDEATKRSNRDSLQAVRTLLGYGY NIEPPDQEPSQVENQSRCDRVRIFAEKSYTV QSGRWYFEFEAVTTGEMRVGWARPELRPDV ELGADELAYVFNGHRAGRWHLGSEPFGRPW QPGDVVGCMIDLTENTUFTLNGEVLMSDSGS ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD VSSLRFFAICGLQEFEPFANMGRPVTTWFS KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR LTHRTWGSONSLVEMLFLRLSLPYQFHGHFR CTAGATPLAPPGLQPPAEDEARAAEPDPDYE NLRRSAGGWSEAENGKEGTAKRGAPGGTPQ AGGEAQPARAENEKDATTEKNKKGFLFAK KKVAMMTQPPATPTLPRLPHDVVPADNRDD PEILINTTTYYSVRVFAGQEPSCWAGWVT PDYHQHDMSFDLSKVRVVTVTMGDEQGNV HSSLKCSNCYMWGGFVSPGQQGRISHTDL VIGCLVDLATGLMTFTANGKESNTFFQVEPN TKLFPAVFVLPTHGNVIQFELGKQKNIMPLSA AMFQSERKNPAPQCPPRLEMQMLMPVSWSR MFNHFLQVETRRAGERLGWAVQCQEPLTMM ALHIPEENRCMDLELSERLDLQRFHSHTLRL YRAVCALGNNRVAHALCSHVQAQLLHALE DAHLPGPLRAGYYDLLISHH FSACRSRSML SEYIVPLTFETRATILFPPGRSTENGHPRHGLP GVGVTTSLRPPHHFSPPCFVAALRM.GEAVRDGGQHA RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE DVKQLKMIEPEVFTEEEEEDBEEGEEBEDEE EKEEDBEEFTAQEKEBEEAAEGEKEEG LEEGLLQMKLPSVKLQMCHLLEYFCDQELQ HRVESLAAFAERTYDKLQANGRSYGLLIKA FSMTAAAFTARTRTERFSPPQCONMLLOFKDG TDEEDCPLPEERROPLLDFHQDLLAHCGIQLD GEBEPEEETTLGSRLMSLEKKVLVKKKEK PEEERSAEESKFRSLGELVSHMVVRWAQEDF VQSPELVRAMFSLHRQQVGIGSLLIVQMGPQE ENLMIQSIGNIMNNVKYPQHPNLMRALGHPA	1						
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EKEEDEETAQEKEDEEKEEEAAEGEKEEG LEEGLLQMKLPESVKLQMCHI.LEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPJPEEIRQDLLDFHQDLLAHCGIQLD GEEEPEETTLGSRLMSLLEKVRLVKKKFEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE	1						·
LEEGLLQMKLPESVKLQMCHILLEYFCDQELQ HRVESLAAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEERQDLLDFHQDLLAHCGIQLD GEEEEPEETTLGSRLMSLLEKVRLVKKKFEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE							
HRVESLÄAFAERYVDKLQANQRSRYGLLIKA FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEPEEETTLGSRLMSLLEKVRLVKKKFEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE							
FSMTAAETARRTREFRSPPQEQINMLLQFKDG TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEPEEETTLGSRLMSLLEKVRLVKKKFEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE							
TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD GEEEEPEETTLGSRLMSLLEKVRLVKKKFEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE			1		' I	ı	
GEEEEPEETTLGSRLMSLLEKVRLVKKKFEK PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE							rsmtaaetarrtreprsppQEQINMLLQFKDG
PEEERSAEESKPRSLQELVSHMVVRWAQEDF VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE							
VQSPELVRAMFSLLHRQYDGLGELLRALPRA YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE							
YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE	1	,			Į		
ENLMIQSIGNIMANKVFYQHPNLMRALGMHE	1						
TVMEVMVNVLOGGESKEIRFPRMVTSCCRFL	1				·	ŀ	
							IVMEVMVNVLOGUESKEIRFPKMVTSCCRFL

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						CYFCRISRQNQRSMFDHLSYLLENSGIGLGM QGSTPLDVAAASVIDNNELALALQEQDLEKV VSYLAGCGLQSCPMLVAKGYPDIGWKPCGG ERYLDFLRFAVFVNGESVEENANVVVRLLIR KPECFGPALRGEGGSGLLAAIEEAIRISEDPAR DGPGIRRDRREHFGEEPPEENRVHLGHAIMS FYAALIDLLGRCAPEMHLIQAGKGEALRIRAI LRSLVPLEDLVGIISLPLQIPTLGKDGALVQPK MSASFVPDHKASMVLFLDRVYGIENQDFLLH VLDVGFLPDMRAAASLDTATFSTTEMALAV NRYLCLAVLPLITKCAPLFAGTEHRAIMVDS MLHTVYRLSRGRSLTKAQRDVIEDCLMSLCR
						YIRPSMLQHLLRRLVFDVPILNEFAKMPLKLL TNHYERCWKYYCLPTGWANFGVTSEEELHL TRKLFWGIFDSLAHKKYDPELYRMAMPCLC AIAGALPPDYVDASYSSKAEKKATVDAEGNF DPRPVETLNVIIPEKLDSFINKFAEYTHEKWAF DKIQNNWSYGENIDEELKTHPMLRPYKTFSE KDKEIYRWPIKESLKAMIAWEWTIEKAREGE EEKTEKKKTAKISQSAQTYDPREGYNPQPPDL SAVTLSRELQAMAEQLAENYHNTWGRKKKQ ELEAKGGGTHPLLVPYDTLTAKEKARDREKA QELLKFLQMNGYAVTRGLKDMELDSSSIEKR FAFGFLQQLLRWMDISQEFIAHLEAVVSSGRV
						EKSPHEQEIKFFAKILLPLINQYFTNHCLYFLS TPAKVLGSGGHASNKEKEMITSLFCKLAALV RHRVSLFGTDAPAVVNCLHILARSLDARTVM KSGPEIVKAGLRSFFESASEDIEKMVENLRLG KVSQARTQVKGVGQNLTYTTVALLPVLTTLF QHIAQHQFGDDVILDDVQVSCYRTLCSIYSLG TTKNTYVEKLRPALGECLARLAAAMPVAFLE PQLNEYNACSVYTTKSPRERAILGLPNSVEEM CPDIPVLERLMADIGGLAESGARYTEMPHVIE ITLPMLCSYLPRWWERGPEAPPSALPAGAPPP CTAVTSDHLNSLLGNILRIIVNNLGIDEASWM KRLAVFAQPIVSRARPELLQSHFIPTIGRLRKR
						AGKVVSEBEQLALEAKAEAQEGELLVRDEFS VLCRDLYALYPLLIRYVDNNRAQWLTEPNPS AEBLFRMVGEIFIYWSKSHNFKREEQNFVVQ NEINNMSFLTADNKSKMAKAGDIQSGGSDQE RTKKKRRGDRYSVQTSLIVATLKKMLPIGLN MCAPTDQDLITLAKTRYALKDTDEEVREFLH NNLHLQGKVEGSPSLRWQMALYRGVPGREE DADDPEKIVRRVQEVSAVLYYLDQTEHPYKS KKAVWHKLLSKQRRRAVVACFRMTPLYNLP THRACNMFLESYKAAWILTEDHSFEDRMIDD LSKAGEQEEEBEEVEEKKPDPLHQLVLHFSRT ALTEKSKLDEDYLYMAYADIMAKSCHLEEG
						GENGEAEEEVEVSFEEKQMEKQRLLYQQARL HTRGAAEMVLQMISACKGETGAMVSSTLKL GISILNGGNAEVQQKMLDYLKDKKEVGFFQS IQALMQTCSVLDLNAFERQNKAEGLGMVNE DGTVINRQNGEKVMADDEFTQDLFRFLQLLC EGHNNDFQNYLRTQTGNTTTINIICTVDYLL RLQESISDFYWYYSGKDVIEEQGKRNFSKAM SVAKQVFNSLTEYIQGPCTGNQQSLAHSRLW DAVVGFLHVFAHMMMKLAQDSQIELLKEL LDLQKDMVVMLLSLLEGNVVNGMIARQMV DMLVESSSNVEMILKFFDMFLKLKDIVGSEAF QDYVTDPRGLISKKDFQKAMDSQKQFSGPEI

SEQ NO: o nucl- eotide seq- uence	of NO: of peptide seq-uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						CFLLSCSEADENEMINCEEFANRFQEPARDIO FNVAVILTNISEHVPHDPRIHNFLELAESILE YFRPYLGRIEIMGASRRIERIYFEISETNRAQW EMPQVKESKROFIFDVVNEGGEAEKMELFVS FCEDTIFEMQIAAQISEPEGEPETDEDEGGAG AEAGAEGAEEGAAGLEGTAATAAAGATARV VAAAGRALRGISYRSLRRVRRLRRLTAREA ATAVAALLWAAVTRAGAAGAGAAAGALGL LWGSLFGGGLVEGAKKVTVTELLAGMPDPT SDEVHGEQPAGPGGDADGEGASEGAGDAAE GAGDEEEAVHEAGPGGADGAVAVTDGGFFR PEGAGGLGDMGDTTPAEPPTPEGSPILKRKLG VDGVEEELPPEPEPEPELEPEKADAENGEK EEVPEPTPEPPKKQAPPSPPPKEEAGGEFWG ELEVQRVKFLNYLSRNFYTLRFLALFLAFAIN FILLFYKVSDSPPGEDDMEGSAAGDVSGAGS GGSSGWGLGAGEEAEGDEDENMVYYFLEES TGYMEPALRCLSLLHTLVAFLCIIGYNCLKVP LVIFKREKELARKLEFDGLYTTEQPEDDDVKG QWDRLVLNTPSFPSNYWDKFVKRKVLDKHG DIYGRERIAELLGMDLATLEITAHNERKPNPP PGLLTWLMSIDVKYQIWKFGVIFTDNSFLYLG WYMVMSLLGHYNNFFFAAHLLDIAMGVKTL RTILSSVTHNGKQLVMTVGLLAVVVYLYTVV AFNFFRKFYNKSEDEDEPDMKCDDMMTCYL FHMYYGVRAGGGIGDEIEDPAGDEYELYRVV FDITFFFFFYIVILLAIIQGLIIDAFGELRDQQEQV KEDMETKCFICGIGSDYFDTTPHGFETHTLEE
501	1851	A	3869	467	665	HNLANYMFFLMYLINKDETEHTGQESYVWK MYQERCWDFFPAGDCFRKQYEDQLS VIVAIYCQLIFDKGAKTIQ*PFQQIAL/CKRMK LGPCFTPCGKINSEWIRELSVRVKTIKHLEIGV
502	1852	A	3888	1042	724	N SGMQWRDLTPLQPLPPRFKQFSCLSLPGSWD YRHAP\PLLTNF\*FLVEMGFCYVGQAGRKLL ASSDQSALASQSAGITGISTAPGPPFFLNFEA
503	1853	A	3891	1773	1193	GSCSVAQAGVQ  EVDSQSGVQ*QAPGSLQLQTPGLK/VSCLLSR QDYRSSLPHLASCCYYYYYYY/VFL*RRGLTTL VQGGLKLLPSSNPFASAP*TAGITGMSHCAGP HFNF*MFRKISCIRE*F*HTRIYDIPFLILFFKET WVLLCYPGWPQIPGLKPSSCLRLLSSWDHRC APPCPASFFIFHVDRVSPPCPGLVSITFKMLLL L
504	1854	В	3896	279	70	MVSKSKSILMSYNHVELTFSDMKKMPEAFRR TQKHTIYLIPYQVIFWSTGKDAMRSFMMPFY QKEYYENO*
505	1855	A	3899	2		EPGVPTKKTWFDKPDFNRTNSPGFQKKVQFG NENTKLELRKVPPELNNISKLNEHFSRPGTLV NLQVAYNGDPEGALIQFATYEEAKKAISSTEA VLNNRFIKVYWHREGSTQQLQTTSPKVMQPL VQQPILPVVKQSVKERLGPVPSSTIEPAEAQS ASSDLPQVLSTLLA*QKQCIIQLL/WKAAQKT LLVSTSAVDNNEAQKKKQEALKLQQDVRKR KQEILEKHIETQKMLISKLEKNKTMKSEDKAE IMKTLEVLTKNITKLKDEVKAASPGRCLPKSI KTKTQMQKELLDTELDLYKKMQAGEEVTEL RRKYTELQLEAAKRGILSSGRGRGIHSRGRGA VHGRGRGRGRGRGVPGHAVVDHRPRALEIS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion AFTESDREDLLPHFAQYGEEDCQIDDSSLHA VITFKTRAEAEAAAVHGARFKGQDLKLAWN KPVTNISAVETEEVEPDEEEQREIIIA
506	1856	A	3911	1952	919	DAELSGTLSLVLTQCCKRIKDTVQKLASDHK DIHSSVSRVGKAIDKNFDSDISSVGIDGCWQA DSQRLLNEVMVEHFFRQGMLDVAEELCQES GLSVDPSQKEPFVELNRILEALKVRVLRPALE WAVSNREMLIAQNSSLEFKLIRLYFISLLMG GTTNQREALQYAKNFQPFALNHQKDIQVLM GSLVYLRQGIENSPYVHLLDANQWADICDIFT RDACALLGLSVESPLSVSFSAGCVALPALINIK AVIEQRQCTGVWNQKDELPIEVDLG*KSAGY HSIFACPILRQQTTDNNPPMKLVCGHIISRDAL NKMFNGSKLKCPYCPMEQSPGDAKQIFF
507	1857	A	3936	439	18	SHPFSPAPGICPDAPPPLPRPSKGLGHPGTAGA PGSGARCHPPSTCSPSWASPG*GAKASPALPR SHGVTLLCKAQAHLCRGEDSKDASGSTSQA WEPG*GAWGMPRCQGPALGSCFCPPGTTVQ RPAKORDKRNRHLGR
508	1858	A	3944	120	412	WCPAGTLDFPGPQEMVLLEIEVMNQLNHRNL IQLYAAIETPHEIVLFME\YECPK*W*GLGGGT TRHGASRGGVCAHSIEGGELFERIVDEDYHLT EV
509	1859	A	3949	31	392	LTKTPSPREKGRGVLSVLLMMI*KCRVIFVKIP MVFFLQNFC/RIILNVA\WTGD*PNTL*KEQRG ITFSDSKS*YKATKIKTMWYCHKNRYID/ERN RIEIPEINPCICDKIIFRKLSMITQ
510	1860	A	3954	1013	885	FSETRACCPRLEHSGRIEAHCSLNIPGSSDPPT SASSVAATTG
511	1861	A	3956	1	1054	PPAWAPRSPLIWAPTSGRHPCRAALPWSTSSV RWQPSEKQPPPPAHRGPADSLSTAAGAAELS AEGAGKSRGSGEQDWVNRPKTVRDTLLALH QHGHSGPFESKFKKEPALTAVARTARKRKPS PEPEGEVGPPK\TTERPSRGCPHPQRGSRSP*L LHPLLCLRHHPLPHLIPTGPHRLKRPRM\P\SP MAALILVADNAGGSHASKDANQVHSTTRN SNSPPSPSSMNQRRLGPREVGQGAGNTGGL EPVHPASLPDSSLATSAPLCCTLCHERLEDTH FVQCPSVYSHKFCYPCSRQSIKQQGASGEVYC PSGEKCPLVGSNVPWAFMQGEIATILAGDVK VKKERDS QDRARLDCSSATSAHCNLRLPGS*DSPASASR
512	1862	A	3957	1086	3	VAGTTDTHIHITWLILGSSVQTGFDHVGQAG LELLTSGDPPISASESAGIMGMSHCVWP*SWG LSHHMAPPQGDGGRARGTPGPEQSFWNLSC H*PRCQVPS*LMTQL/FWGRHQYNPTMKRGK LRHREACSLPLPGEGEPGLQPSS\*SQNPCSSPL FHHGL*AWLWCPELLLQGQARRH*RSPPS/FK CPATLSLTAWSQTKRLRSQFLLLPWL*RAL*H PP\CHWPSRRSLGDPLLPRSQG*RDGT*ASTFC SYF*DTESHLVAQAGVQWRDLGSLQPPCPRL K\RFSRLSPPSSYTHRYVPSHLAESCISSRDRIP PSRPDRSRNSNSLSR
513	1863	A .	3961	3038	476	VALTTSMCCNKQVIVIDKIKSASIADRCGALH VGDHILSIDGTSMEYCTLAEATQFLANTTDQ VKLEILPHHQTRLALKGPDHVKIQRSDRQLT WDSWASNHSSLHTNHHYNTYHPDHCRVPAL TFPKAPPPNSPPALVSSSFSPTSMSAYSLSSLN MGTLPRSLYSTSPRGTMMRRRLKKKDFKSSL

	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	
	NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
	nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
	eotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq-	uence		09/496	correspondi		M=Methionine, N=Asparagine, P=Proline,
	uence	ļ	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		}	1	l	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
		l	ł	1	peptide		/=possible nucleotide deletion. \=possible
- 1					sequence		nucleotide insertion
١		ļ ·	1				SLASSTVGLAGQVVHTETTEVVLTADPVTGF
- 1			1	1	{	1	GIQLQGSVFATETLSSPPLISYIEADSPAERCG
- 1		ĺ	1			1	VLQIGDRVMAINGIPTEDSTFEEASQLLRDSSI
ļ		l	1				TSKVTLEIEFDVAESVIPSSGTFHVKLPKKHN
ł		ľ	1			1	VELGITISSPSSRKPGDPLVISDIKKGSVAHRT
- 1						j	GTLELGDKLLAIDNIRLDNCSMEDAVQILQQC
- [			İ	1 1		ł	EDLVKLKIRKDEDNSDEQESSGAIIYTVELKR
- [			1			j	YGGPLG\ITISGTEEP\FDL*IISSLTKGGLAERT
			1.			1	GAIHIGDRIL\AINSSSLKGKPLSEAIHLLOMAG
- 1			ł	]		ł	ETVTLKIKKQTDAQSASSPKKFPISSHLSDLGD VEEDSSPAQKPGKLSDMYPSHGCPSVDSAVD
-				!			SWDGSA/IDTS/YGTEGT/SFQASGY/NFNTYD
I			ł	j			WRSPKQRGS/LSPVT/KPRSQTYPDVGLSYED
	- 1			1 1		1	WDRSTASGFAGAA\DSAETEQEENFWSQALE
-			1				DLETCGQSGILRELEATIMSGSTMSLNHEAPT
-1				ĺ			PRSPAGSDRPSFQERSSSRPHYSQTTRSNTLPS
- 1	l		l				DVGRKSVTLRKMKQEIKEIMSPTPVELHKVT
							LYKDSDMEDFGFSVADGLLEKGVYVKNIRPA
-	1			. [		ł	GPGDLGGLKPYDRLLQVNHVRTRDFDCCLV
- 1	ļ		) )	j		l	VPLIAESGNKLDLVISRNPLASOKSIDOOSLPG
-	514	10/4		20/6	***		D*SEQNSAFFQQPSHGGNLETREPTNTL
-	314	1864	Α	3967	833	800	LEKQGVSGMATKRLARQLGLIRRKSIAPANG
-			] ]				NLGRSKSKQLFDYLIVIDFESTCWNDGKHHH
-				.		1 .	SQEIIEFPAVLLNTSTGQIDSEFQAYVQPQEHPI
- 1	Ì			.			LSEFCMELTGIKQAQVDEGVPLKICLSQFCK
-	J	•					WIHKIQQKNIIFATGISEPS/DF*SKIMCICYL
	515	1865	A	3969	492	182	VR*RISYTY*SKHKSKGC
1	- 1				1,52	162	CRFWGISTHCDTCDPLSPQTTEG**EGDLWSL
	1						DLLGPEFLARKPLFKTKTYQSTF*SISKNE/FTC
L							PNFIIEEGTDLIF\*QVKHNPCHRLTPEEGTVQL NRADS
-[-	516	1866	A	3977	2	1357	KMLC/QKESNYIRLKRAKMDKSMFVKIKTLGI
							GAFGEVCLARKVDTKALYATKTLRKKDVLL
1	.			i			RNQVAIIVKAERDILAEADNEWVVRLYYSFQ
1	1	1	- 1	1			DKDNLYFVMDYIPGGDMMSLLIRMGIFPESL
1			1	ļ			ARFYIAELTCAVESVHKMGFIHRDIKPDNILID
	ì	ł	- 1		l		RDGHIKLTDFGLCTGFRWTHDSKYYOSGDHP
	ļ						RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA
	Ì		ĺ				RQHQRCLAHSLVGTPNYIAPEVLLRTGYTOL
		1	.				CDWWSVGVILFEMLVGQPPFLAQTPLETOM
1	.	ľ	- 1			ĺ	KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE
		}	J	ŀ		·	DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS
	- 1	ŀ	1	ì		l	AFKQFP*NHTTPTDTSNFDP\VDPDKLWSDDN
		ł	1				EEENVNDTLNGWYKNGKHPEHAFYEFTFRRF
		f	- 1	- 1	. 1		FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD QNTGSEIKNRDLVYV
5	17	1867	A	3980	1358	1022	FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY
		j					VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD
1			- 1	1	İ	•	*RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA
L			}		1		QAIFQPQPPKVLGLQV
5	18	1868	A	3986	974	666	SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F
	1		-		Ì	[	SCFSLPE*LGYRHVPPCLANSVFSVEMGVFLH
1	1	1	- 1	]	j	!	VGQAGLELLTSGDLPALASQSAGITG\SHRAR
Ļ						1	PENGFENIF
5	19	1869	A	3994 ′	751	126	NQGLRHVGLCRTCLVNQMFASSILGKSHHHS
		1	- 1		ļ		LISINQGHNALWKAAG\PLPLKAGYC\OSESPC
1			- 1	1	1		DSLKYG\SWDEKDLTVPORDTHKRSVLRWIS
1		- 1	- 1	1	1		QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV
L.							HLFSSEMGE\NRPMVG\ARHVYSNAALLSFTP

			• • • • • •			
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	<b>,</b>		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
ŧ		[		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/-possible nucleotide deletion, \-possible
,			ļ ·	peptide sequence		nucleotide insertion
	ļ	ļ	ļ	Sequence		LRCLGGEKHKSGLHARPVIVPSLELHYDMDSI
	ļ				1	AHV\FADLLLIITLPSYYIPFC
	1000	<del>                                     </del>	3999	882	698	QSFRLSLLSSWDYRHM*PRLANF*TVFFCRDR/
520	1870	A	3999	602	1 0,0	SLALLPRLVSNSWPQAILPPRPPKVLGLQT
<u> </u>	1871	A	4011	1346	1178	FFF*ETVSCSAS*AGVRSHDNSSLQPPSPG\SSN
521	18/1	Ι Α	4011	1340	11.70	PPTSASHVAGATGTHHHAWLLSV
500	1872	A	4015	2	377	QGIALLTRMGESVKHVTGGYKLRTRPLEFAA
522	18/2	Α.	4015	1	1 37.	IGDYLDTFALKLGTIDRIAQRIIKEEIEYLVELR
	1	1	İ		1	EYGPVYSTWSALEGELAEPLEGVSACIGNCST
	İ	1		1		AL*ELTDDMTEDFLFVLREYILYSDSMK
523	1873	A	4018	341	19	ERVIHNOIOOAORSPHIFNARRSS/PRPNIVELP
343	10/3	1	7010	"	1	KVKEVCKTSKS/GOVIYKGVSIRLRANFLAEP
	1	1	Į	1	1	L*NRREWDEAIKVLKEKQ\FLSKMVYPANLSF
	1	1				GNEGDITSFPAK
524	1874	A	4020	1067	743	FFLRWSL/DSVAQAGVKWCNLGSLQAPPPGF
324	10/4	1 ^	4020	1007	1	TPFSCLSLPSSWDYRHPPPRLAN*LTNFLCF**
	,	1		1		RQGFTVLARMVLIS*PHDLPASASQSAGITGL
	į	1	1			SHCSWPTSSILS
525	1875	A	4021	781	351	OFRVIFFFLRRSHSVAOAGMOWHDHSLLQPL
323	10/3	^	7021	701	1	PPRLKO/F/SHLSPPSIWDYRRVPPCLVNFSIFF
	ı	ŀ		Į		VETGSCOPCLOLLGSSNPPASASQSAGIAGISH
	j	ı			1	OGOPE*SFDIRFACVIAALRETFQCLCSASRVN
		ŀ				NKIINRPTHPVESSF
526	1876	<del> </del> A	4024	80	341	TPSSTSRGTEEOOSSKMAWQRREEKEHLNVR
320	1070	1 "	1021		1	RSSAEDGWKADKP/VDG*TPGEDHLPTPSPFQ
1	1	1	1	•	1	LHIHSSESQLHHSVKSPPSLSFRLM
527	1877	A	4026	593	230	DFYLYPERKKRGQMMTAVSLTTRPQESVAFE
327	10,,	1"	1020			DVAVYFTTKEWAIMG\PAERALYRDVMLEN
	ì					YGGCGPL*CHPTSKPALVFS\LEQGKESCFSPA
		1	1			TGSSLSRNDWRAGWIGYLELRRYTYLS
528	1878	A	4028	1160	242	GTSELLCIQRWNWGPAFPPRPGLALAPTLQLL
1 320	1.0	1		}		VEMGSAKSVPVTPARPPPHNKHLARVADPRS
	1	İ	ı		[	PSAGILRTPIQVESSPQPGLPAGEQLEGLKHAQ
1					Ì	DSDPRSPTLGIARTPMKTSSGDPPSPLVKQLSE
	i					VFETEDSKSNLPPEPVLPPEAPLSSELDLPLGT
1		1	İ			QLSVEEQMPPWNQTEFPSKQVFSKEEARQPT
ļ	1		1	ì	ì	ETPVASQSSDKPSRDPETPRSS\GSMRNRWKP\
ł		ł			ł	NSSKVL\GKSPLHPSCQDDNSPGTLTLRQGKA
ļ		1	1	,		AFKPLSENVSELK\EGA\ILGTGR\LLKTEGRA
İ		1				WEQGQD\HDKENQHFPLVES
529	1879	A	4039	2	366	KDMVLIMEMQSMITMKCPQYL*E*RKIPDITK
		1			l	CW*GCGSTGILIFC/WS*PL*KTI*QPR*FKQI*T
1	Ì	1.		1		ILTIIYSIM*EHTFHNAGV*LSDIYPRFMKGYV
	1	1	-	1		HTEICT*MFIAVLFVVVKTWKQF
530	1880	A	4057	358	3	LLEVNONTIVTVFTKAQNKKNKGSRSILFKQL
						RKYGSRINLLKSKHDKNICTENYKT*MKEIEA
1		ł		1		/DTDKWKDILCSWIRRIHMKDILCSWIGRTHV
		1		1 .		VKISILPKVNYRFYLISIKIIMAI
531	1881	A	4061	50	278	TQGTEEIYKISSCEWVQASFSTPLITLHDFKIY
1		1		1		HKATVIKMVWYWHRQ*KFSKN/RIESSEIEPH
1			1	1	1	IYDQFIFDKGEKIIQEKGNSFFNN/MCWKNWIF
]		1			_	T*KR
532	1882	A	4069	19	368	NDLLENFKFWE*FKE*LENINGTVTEKETGGV
		1		1		YKELSSPKYSGTRQFYGQTISNFPGKIISMVY
1		1		1		KLFQNTE/TEGRHPISLYEFRITLITIPNKDNIYL
1		1	1	· ·		OIWMPVSLMNIVTLKCPT
1			1000	1	355	PIRKFTKVAG*KSNTPK*LAFLHINNEQFENKI
533	1883	ΙA	4076	) <u>1</u>	, 333	
533	1883	Α	4076	1.	1 333	ITNI/PFIIASKRIKYSGISLTKEMKDLYTETLLR KIKEDTNKWKDI/SCFWVGR/LNIVKMPK/VIC

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine O=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	•	İ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	Sequence	/=possible nucleotide deletion, \=possible
1	1.			sequence		nucleotide insertion
	<del></del>	╅╌┈	+	Sequence	<del></del>	IPNAIPIKMPMMCMAKIEKNSS
534	1884	A	4088	3	1931	UDGGTDD GGDD ON UDGGTD ON
] **	100.	1 4	4000	] -	1931	IIDSSTRRMESERSPLYRQLIDLGYLSSSHWNC
			1	l .	1	GAPGQDTKAQSMLVEQSEKLRHLSTFSHQVL
		1				QTRLVDAAKALNLVHCHCLDIFINQAFDMQR
	ł					DLQITPKRLEYTRKKENELYESLMNIANRKQE
		i				EMKDMIVETLNTMKEELLDDATNMEFKDVI
1	1	1	1 '	1	i	VPENGEPVGTREIKCCIRQIQELIISRLNQAVA
ļ	l	1	1	l	l	NKLISSVDYLRESFVGTLERCLQSLEKSQDVS
İ		l				VHITSNYLKQILNAAYHVEVTFHSGSSVTRM
		ĺ			1	LWEQIKQIIQRITWVSPPAITLEWKRKVAQEAI
1		].		l	İ	ESLSASKLAKSICSQFRTRLNSSHEAFAASLRQ
		l		ļ		LEAGHSGRLEKTEDLWLRVRKDHAPRLARLS
		İ	1	ĺ		LESRSLQDVLLHRKPKLGQELGRGQYGVVYL
ł		i	ļ		1	CDNWGGHFPCALKSVVPPDEKHWNDLALEF
İ	1	ļ.				HYMRSLPKHERLVDLHGSVIDYNYGGGSSIA
İ	l	1	ľ		1	VLLIMERLHRDLYTGLKAGLTLETRLQIALDV
[.						VEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKI
ľ						TDLGFCKPEAMMSGSIVGTPIHMAPELFTGK
	,					YDNSVDVYAFGILFWYICSGSVKLPEAFERCA
1			}		i	SKDHLWNNVRRGARPERLPVFDEECWQLME
			'			ACWDGDPLKRPLLGIVQPMLQGIMNRLCKS\
535	1005	ļ. <u></u>	4000			NSEQPNRGLDDST
333	1885	Α	4090	2	417	ALMPHEANYEEIFLKTDKDMDGFESGLEVRE
						IFLKTR/GLPSTLLAHIWALCDSKDCGKLSKD
ł	ŀ	l	1 1		ŀ	HFALAPHLIT\QKLIKGIDPPLVLTPEKISPSNR
				· ·		ASLQKVTELTRKPVCIIFKGTILWRITDSIWMK
536	1886		4100			HNRKRIWLRA
330	10,00	A	4102	569	829	DHQK*KNIPCSWIGRINIVKMSILPKAIYRFSAI
<b>!</b> .						PIKIPMTFFTEI*S*NVYRTTKTQE*AKAILSKK
537	1000		1201			EQNLEESHYLDFK*YYRAV
337	1887	Α	4104	54	281	SIDCEHLIRRMLVLDPSKRLTIAQIKEHKWML
			1 1			IEVPVQRPVLYPQEQENEPSIGEFNEQVLRLM
520	1000		<u> </u>	·		HSLGIDQQKTIE
538	1888	A	4109	141	314	IRHIPLKIRSVVSHLKCFYKFILTFFFAGCSQPL
	1000					VPRENITAWMNAIGLIITALPVS
539	1889	A	4111	268	1	ASRPWGHSYP*FNQQEVDTLKRPIASSEI*MM
					j	I*KFAT\KKSPGPYRFTAEFSHTFKEDLVPILW
						PLFPKIYREGTLPHSFYEASITL
540	1890	A	4142	198	2064	PEPGAGRAATPWGPLFWRGRGSGRCEKAAE
				- 1	j	AALGDFLGLHRRTOOPAVDRLLSDASAOWR
	- 1			İ		VRGHGGVRESGRAPQQPGRRRGRRPRKRPR
.				ļ	j	GRWRREGCGAGGRGVCVAAWSQRSIAGNN
				- 1		DYRLFHKMSNSHPLRPFTAVGEIDHVHILSEH
						IGALLIGEEYGDVTFVVEKKRFPAHRVILAAR
. ]					l	CQYFRALLYGGMRESQPEAEIPLQDTTABAFT
ł	1			Í	- 1	MLLKYIYTGRATLTDEKEEVLLDFLSLAHKY
				ŀ		GFPELEDSTSEYLCTILNIQNVCMTFDVASLY
.		į		l	į	SLPKLTCMCCMFMDRNAQEVLSSEGFLSLSK .
				ŀ		TALLNIVLRDSFAAPEKDIFLALLNWCKHNSK
ļ	}			J	j	ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSP
	1		Į	1	ĺ	DAILDAIKVRSESRDMDLNYRGMLIPEENIAT
ł	ļ		ŀ	į	İ	MKYGAQVVKGELKSALLDGDTQNYDLDHG
ļ		- 1			l	FSRHPIDDDCRSGIEIKLGQPSIINHVRILLWDR
	j		- 1	1	İ	DSRSYSYFIEVSMDELDWVRVIDHSQYLCRS
1	ļ		ł	ł	ļ	WQKLYFPARVCRYIRIVGTHNTVNKIFHIVAF
			1	ŀ		ECMFTNKTFTLEKGLIVPMENVATIADCASVI
1	ļ		ŀ	l l	Į	EGVSRSRNALLNGDTKNYDWDSGYTCHOLG
		İ	- 1		,	SGAIVVQLAQPYMIGSIRVLLWDCDDRSY
541	1891	A	4146	282	778	GTLGYPNGARGQPQDNFFAHQ\VSHHPPISAC
				<del></del>	•••	OYSOLITIOUS AND LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LIVE AND THE LI

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mode- entidd seq- uence  USSN   09/496   14   18   18   18   18   18   18   18	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,							
Seq-   unnec		NO: of	hod	ID NO:			D-Aspartic Acid, E-Glutamic Acid,							
1892 A   1417   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418   1418	nucl-	peptide					P=Phenylalanine, G=Glycine, H=Histidile,							
1914	eotide	seq-					l=Isoleucine, K=Lysine, L=Leucine,							
### ### ### ### ### ### ### ### ### ##	seq-	uence	1				M=Methionine, N=Asparagine, P=Profite,							
residue of poptide   sequence	uence	ļ		914			Q=Giutamine, R=Arginine, S=Scrine,							
Poptide			Í	1			I Timeonine, V=Vaine, W=Typiophan,							
			Ì	ŀ		sequence	Y=1yrosine, X=Unknown,sup codon,							
1892			ł	1		1								
1892					sequence		TYATECHIE A BWODMY WYNIK CWGK SI FIVPVG							
BEHYGEVLINNTQDSSCHENTFCKAKYWSN   PIPOGQCUMKP		i	1	!		1	TUNIVEL DESCRIPE WINK VTSCHINVI SGORW							
VHEWQGAVISRSGRVLIRRIFGKWHEGLYRG			1		ļ		THE						1	VERVOGAVI SPEGRVI HRI FOKWHEGI.YRG
542         1892         A         4147         44         433         SVDAYVCNDIVESYRTITILEGA-RITERSOGGUSSITISTSCR QPEROGUSSILITICOS-ANGSOGGUSSTISCR DIHLIFROGAQUTELATEDSPKAVLGDRILLT ANVSSISCHTTRISKTIFQLELSVKDAVYTVV SH           543         1893         A         4153         678         11         TISYPQCITQMYRISRANDTPILIPIMALDH YVAICSALQ*CSITIPELCQGLPVLA*AGSSILSI-PINGTPILIPIMALDH YVAICSALQ*CSITIPELCQGLPVLA*AGSSILSI-PINGTPIVITYMSULAFCSSAQISIITYRDAYLLMKIA CSH*YMQHYLGAVVLLARCALLVSYRIA AALLRIPSPTRRRKACSICSSHISLVTLFYGTV           544         1894         A         4158         3         538         LLYAQAGQ*Q*LASSIGGPQ*ACALLVSYRIA AALLRIPSPTRRRKACSICSSHISLPUSSGG LIGHLLCLPMVPFILCYFVLISSSI.AGEEAA QUDIASAM*CLPYPYTSIGSMAGGILSGGSUSVUE LKVGREGHVLPWQAHVVEF           545         1895         A         4160         1         412         HFIGIGLIVPSEFISPQDKKAADGSILAPARGE DILEAGIGLYSSEFISPQDKXADGSILAPARGE DILEAGIGLYSSEFISPQDKXADGSILAPARGE DILEAGIGLYSSEFISPQDKXADGSILAPARGE DILEAGIGLYSSEFISPQDKXADGSILAPARGE DILEAGIGLYSPTSPGDKXADGSILAPARGE DILEAGIGLYSPTSPGDKXADGSILAPARGE DILEAGIGLYSPTSPGDKXADGSILAPARGE DILEAGIGLYSPTSPGDKXADGXAGSSAGGSSGGGW ELLISGEPAGWOULAGYTYTQARYLRDASE ANVOQUERPDDRY           346         1896         A         4174         1252         1190         FFQVFELFLEFKTEFHSCCCGAVQWIDLDS: QPPPRPRKGSCSCCGAVQWIDLDS: QPPPRPRKGSCSCCGAVQWIDLDS: QPPPRPRKGSCGGSCGGSGCGGGGGGGGGGGGGGGGGGGGGGGGGG						Į.								
Opprogogurshititodsprayascic   NHLIPROGAQUITLATIDDSPKAYLOBRILLT   ANYSSENTPRISKTTFQLELSVKDAVYTVV   SSH			ļ	1.15		422	SVDAVVCNDIVESVRTTITI.LEGA*LTHRYVA							
INHLIFRGGAQITTLATIPDDSPKAVLGDRLLLT	542	1892	A	4147	44	433	ODDROGOL BSI HI TCDSAPAGSOGTWSTSCR							
ANYSSENTPRISKTITQLELSVKDAVYTVV					<b>!</b>		DIFFUER GAOITELATEDDSPKAVLGDRLLLT							
SSH			1				ANVSSENNTPRTSKTTFOLELSVKDAVYTVV							
1893   A   4153   678   11	Į.			ļ										
YVAICSALQ*CSIITPELCQGLPVI.A*GASSILS   PVIITVIMSILAFCSAQISIITYRDAYLLMKIA   CSHT*NQHYFLGAVVLFLAPCALILV\$YIRIA   AAILRIPSITRRKACSICSSHLSVTLFYGTV   LGICI*PPDSFSAQDAIATIM*TVVTSMLNPFIY   SIMNKEVQBAVRLFSRGSHSSWCD*   SIMNKEVQBAVRLFSRGSHSSWCD*   SIMNKEVQBAVRLFSRGSHSSWCD*   SIMNKEVQBAVRLFSRGSHSSWCD*   SWDYRYSTFH*PANFYEMEFHHYQAQALEL   LGSGDL*PTSTHSAGITGYSHHAPPRLISSEGS   LLGHLLCL*PMVFPLLCVFVLSSSLAGERAAG   LRVQKLW*PAVVLSHLPVCWFHCSGIWSEVIE   LVGGBGL*PTSTHSAGITGYSHHAPPRLISSEGS   LLGHLLCL*PMVFPLLCVFVLSSSLAGERAAG   LRVQKLW*PAVVLSHLPVCWFHCSGIWSEVIE   LWGGBGHVLPWQAHVVEF   HPLGLGL*VPSEIFS*PQDKKAADGSILAPARGE   DLEAGLKGS*FMODRLQAS*VVFRIQR*VGSAM   QDTA\$AMPCL*PYYPTSHCFMAGGKSS*SQGW   ELELSGE*PAGWQVLAGYTYTQAS*SLGFAM*   QDTA\$AMPCL*PYYPTSHCFMAGGKSSQGW   ELELSGE*PAGWQVLAGYTYTQAS*SLGFAM*   QDTA\$AMPCL*PYYPTSHCFMAGGKSSQGW   ELELSGE*PAGWQVLAGYTYTQAS*SLGFAM*   QDTA\$AMPCL*PYYPTSHCFMAGGKSSQGW   ELELSGE*PAGWQVLAGYTYTQAS*SLGFAM*   QDTA\$AMPCL*PYYPTSHCFMAGGKSSQGW   ELELSGE*PAGWQVLAGYTYTQAS*SLGFAM*   QDTA\$AMPCL*PYYPTSHCFMAGGKS*SQGWAGGTGY*NFGAFSWLAP   GSHHASEQLAPGVQPAGGVAQHLTAPPQBG   WGGAPAAPSCSCLSPLGFAM*   QDTA*APPCSDE*CKQGHLW*HCPWPQ   PSHLPLT*TAQLLQGPQVLAPPG*PYPGFAM*   QGSPMLPAPPSSPRS*PAGSTATAAASSTFESQCP*SAPSASSAPAS   TMA*PISALAVWE*PAGSS*PQLSAPADSSVLP*   ALVGPHHYP*SQCP*GSSY*PLGGGPCP*PL*APPLD*   AASSLFWMFCQPPPHPGFLSAP*   AASSLFWMFCQPPPHPGFLSAP*   AASSLFWMFCQPPPHPGFLSAP*   AASSLFWMFCQPPPHPGFLSAP*   AASSLFWMFCQPPPHPFQFLXAPPLD*   PFPASGTSDSSDSSRS*SASAARVWPPASPPP   AARRIPHPPF*SQCP*SQSYPLIGR*PRPQ   ALGPFARWCD*PPSSPAQ*PCLW*GHPP*   PFPASGTSDSSDSSRS*SASAARVWPPASPPP   AARRIPHPPF*SQCP*SQSYPLIGR*PRPQ   ALGPFARWCD*PPSSPAQ*PCLW*CG*PPP*   PFPASGTSDSSDSSRS*PASSAARVWPPASPPP   AARRIPHPPF*SQCP*SQC*PCL*PAFR*PPC*   AARRIPHPPP*SQCP*SQS*PCLT*PARQ*PCL*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGT*   PFPASGTSDSSQC*PCL*   PFPASGTSDSSQC*PCL*PARPSC*   PFPASGT*   P		1000	<del> </del>	41.52	679	<del>  11                                  </del>	TISYPOCI TOMYFLISFANYDTFLLPIMALDH							
PVIITVIMSRLAFCSSQISHITYRDAYLLMKIA	543	1893	A	4155	0/0	111	VVAICSALO*CSITP/ELCOGLPVLA*AGSSLIS							
CSHT*NQHVELGAVVLELAPCALLUSYIRIA				1			PVITVIMSRI AFCSSAOISHFYRDAYLLMKIA							
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LQPLHLRAAQPLDPCCSLSPPGPPLPVPALPS WPGRP*SPSPASSQPPYHAGLPGPQSSPLPPGL PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ PLSPHPPPF/ARTQTFPVASRSLSPGTAPYSVCL TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT		ļ	1		1		RPVGHS*SGPPHSPPL*APPOAWPLELPPSRQC							
WPGRP*SPSPASSQPPYHAGLPGPQSSPLPPGL PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT		1					LOPLHLRAAOPLDPCCSLSPPGPPLPVPALPS							
PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL TPSRSASSLPEVVLASSLPKIPQSSGSVPLGPTSP MP*CFHRPSPPLP/LSSPFPAVLRPQAPQFPLHLP P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT	1		1				WPGRP*SPSPASSOPPYHAGLPGPQSSPLPPGL							
PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT	1		1		1	1	PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ							
TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT					1		PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL							
MP*CFHRPSPPLP/LSSPFPA/LRPQAPQFPLHLP P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT			- 1		1	1	TPSRSASSLPEVVLASSLPKIPOSSGS\PLGPTSP							
P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT			- 1	-	ŀ		MP*CFHRPSPPLP/LSSPFPA\LRPOAPQFPLHLP							
PPLWPSLALLP*PLPPPPPVPSFSASLLCSLPAH			- 1	.	1	1	P*PPAPSPGCPLPPLAOOHOPSPPSPHARSTLT							
			- !	İ	1	1	PPLWPSLALLP*PLPPPPPVPSFSASLLCSLPAH							

SEQ ID	SEOID	Met	SEQ	Predicted	Predicted end	1 1 - 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1 - 2 1
NO: of	NO: of	hod	ID NO:	beginning	nuclcotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1,100	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid,
cotide	seq-		USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ł	1	ł		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	peptide		/=possible nucleotide deletion. \=possible
1			i	sequence	1	nucleotide insertion
		1			<del>                                     </del>	GTPASPGLGRSCLGKPQTLPWISFWPPSGRLA
	1	1				PGTWQPW/PVSPAPLSCLSAWDPWELPSPQPQ
	1	1				VCSTAELPTSCLLSSPGPPAFQPPRFGCL*GPP
	1.	-			i	GPPGLPPLQSSLSFPPPPPPVPQPPAPPALQWG
						LHLPGGRTK
548	1898	A	4180	2369	844	RIHREEDFQFILKGIARLLSNPLLQTYLPNSTK
1		1				KIQFHQELLVLFWKLCDFNKVGQPRGALQGD
}						GEQLPQ*PGGRDSVRLRGVGQSCPSLELSPLG
i		į				PSPHP*KFLFFVLKSSDVLDILVPILFFLNDAR
}	1	l			1	ADQSRVGLMHIGVFILLLLSGECNFGVRLNKP
		1			}	YSIRVPMDIPVFTGTHADLLIV\VFHKIITSGHO
1			1			RLQPLFDCLLTIVVNVSPYLKSLSMVTANKLL
1	1					HLLEAFSTTWFLFSAAQNHHLVFFLLEVFNNI
Ì	1	1			ľ	IQYQFDGNSNLVYAIIRKRSIFHQLANLPTDPP
· ·	1	1	1 1			TIHKALQRRRRTPEPLSRTGSQGGAPPWRAPA
	1					PLPLQSQAPSRPVWWLLQALTS*PRSPRCOR
						MAPCGPWNLSPSRAWRMAARLRGSPARHGG
	İ		1 1		1	SSGDRP/HSSASGQWSPTPEWVLSWKSKLPLQ
l	1	1	1 1		}	TIMRLLQVLVPQVEKICIDKGLTDESEILRFLQ
	İ					HGTLVGLLPVPHPILIRKYQANSGTAMWFRT
1	1					YMWGVIYLRNVDPPVWYDTDVKLFEIQRV
549	1899	A	4191	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKT
]		İ				ALLQDGRRKVHYLFPDGKEMAEEYDEKTSE
İ	İ	l				LLVRKWRVKSALGAMGQWQLEVGDPAPLG
	1	1				AGNLGPELIKESNANPIFMRKDTKMSFQWRIR
		1				NLPYPKDVYSVSVDQKERCIIVRTTNKKYYK
						KFSIPDLDRHQLPLDDALLSFA\TPTAP
550	1900	Α	4192	1	1980	IRHTGSDIAGVCGWLLLSGPCGVGLDLDSRLL
			1 [			GASAMRRSEVLAEESIVCLQKALNHLREIWE
•						LIGIPEDQRLQRTEVVKKHIKELLDMMIAEEE
						SLKERLIKSISVCQKELNTLCSELHVEPFQEEG
ļ.						ETTILQLEKDLRTQVELMRKQKKERKQE\LKL
						LQEQDQELC\EILCMPHYDIDSASVPSLEELNQ
			1			FRQHVTTLRETKASRREEF/VSSIKRQIILCME
	:					ELDHTPDTSFERDVVCEDEDAFCLSLENIAT\L
			1			QKLLRQ\LEMQKSQNEAVCEG\LRTQI\RELW
	[		1 1			DRLQIPEEEREAVATIMSGSKAKVRK\ALO\LE
			ļ	l		VDRLEELEKCKTMKKVIEAIRVELVQYWDQC
						FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR
						LKNYYEVHKELFEGVQKWEETWRLFLEFER
						KASDPNRFTNRGGNLLKEEKQRAKLQKMLP
						KLEEELKARIELWEQEHSKAFMVNGQKFME
					1	YVAEQWEMHRLEKERAKQERQLKNKKQTET
					1	EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT
					į.	TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK
				j	ľ	PVAASTCSGKKTPRTGRHGANKENLELNGSI
				İ	Ì	LSGGYPGSAPLQRNFSINSVASTYSEFADPSLS
					ŀ	DSSTVGLQRELSKASKSDATSGILNSTNIQS
551	1901	A	4194	3	1008	AWHEGLVSSPAIGAYLSASYGDSLVVLVATV
ı				1		VALLDICFILVAVPESLPEKMRPVSWGAQISW
-				1	İ	KQADPFASLKKVGKDSTVLL\ICITVCLSYLPE
ļ				İ	·	AG/QYSSFF/LYLR/QVIGFG/TVKIAAFIAMVGI
				I		LSIVAQTAFLSILMRSLGNKNTVLLGLGFQML
	1			ļ	ļ	QLAWYGFGSQAWMMWAAGTVAAMSSITFP
	l				-	AISALVSRNAESDQQGVAQGIITGIRGLCNGL
	1				1	GPALYGFIFYMFHVELTELGPKLNSNNVPLQ
	ł					GAVIPGPPFLFGACIVLMSFLVALFIPEYSKAS
	.					GVQKHSNSSSGSLTNTPERGSDEDIEPLLQDS
- 1	- 1	1		l	ŀ	SIWELSSFEEPGNQCTEL
	1		<u> </u>			PLIL PROPERELONACTED

SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
•	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of nucl-	peptide	1100	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
		ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ł		ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		ļ	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
		i		amino acid residue of	, , ,	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			******	sequence	/=possible nucleotide deletion, \=possible
		·		peptide		
	ļ			sequence		nucleotide insertion
552	1902	Α	4197	2	14302	ARPPPAPGSRQKQKAAPGAAAAAELRGAR
			1			EPAPARRRGTMADGGEGEDEIQFLRTDDEVV
	j	l				LQCTATIHKEQQKLCLAAEGFGNRLCFLESTS
	1					NSKNVPPDLSICTFVLEQSLSVRALQEMLANT
		1				VEKSEGQVDVEKWKFMMKTAQGGGHRTLL
*		ļ				YGHAILLRHSYSGMYLCCLSTSRSSTDKLAFD
	1	1				VGLQEDTTGEACWWTIHPASKQRSEGEKVR
	ļ	1	ì		j	VGDDLILVSVSSERYLHLSYGNGSLHVDAAF
	1	1		!		QQTLWSVAPISSGSEAAQGYLIGGDVLRLLH
	ľ			l		GHMDECLTVPSGEHGEEQRRTVHYEGGAVS
		1		ĺ	<u> </u>	VHARSLWRLETLRVAWSGSHIRWGQPFRLR
	Ţ	ĺ	1			HVTTGKYLSLMEDKNLLLMDKEKADVKSTA
	1		1		1	FTFRSSKEKLDVGVRKEVDGMGTSEIKYGDS
		1	ł	1	I	VCYIQHVDTGLWLTYQSVDVKSVRMGSIQR
		1	ĺ	1	f "	KAIMHHEGHMDDGISLSRSQHEESRTARVIRS
	1	1		Į	Į.	TVFLFNRFIRGLDALSKKAKASTVDLPIESVSL
1				-	1	SLQDLIGYFHPPDEHLEHEDKQNRLRALKNR
ì		1		i		ONLFQEEGMINLVLECIDRLHVYSSAAHFAD
				[	Ì	VAGREAGESWKSILNSLYELLAALIRGNRKN
ĺ	1	ĺ	1	[		CAOFSGSLDWLISRLERLEASSGILEVLHCVL
Ì		1		İ		VESPEALNIIKEGHIKSIISLLDKHGRNHKVLD
				l		VLCSLCVCHGVAVRSNQHLICDNLLPGRDLL
	1		i	ł	1	LOTRLVNHVSSMRPNIFLGVSEGSAQYKKWY
ł		1				YELMVDHTEPFVTAEATHLRVGWASTEGYSP
		1				YPGGGEEWGGNGVGDDLFSYGFDGLHLWSG
1	1	1	1	ł	1	CIARTVSSPNQHLLRTDDVISCCLDLSAPSISF
ļ		İ		l .		RINGQPVQGMFENFNIDGLFFPVVSFSAGIKV
Ì						RFLLGGRHGEFKFLPPPGYAPCYEAVLPKEKL
j		}	ļ	1		KVEHSREYKQERTYTRDLLGPTVSLTQAAFT
						PIPVDTSQIVLPPHLERIREKLAENIHELWVMN
	l	l	l	į.	ł	KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ
1	1					ERNYNLOMSLETLKTLLALGCHVGISDEHAE
	1					DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT
ļ	}	1		}		PSQEAMVDKLAENAHNVWARDRIRQGWTY
	1	}				GIOODVKNRRNPRLVPYTPLDDRTKKSNKDS
		İ	ļ	1		LREAVRTLLGYGYNLEAPDQDHAARAEVCS
J	]	}		1		GTGERFRIFRAEKTYAVKAGRWYFEFETVTA
				l		
1		1		1		GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM
1	1			1	1	NEHTMMFTLNGEILLDDSGSELAFKDFDVGD
		1	1	I		
		]	[	1		GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC
	1			1		GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV
	1	1	Į	1		PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN
			1		ŀ	SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG
	1					LFGPKNDLEDYDADSDFEVLMKTAHGHLVP
1	1	1	1	1	1	DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ
	l	ĺ	1		1	RFLLRRTKPDYSTSHSARLTEDVLADDRDDY
1	1		1	1	1	DFLMQTSTYYYSVRIFPGQEPANVWVGWITS
	1	1	1		1	DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE
1	1	1	1	!		SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC
1	1	1	1	l	1	VVDAASGLLTFIANGKELSTYYQVEPSTKLFP
1		1	1	1	1	AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS
ł	1	1	1		1	EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL
1	1	1	1		1	KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN
	1	1	1	Î	1	RSVDILELTEQEELLKFHYHTLRLYSAVCALG
	1	1	ł	{	1	NHRVAHALCSHVDEPQLLYAIENKYMPGLLR
					1	AGYYDLLIDIHLSSYATARLMMNNEYIVPMT
			1		1	EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF
		1	1	1	1	SSPSFVSISNECYOYSPEFPLDILKSKTIOMLTE
	1	1	1	1	1	AVKEGSLHARDPVGGTTEFLFVPI.IKLFYTLLI
L	<u> </u>			J		

SEQ ID NO: of nucl- cotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	иепсе		09/496 914	ng to first amino acid residue of	to last amino acid residue of peptide sequence	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide sequence		/=possible nucleotide deletion, \=possible nucleotide insertion
						MGIFHNEDLKHILQLIEPSVFKEAATPEEESDT LEKELSVDDAKLOGAGEEAKGGKRPKEGLL
						QMKLPEPVKLQMCLLLQYLCDCQVRHRIEAI VAFSDDFVAKLQDNQRFRYNEVMQALNMSA
						ALTARKTKEFRSPPQEQINMLLNFKDDKSECP CPEEIRDQLLDFHEDLMTHCGIELDEDGSLDG
						NSDLTIRGRLLSLVEKVTYLKKKQABKPVES DSKKSSTLQQLISETMVRWAQESVIEDPELVR
						AMFVLLHRQYDGIGGLVRALPKTYTINGVSV EDTINLLASLGQIRSLLSVRMGKEEEKLMIRG
						LGDIMNNKVFYQHPNLMRALGMHETVMEV
						MVNVLGGGESKEITFPKMVANCCRFLCYFCR ISRQNQKAMFDHLSYLLENSSVGLASPAMRG
						STPLDVAAASVMDNNELALALREPDLEKVVR YLAGCGLQSCQMLVSKGYPDIGWNPVEGER
						YLDFLRFAVFCNGESVEENANVVVRLLIRRPE CFGPALRGEGGNGLLAAMEEAIKIAEDPSRD
						GPSPNSGSSKTLDTEEEEDDTIHMGNAIMTFY SALIDLLGRCAPEMHLIHAGKGEAIRIRSILRS
				-		LIPLGDLVGVISIAFQMPTIAKDGNVVEPDMS AGFCPDHKAAMVLFLDRVYGIEVQDFLLHLL
			-			EVGFLPDLRAAASLDTAALSATDMALALNRY LCTAVLPLLTRCAPLFAGTEHHASLIDSLLHT
						VYRLSKGCSLTKAQRDSIEVCLLSICGQLRPS MMQHLLRRLVFDVPLLNEHAKMPLKLLTNH
						YERCWKYYCLPGGWGNFGAASEEELHLSRK LFWGIFDALSQKKYEQELFKLALPCLSAVAG
					i	ALPPDYMESNYVSMMEKQSSMDSEGNFNPQ PVDTSNITIPEKLEYFINKYAEHSHDKWSMDK
						LANGWIYGEIYSDSSKVQPLMKPYKLLSEKE KEIYRWPIKESLKTMLARTMRTERTREGDSM
						ALYNRTRRISQTSQVSVDAAHGYSPRAIDMS NVTLSRDLHAMAEMMAENYHNIWAKKKKM
				•		ELESKGGGNHPLLVPYDTLTAKEKAKDREKA QDILKFLQINGYAVSRGFKDLELDTPSIEKRFA
						YSFLQQLIRYVDEAHQYILEFDGGSRGKGEHF PYEQBIKFFAKVVLPLIDQYFKNHRLYFLSAA
						SRPLCSGGHASNKEKEMVTSLFCKLGVLVRH RISLFGNDATSIVNCLHILGQTLDARTVMKTG
						LESVKSALRAFLDNAAEDLEKTMENLKQGQF THTRNQPKGVTQIINYTTVALLPMLSSLFEHI
						GQHQFGEDLILEDVQVSCYRILTSLYALGTSK SIYVERQRSALGECLAAFAGAFPVAFLETHLD
						KHNIYSIYNTKSSRERAALSLPTNVEDVCPNIP
						SLEKLMEEIVELAESGIRYTQMPHVMEVILPM LCSYMSRWWEHGPENNPERAEMCCTALNSE
						HMNTLLGNILKIIYNNLGIDEGAWMKRLAVF SQPIINKVKPQLLKTHFLPLMEKLKKKAATVV
					·	SEEDHLKAEARGDMSEAELLILDEFTTLARDL YAFYPLLIRFVDYNRAKWLKEPNPEAEELFR
						MVAEVFIYWSKSHNFKREEQNFVVQNEINN MSFLITDTKSKMSKAAVSDQERKKMKRKGD
						RYSMQTSLIVAALKRLLPIGLNICAPGDQELIA LAKNRFSLKDTEDEVRDIIRSNIHLQGKLEDP
						AIRWQMALYKDLPNRTDDTSDPEKTVERVL DIANVLFHLEQKSKRVGRRHYCLVEHPQRSK
						KAVWHKLLSKQRKRAVVACFRMAPLYNLPR HRAVNLFLQGYEKSWIETEEHYFEDKLIEDLA
						KPGAEPPEEDEGTKRVDPLHQLILLFSRTALT EKCKLEEDFLYMAYADIMAKSCHDEEDDDG

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
					·	EEEVKSFEEKEMEKQKLLYQQARLHDRGAA EMVLQTISASKGETGPMVAATLKLGIAILNGG NSTVQQKMLDYLKEKKDVGFFQSLAGLMQS CSVLDLNAFERQNKAEGLGMVTEBGSGEKV LQDDEFTCDLFRFLQLLCEGHNSDFQNYLRT QTGNNTTVNIIISTVDYLLRVQESISDFYWYY SGKDVIDEQGQRNFSKAIQVAKQVFNTLTEYI QGPCTGNQQSLAHSRLWDAVVGFLHVFAHM QMKLSQDSSQIELLKELMDLQKDMVVMLLS MLEGNVVNGTIGKQMVDMLVESSNNVEMIL KFFDMFLKLKDLTSSDTFKEYDPDGKGVISK RDFHKAMESHKHYTQSETEFLLSCAETDENE TLDYEEFVKRFHEPAKDIGFNVAVLLTNLSEH MPNDTRLQTFLELAESVLNYFQPFLGRIEIMG SAKRIERVYFEISESSRTQWEKPQVKESKRQFI FDVVNEGGEKEKMELFVNFCEDTIFEMQLAA
				·		QISESDLNERSANKEESEKERPEEQGPRMAFF SILTVRSALFALRYNILTLMRMLSLKSLKKQM KKVKKMTVKDMVTAFFSSYWSIFMTLLHFV ASVFRGFFRICSLLLGGSLVEGAKKIKVAELL ANMPDPTQDEVRGDGEEGERKPLEAALPSED LTDLKELTEESDLLSDIFGLDLKREGGQYKLIP HNPNAGLSDLMSNPVPMPEVQEKFQEQKAK EEEKEEKEETKSEPEKAEGEDGEKEEKAKED KGKQKLRQLHTHRYGEPEVPESAFWKKIIAY QQKLLNYFARNFYNMRMLALFVAFANFILL FYKVSTSSVVEGKELPTRSSSENAKVTSLDSS SHRIIAVHYVLEESSGYMEPTVRILPILHTVISF FCIIGYYCLKVPLVIFKREKEVARKLEFDGLYI TEQPSEDDIKGQWDRLVINTQSFPNNYWDKF VKRKVMDKYGEFYGRDRISELLGMDKAALD FSDAREKKKPKDSSLSAVLNSIDVKYQMW KLGVVFTDNSFLYLAWYMT
553	1903	A	4199	31	767	LPELNGRGAGLRRAEPSERGGGAERTQQVAA LPLSHGHSHGGGGCRCAAER/VGAARGSAAC AYGLYLRIDKGRLQCLNESREGSGRGVFKPW ERAD\DRSKPVESDADEELLFNIPFTG\HVKLK GIIIMGEDDDSHPSEMRLYKNIPQMSFDDTER EPDQTFSLNRDLTGELEYATKISRFSNVYHLSI HISKNFGADTTKVFYIGLRGEWTELRRHEVTI CNYEASANPADHRVHQVTPQTHFIS
554	1904	A	4200	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSL EICIKACKNLAYGEEKKKKCNPYVKTYLLPD RSSQGKRKTGVQRNTVDPTFQETLKYQVAPA QLVTRQLQVSVWHLGTLARRVFLGEVIIPLAT WDFEDSTTQSFRWHPLRAKADKYEDSVPQS NGELTVRAKLVLPSRTRKLQEAQEGTDQPSL HGQLCLVVLGAKNLPVRPDGTLNSFVKGCLT LPDQQKLRLKSPVLRKQACPQWKHSFVFSGV TPAQLRQSSLELTVWDQALFGMNDRLLGGT\ RLGSKGDTAVGGDACSQSKLQWQKVLSSPN LWTDMTLVLH
555	1905	A	4211	331	2419	KENKKARNLRMNQSRSRSDGGSEETLPQDH NHHENERRWQQERLHREEAYYQFINELNDE DYRLMRDHNLLGTPGEITSEELQQRLDGVKE QLASQPDLRDGTNYRDSEVPRESSHEDSLLE WLNTFRRTGNATRSGQNGNQTWRAVSRTNP NNGEFRFSLEIHVNHENRGFEIHGEDYTDIPLS DSNRDHTANRQQRST\SPVARRTRSQTSVNFN GSSSNIPRTRI.ASRGQNPAEGSFSTLGRLRNGI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Dundistad and	1 4 - i mid
NO: of	NO: of	hod	ID NO:	beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	nou.	in in	nucleotide	location	
eotide	seq-		USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence		09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine,
uence	ualcc	l	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline,
delle	ľ		714	amino acid		Q=Glutamine, R=Arginine, S=Serine,
	[			residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		l				/=possible nucleotide deletion, \=possible
		<del> </del>	. <del> </del>	sequence	<u> </u>	nucleotide insertion
1	ŀ	}	) .	}	1	GGAAGIPRANASRTNFSSHTNQSGGSELRQRE
						GQRFGAAHVWENGARSNVTVRNTNQRLEPI
	ļ	1				RLRSTSNSRSRSPIQRQSGTVYHNSQRESRPV
	1	1				QQTTRRSVRRRGRTRVFLEQDRERERRGTAY
	1	1			1	TPFSNSRLVSRITVEEGEESSRSSTAVRRHPTIT
		i			1	LDLQVR\RIRPGENRDRDSIANRTRSRVGLAE
		1				NTVTIESNSGGFRRTISRLERSGIRTYVSTITVP
		į.			!	LRRISENELVEPSSVALRSILRQIMTGFGELSSL
		ł				MEADSESELQRNGQHLPDMHSELSNLGTDN
					1	NRSQHREGSSQDRQAQGDSTEMHGENETTQP
1	l				İ	HTRNSDSRGGRQLRNPNNLVETGTLPILRLAH
	1	1			[	FFLLNESDDDDRIRGLTKEQIDNLSTRHYEHN
i		1				SIDSELGKICSVCISDYVTGNKLROLPCMHEF
						HIHCIDRWLSENCTCPICRQPVLGSNIANNG
556	1906	A	4212	3	462	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKR
		1	i i		1	KSPENTEGKDGSKVTKQEPTRRSARLSAKPA
		İ			ļ	PPKPEPKPRKTSAKKEPGAKISRGAKGKKEEK
		l	}			QEAGKEGTAPSENGETKAEEIHISRSTVNVST
1			1			SRGTPPSTLSVKGQIETVRVKGTEN
557	1907	A	4213	774	507	ARRESCLTLQTSWGHRH\GPPRP\ANFVFLVET
1	1 ., .,	' '	1.2.3	,,,	307	GFLHIGQAGHKLPTSGDPPASASOSARITGMS
			1			HRTWFLASFLIDSCKNFIVYKIMYTL
558	1908	A	4225	3	1253	TICL WILLAST LIDSCRINT VILLAND VILLAST TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF TH
330	.,,00	<u> </u>	4223	,	1233	TYRHAEREHPETSSATKVSYDYRHKRPKLLD
						GDQDFSDGRTQKYCKEEDRKYSFQKGPLNRE
(			1 1			LDCFNTGRGRETQDGQVKEPFKPSKKDSIAC
						TYSNKNDVDLRSSNDKWKEKKKKEGDCRKE
						SNSSSNQLDKSQKLPDVKPSPINLRKKSLTVK
1						VDVKKTVDTFRVASSYSTERQMSHDLVAVG
1 1			1 1			RKSENFHPVFEHLDSTQNTENKPTGEFAQEIIT
	i					IIHQVKANYFPSPGITLHERFS\KMADIHKADV
l ï			1			NEIPLNSDPEIHRRIDMSLAELQSKQAVIYESE
						QTLIKIIDPNDLRHDIERRRKERLQNEDEHIFHI
			1 1			ASAAERDDQNSSFSKNYTTQRKDIITHKPFEV
1 1						EGNHRNTRVRPFKSNFRGGRCQPNYKSGLVQ
	•		1 1			KSLYIQAKYQRLRFTGPRGFITHKFRERLMRK
L	- 1000					KKVP
559	1909	A	4235	1	323	KFSIPFFLRWSFTLV\PRLEGNDMISVHCNLGL
			1 1			LGLSHSPASASQVGGITGTQHHTGLIFGFLIET
			.			EFHHVGQAGLELLTSGDPPALAFQSAGITGVS
						HHAWLQVLNS
560	1910	A	4246	2	1569	TLSLLERVLMKDIVTPVPQEEVKTVIRKCLEQ
						AALVNYSRLSEYAKIEGKKREMYELPVFCLA
				ł		SQVMDLTIQNQKDAENVGRLITPAKKLEDTIR
	1		1			LAELVIEVLQQNEEHHAEAFAWWSDLMVEH
						AETFLSLFAVDMDAALEVQPPDTWDSFPLFQ
	ľ	•				LL\NDFLRTGLLICGNGK\FHKHLQDLFAPLVV
			l			R/YMWDLDGSSPIAQSIHRGLLSRESWEPVNN
			ľ			GSGTSEDLFWKLDALQTFIRDLHWPEEEFGK
						HLEQRLKLMASDMIESCVKRTRIAFEVKLQK
	ţ			'		TSSIQQIFRVPQFNMAPCFNVMGLMAKGSIQP
	İ			1		KL\CSMEMGQEFAKMWHQYHSKIDELIEETV
	1	•		ł	l	KEMILI I AVEALI BOA VA DESTREON SO
ľ	i			1	l	KEMITLLVAKFVTILEGVLAKLSRYDEGTLFS
	1	ı		ľ	!	SFLSFTVKAASKYVDVPKPGMDVADAYVTF
				1	ĺ	VRHSQDVLRDKVNEEMYIERLFDQWYNSSM
- 1	ļ			ì	İ	NVICTWLTDRMDLQLHIYQLKTLIRMVKKTY
ļ	i	ļ		ı		RDFRLQGVLDSTLNSKTYETIRNRLTVEEATA
561	1011		1055			SVSEGGGLQGISMKDSDEEDEEDD
561	1911	A	4257	1300	654	SELVQFLLIKDQKKIPIKRADILKHVIGDYKDI
		1				FPDLFKRAAERLQYVFGYKLVELEPKSNTYIL

SEQ ID NO: of nucl- cotide seq-	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496	Predicted beginning nucleotide location correspondi	Predicted end nucleotide location corresponding to last amino	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid residue of peptide sequence	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y='Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion INTLEPVEEDAEMRGDQGTPTTGLLMIVLGLI
						FMKGNTIKETEAWDFLLAL\GVYPTKKHLIFG DPKKLITEDFVRQRYLEYRRIPHTDPVDYEFQ WGPRTNLETSKMKVLKFVAKVHNQDPKDW PAQYCEALADEENRARPQPSGPAPSS
562	1912	A	4260	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQF WLHARLQKCFLSRGCGSYCAGAKASPLPGK MAMGLMCGRRELLRLLQSGRRVHSVAGPSQ WLGKPLTTRLLFPAAPCCCRPHYLFLAASGPR SLSTSAISFAEVQVQAPPVVAATPSPTAVPEV ASGETĄDVVQTAAEQSFAELGLGSYTPVGLI QNLLEFMHVDLGLPWWGAIAACTVFARCLIF PLIVTGQREAARIHNHLPEIQKFSSRIREAKLA GDHIEYYKASSEMALYQKKHGIKLYKPLILPV TQAPIFISFFIALREMANLPVPSLQTGGLWWF QDLTVSDPIYILPLAVTATMWAVLELGAETG VQSSDLQWMRNVIRMMPLITLPITMHFPTAV FMYWLSSNLFSLVQVSCLRIPAVRTVLKIPQR VVHDLDKLPPREGFLESFKKGWKNAEMTRQ
563	1913	A	4265	623	116	LREREQRMRNQLELAARGPLRQTFTHNPLLQ PGKDNPPNIPSSISSSSSKPKSKYPWHDTLG MGGLAPTQTLEPTNEYQNTQLSVSYLLPEQN THGTRRTLSSQPSNNLPLPLSSSATMPSMQCK HRSPNGGLFRQSPVK/TPPIPMSFQPVPGGV/L PRGSGNPPHGTSILTAPPALLPHPPTHPTQQSF LIQENNNTNHTHSHTHTYTETLSFFLYICVNN
564	1914	A	4270	3	368	DRMEWGKSVF  ILKRKLSSLNSEVSTIQNTRMLAFKATAQLFIL GCTWCLGLLQVGPAAQVMAYLFTIINSLQGF FIFLVYCLLSVQQVQKQYQKWFREIVKSKSES ETYTLSSKMGPDSKPSEGDVFPRTSE
565	1915	A	4288	83	406	RNSRPLWCSPPASQPRQAPVSQSCCCPLPSSSS PPSALLAPTKPRALGTLRLYECSPELCTTMLP PAWLLMLCQAPRPQDPDPRLTQPEKSLQEAP GQTGASRTPRT
566	1916	A	4298	1041	229	LNSSQKLACLIGVEGGHSLDSSLSVLRSFYVL GVRYLTLTFTCSTPWAESSTKFRHHMYTNVS GLTSFGEKVVEELNRLGMMIDLSYASDTLIRR VLEVSQAPVIFSHSAARAVCDNLLNVPDDILQ LLKKNGGIVMVTLSMGVLQCNLLANVSTVA DHFDHIRAVIGSEFIGIGGNYDGTGRFPQGL\B DVSTYPVLIEELLSRSWSEEELQGVLRGNLLR VFRQVEKVREESRAQSPVEAEFPYGQLSTSCH FHLGASEWTPRLLIWR
567	1917	A	4299	1	1106	GATPLGSVGGRTGKMDAATLTYDTLRFAEFE DFPETSEPVWILGRKYSIFTEKDEILSDVASRL WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ MIFAQALVCRHLGRDWRWTQRKRQPDSYFS VLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQ WYGPNTVAQVLKKLAVFDTWSSLAVHIAMD NTVVMEEIRRLCRTSVPCAGATAFPADSDRH CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAYVETLKHCFMMPQSLGVIGGKPNSAHY FIGYVGBELIYLDPHTTQPAVEPTDGCFIPDES FHCQHPPCRMSIAELDPSIAVVRGGIILSTQAF GAECCLGMTRKTFGFLRFFSMLG
568	1918	A	4300	2012	1843	SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY
569	1919	A	4302	186	531	WTFCLFL/WWVPESARWLLTQGHVKEAHRY

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, i=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion  LLHCARLNGRPVCEDSPSQEVRVNVCVSMIII  CVWWGVGCVKCLPPRAHHIWQEKPLGPHRT  VTESKLEAEGKTKEKAREKERKKKS
570	1920	A	4308	3		RSGQGKVYGLIGRRRFQQMDVLEGLNLLITIS GKRNKLRVYYLSWLRNKILHNDPEVEKKQG WTTVGDMEGCGHYRVVKYERIKFLVIALKSS VEVYAWAPKPYHKFMAFKSFADLPHRPLLV DLTVEEGQRLKVIYGSSAGFHAVDVDSGNSY DIYIPVHIQSQITPHAIIFLPNTDGMEMLLCYE DEGVYVNTYGRIIKDVVLQWGEMPTSVAYIC SNQIMGWGEKAIEIRSVETGHLDGVFMHKRA QRLKFLCERNDKVFFASVRSGGSSQVYFMTL NRNCIMNW
571	1921	A	4309	9	524	ASREMDVTKVCGEMRYQLNKTNMEKDEAE KEHREFRAKTNRDLEIKDQEIEKLRIELDESK QHLEQEQQKAALAREECLRLTELLGESEHQL HLTRQEKDSIQQSFSKEAKAQALQAQQREQE LTQKIQQMEAQHDKTENEQYLLLTSQNTFLT KLKEECCTLAKKLEQISQ
572	1922	A	4318	1	1119	GATPLGSVGGRTGKMDAATLTYDTLRFAEFE DFPETSEPVWILGRKYSIFTEKDEILSDVASRL WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ MIFAQALVCRHLGRDWRWTQRKRQPDSYFS VLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQ WYGPNTVAQVLKKLAVFDTWSSLAVHIAMD NTVVMEEIRRLCRTSVPCAGATAFPADSDRH CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLAT DINEAYVETLKHCFHGWPQFPG/VVHREGK PNSAHYFIGYVGEELTYLDPHTTQPAVEPIDG CFIPDESFHCQHPPCRMSIAELDPSIAVVRGGH LSTQAFGAECCLGMTRKTFGFLRFFFSMLG
573	1923	A -	4333	363	1066	GGVPVGLASKPFQILYGHTNEVLSVGISTELD MAVSGSRDGTVIIHTIQKGQYMRTLRPPCESS LFLTIPNLAISWEGHIVVYSSTEEKTTLKÆRM HYICFSINGKYLGSQILKEQVSDICLIGEHIVTG SIQGFLSIRDLHSLNLSINPLAMRLPIHCVCVT KEYSHILVGLEDGKLIVVGVGKPAEVKPSISN FISHAVGDYFGSPSFQLIEKSPLGINKLKAKFD FSKGSK
574	1924	A	4346	359	1234	MDTLEEVTWANGSTALPPPLAPNISVPHRCLL LLYEDIGTSRVRYWDLLLLIPNVLFLIFLLWK LPSARAKIRITSSPIFITFYILVFVVALVGIARA VVSMTVSTSNAATVADKILWEITRFFLLAIEL SVIILGLAFGHLESKSSIKRVLATTTVLSLAYSV TQGTLEILYPDAHLSAEDFNIYGHGGRQFWL VSSCFFFLVYSLVVILPKTPLKERISLPSRRSFY VYAGILALLNLLQGLGSVLLCFDIEGLCCVD ATTFLYFSFFAPLIYVAFLRGFFGSEPKILF
575	1925	A	4360	2038	1512	GCWWRHPWLASQRDCLDCRIQLAEKFVKAV SKPSRPDMNPIRVKEVYRLEEMEKIFVRLEM KIIKGSSGTPKLSYTGRDDRHFVPMGLYIVRT VNEPWTMGFSKSFKKKFFYNKKTKDSTFDLP ADSIAPFHICYYGRLFWEWGDGIRVHDSQKP QDQDKLSKEDVLSFIQMHRA
576	1926	A	4365	69	500	QVEGRQGREVKRTAWRISPVWRPARCRRRST PQP/PE/PGAQQQERHRQGEAPMQALDPRAEP GPQAQSHAACQEPEPPRVLLDPTAARGGVQ GRP/GLSRHPGLAPHPQTHTPWPQSGRLPCAS EPLPLGGIRPTPGLEPKGRDLM

020 10	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Clutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	<u> </u>	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	Ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ļ	•	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
		1	İ.,	peptide	i ·	nucleotide insertion
577	1927	A	4366	sequence 785	502	SAPPKKKNGVLFLSPRLKSSGAIWVHSTPTLW
3//	1927	^	4300	703	302	ASSNSRASTPKVAGITGARPHARIIFVFLIEMG
ł					1	FHNVGQAGL/DTLTLVICPPQPPKLLGLQM
578	1928	A	4367	1	221	FFFFLKKSRCVTQAGVQG\PISLHPPPPGFKRF
		1	'''	}		SRLSLLSSWDYRHP/HAANFCIFSRDG\VSPYW
		l				SGWSRTPDLR
579	1929	A	4383	1	224	FETESHSVTQAGMQWHNLGSLQPMP/PGLKR
ĺ	ľ	1			ĺ	FSCLRLQSSWDHRHAPPHLAHFCIFSRDGVSP
		<u> </u>				CWPGWSSTPDLK
580	1930	Α	4397	410	94	SRLKPYSTNVTAKKLPATNIPNLDCFTAKLYQ \VFKKGNIHILHELFQNKEEGAFPNS/FYEASFT
				1		LRPKSDRDIAKEESYSTISLLSTDTKILMSKYK
		١.			İ	OLKSSDL
581	1931	A	4414	670	3	VLVHROCGGILRLRRKEAVSVLDSADIEVTDS
301	1331	^	4414	1 070		RLPHATIVDHRPQHRWLETCNAPPQLIQGKA
						RSAPKPSQASGHFSVELVRGYAGFGLTLGGG
1		1	1	į.	l	RDVAGDTPLAVRGLLKDGP\AQRCGRLEVGD
1					ĺ	LVLIIINGESTQGLT\IIAQAVERIRAGGPQLHL
1					1	VIRRPLETHPGKPRGVGEPRKGVVPSWPDRSP
		İ		1		DPGGPEVTGSRSSSTSLVQHPPSRTTLKKTRG
		<u> </u>	1	<u> </u>		SPE
582	1932	Α	4424	194	449	VLYIRKKKRLEKLRHQLMPMYNFDPTEEQDE LEQELLEHGRDAASVQAATSVQAMQGKTTL
	1	ł			1	PS\OGPLORPSRLVFT\DVANAIHV
583	1933	A	4435	<del>  1                                   </del>	166	APGPPVPPPGSPPEQMPGPCPASMPP/DPPPGS
363	1755	l ^ _	1733	1	100	PPEOMPGPCPVSAPP/GPPPGSPPEQMPGPCPV
·		ì		Į		SAPPALLQDTSV
584	1934	A	4439	1	628	SATPQQPSAPQHQGTLNQPPVPGMDESMSYQ
1			}			APPQQLPSAQPPQPSNPPHGAHTLNSGPQPGT
						APATQHSQAGPATGQAYGPHTYTEPAKPKK
				1		GQQLWNRMKPAPGT\EV\$SST\$R\$DPLLLPPR
		1				ALAPTQRASTVVLAPSPT/SEKVQNHSGSSAR GNLSGKPDDWP/LGHERVCGALLHRL*VGGG
ŀ		1		}	]	OGPHGKAAOGGAAGAAAGRLGLYH
585	1935	A	4463	10	144	HKPVTNSRDTQEVPLEKAKQVLKIIATFKHTT
303	1755	1	1.00	"	***	SIFDDFAHYEKRQ
586	1936	A	4464	1309	103	LNAESYVSFTTKLDIPTAAKYEYGVPLQTSDS
						FLRFPSSLTSSLCTDNNPAAFLVNQAVKCTRK
	İ	1		1		INLEQCEEIEALSMAFYSSPEILRVPDSRKKVPI
1		1		· ·		TVQSIVIQSLNKTLTRREDIDVLQPTLVNAGH
İ		1		1		FSLCVNVVLEVKYSLTYTDAGEVTKADLSFV
	'	1				LGTVSSVVVPLQQKFEIHFLQENTQPVPLSGN
1				1		PGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLT ILHSTTEQDCLALEGVRTPVLFGYTMQSGCK
			.			LRLTGALPCQLVAQKVKSLLWGQGFPDYVA
			1		}	PFGNSOGP/ADMLDWVPIHFITQSFNRKDSCQ
						LPGALVIEVKWTKYGSLLNPQAKIVNVTANLI
1						SSSFPEANSGNERTILISTAVTFVDVSAPAEAG
			1			FRAPPAINARLPFNFFFFFV
587	1937	A	4471	614	387	LLGRASAC/LQLQSSW/D/HRPMLPYLANFVF
	1		1			CKDR/SFTWLPRLVLNSWLQVILLPWPPTGCD
	<u> </u>					NKHEPPCPATKRRHSGSI
588	1938	A	4480	1720	1458	HDLGSLQPPPPGFKRFSCLSLPSSWDYRLMPP
		1				CPANFCIII/DFLVETGFHHVGQASHELLTSGD
	1000	4	1	1	220	PPTSASQSAGITGMSYHTWFGES
589	1939	A	4487	922	332	APVTTSPRVGQPW/RTALALRSLYRARPSLRC
1	}	1		1		PPVELPWAPRRGHRLSPADDELYQRTRISLLQ REAAQAMYIDSYNSRGFMINGNRVLGPCALL
1	1			1		PHSVVQWNVGSHQDITEDSFSLFWLLEPRIEI
1	1	1	1	1	1	TITO A LA M'ALA COLIMENTI DE DOLORIA MERIDICIONE

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Deptide   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence							
Solution	nucl-	peptide	į	in	nucleotide	location	
Sequence	eotide	seq-		USSN	location	corresponding	
September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   Sept	seq-	uence	ľ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
	uence	l		914	ng to first		O=Glutamine, R=Arginine, S=Serine
Persidue of peptide sequence	}						
poptide	1	1	1	1.			Y=Tyrosine X=Linknown *=Ston codon
	1	}		1			
1940	1						
DITMACATFIFICHEGRYTGAALIPPEGTSL   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ   TSLGQAAQ			<del> </del>	<del> </del>		<del> </del> -	
1940   A   4492   1   472   FFFEEERSYAQAGYQWRDLGSLQAPPGGT   FFFEEERSRYAQAGYQWRDLGSLQAPPGGT   FFFEEERSRYAQAGYQWRDLGSLQAPPGGT   FFFEEERSRYAQAGYQWRDLGSLQAPPGGT   FFFEEERSRYAQAGYQWRDLGSLQAPPGGT   FFFEETRSRYAQAGYQWRDLGSLQAPPGGT   FFFEETRSRYAQAGYQWRDLGSLQAPPGGT   FFFEETRAR   FFFEETRSRYAQAGYQWRDLGSLASQCFPGR   FFFEARSAGQRLASQCFPGR   FFFEARSAGQRLASQCFPGR   FFFEARSAGQRLASQCFPGR   FFFEARSAGQRLASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSAGGRASQCFPGR   FFFEARSCSVPGAGVGRAGGRASGGRASGCFPGR   FFFEARSCSVPGAGVGRAGGRASGGRASGGRASGGRASGGRASGGRASGGR	1	1	i	1	İ	[	DTPNACATENET CHECENTER AT IDDDCCTOT
1940   A   4492   I   472	i		İ	<u> </u>		<b>!</b>	
PPSCLSLPSSWDYRRPPLRPARFEVELVETGFP   RPSRDdclDLIPIGDPPTSASQSAGITGVSER   APPKRIGEPRRKGGNAVWPSTSLGDHRVTS   VPHQCGLPCPRVAPSSAGQREASQCPPGR   PVHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQREASQCPPGR   VPHQCGLPCPRVAPSSAGQRV   VPHQCGLSLANAWQLSVGAKQKKWKPLEFL   LCTLAATHMINVAVPIATYSVQLRQRPDF   SWNBGLCKVPVSTFYTLTILATCRSVSTSLSYHR   MPMWVCWPVNYRLSNAKKQAGHTVMGIWM   GSFLSALPAVGWHDTSRFYTHIGCFIVAE   GLGFGVCFLLLVGGSVAMGWICTAIALFQTL   AVQVGRQADIRAFTYTHIVVEDAGRRSSIS   DOSEPAKTSLQTTGLVTTIVFTDGRSGACVM   GFFLAADHIN SDLPTVTTIVVEDAGRRSSIS   DOSEPAKTSLQTTGLVTTIVFTDGRSGACVM   GFFLAADHIN SDLPTVTTIVOFDROSGACVM   GFFLAADHIN SDLPTVTTIVOFDROSGACVM   GFFLAADHIN SDLPTVTTIVOFDROSGACVM   GFFLAADHIN SDLPTVTTIVOFDROSGACVM   GFFLAADHIN SDLPTVTTIVOFDROSGACVM   GFFLAADHIN SDLPTVTTVGCPRGACVM   GFFLAADHIN SDLPTVTTVGCPRGACVM   GFFLAADHIN SDLPTVTTVGCPRGACVM   GTFKWVGCMILAHFPRWGLAADRAFVLGP   VAGTASGKLFSFGGLGWTLLDVLLIGVGGVGVG   RYPANCTVRLDHVHCLGRATFFRMI VCNWT   GGYKWVGCMILAHFPRWGLAADRAFVLGP   VAGTASGKLFSFGGLGWTLLDVLLIGVGGVGG   RYPANCTVRLDHVHCLGRATFFRMI VCNWT   GGYKWVGCMILAHFPRWGLAADRAFVLGP   VAGTASGKLFSFGGLGWTLLDVLLIGVGGVG   PADGSLYI   FFFRMESYSVARLECSGAISAPCNLHLLGSNN   SPASASRVAGRIGARHTQQFVLLVVGMRVH   SVSTINCHRWGFQCDUGTDQDDLLAND   NHUMENTA   SPASASRVAGRIGARHTQQFVLLVVGMRVH   SVSTINCHRWGFQCDUGTDQDDLLAND   NHUMENTA   SPASASRVAGRIGARHTQQFVLLVVGMRVL   VAGNAGAGARHTQQFVLLVVGMRVL   VAGNAGAGARHTQQFVLLVVGMRVL   VAGNAGAGARHTQQFVLLVVGMRVL   VAGNAGAGARHTQQFVLLVVGMRVSL   VARNKRQLAGSSVVQEERKFKLD   PEDRACOLVFAGTAGAGAGAGAGARHTQQFVLLVVGMRVSL   VARNKRQLAGSSVVQEERKFKLD   VAGNAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	590	1940	Δ	4492	1	472	
RPSRDGLDLIT/IS/GDPPTISAGS/AGITGV/SIR		** ''	1 .	77/2	*	472	
APPKRIGEPRIKCONAVWPETSLGDHRVTS   SP1	ł			1		ŀ	
1941   A   4495   1444   1116							APPRIORPD VOCALAR REPORTS
1941   A   4495   1444   1116							ARPARIGEPRIKCGNAVVWPSISLGDHRVIS
	501	10/1	<u> </u>	1405	1444	1116	VPHQGGLPGPIRVAPSSAGQREASQGPPGR
LKDNWVEDTIPQGAVPCTATAEGMKRLLFAL	331	1741	A	4493	1444	1110	
1942   A   4496   2   919   RTRPLFSGRYTMOMERILPGSAVGWL   VCOGLSLLANAWGILSVGAKQKKWRLERL   LCTLAATIMI.NVAVPIATYSVVQLRRQRPDF   EWNEGLCKVYVSTFYITLITATCFSVTSLSYHR   MWMCWPVNYSLSNAKKQAGHTVMGIBW   GSFILSALPAVGWHDTSERFYTHCGRIVAE    GLGFGVCFLLLVGGSVAMGVICT.AIALFQTL   AVQVGRQADHRAFTVYTIVVEDAQGKRSSI   DGSFPAKTSLQTTGLVTTIVYDCLMGFPVL   GFFSLADTHLSDLPYTWGDRDSGGACVM   FFFFAESCSVPGAGVQRDJEHAPPPGSC   FFFAESCSVPGAGVQRDJEHAPPPGSC   FFFAESCSVPGAGVQRDJEHAPPPGSC   FFFAESCSVPGAGVQRDJEHAPPPGSC   FFFAESCSVPGAGVQRDJEHAPPPGSC   FFFAESCSVPGAGVQRDJEHAPPPGSC   FFFAESCSVPGAVGRDJECKJAPATICCTINFS   CTYGRV*TFDCAVKPSVTCVDQDFKSQKNPIL   NMTCRFCWQLPETDYBCTNSTSCMTVSCPRQ   RYPANCTVRDHYHCLGNTFFFKML / YCONG   RYPANCTVRDHYHCLGNTFFFKML/CNWT   GGYKWYGLWLRHHFPRWGLGADRPYLOP   VAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   FFFRMESTSVARLECSGAISAPCNLHILGSNN   SPASASRVAGNIGARHHTQGIPVLLVGMRYH   YVQQDGLDLLANMHPPRSFVLGLQA   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PADGSLYI   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PAGTASGKLFSFGGLGIWTLIDVLLIGGGYVG   PAGTASGKLFSFGGLGIWTLIANGGFTEKFKLD   PAGTASGKLFSFGGLGIWTLIANGGFTEKFKLD   PAGTASGKLFSFGGLGIWTLIANGGFTEKFKLD   PAGTASGKLFSFGGLGIWGHT   PAGTASGKLFSFGGLGIWGHT   PAGTASGKLFGGADFCV   PAGTASGKLFGGADFCV   PAGTASGKLFGGADFCV   PAGTASGKTGGATGHT   PAGTASGKTGGATGHT   PAGTASGKTGGATGATGHT   PAGTASGKTGGATGATGHT   PAGTASGKTGGATGATGHT   PAGTASGKTGGATGATGHT   PAGTASGKTGGATGATGTT   PAGTASGKTGGATGATGATGT   PAGTASGKTGGATGATGATGATGATGATGATGATGATGATGATGATGA							
1942	1						
VCGGLSLLANAWGILSVGAKQKKWRPLEFL   LCTLAATIMLINVAVPIATYSVVQLRQRPDF   EWNEGLCKVYVSTFYTLIATCFSVTSLSYHR   MWMVCWPVNYRLSNAKKQAGHTVMGIWM   GSFILSALPAVGWHDTSRFYTHCGRIPVAEI   GLGFGVCPLLLVGGSVAMGVICTAIALFQTL   AVQVGRQADFRAFTVPTIVVEDAQGKRRSIS   DGSEPAKTSLQTFGLVTTIVFYLCHGMGPVL   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GPFSLADTHLSDLPYTWGDRDGGGACVM   GFFSLADTHLSDLPYTWGDRDGGGACVM   GFFSLADTHLSDLFYTHALPALVENGL   C	500	1040		1404			
LCTLAATIMI.NVAVPIATYSVVQLRRQPPDF	392	1942	Α	4496	2	919	RTRPLFSGRPTRPVCTMSDERRLPGSAVGWL
LCTLAATIMI.NVAVPIATYSVVQLRRQPPDF			1	] . [			VCGGLSLLANAWGILSVGAKQKKWKPLEFL
MWMVCWPVNYRLSNAKKQAGHTVMGIWM GSFLSALPAVGWHDTSERFYTHGCRFIVAEI GLGFGVCFLLLVGGSVAMGVICTAIALFQTL AVQVGRQADIRAFTVTTIVYEDAGKRRSSI DGSEPAKTSLQTIGLVTTIVYEDAGKRRSSI DGSEPAKTSLQTIGLVTTIVYEDAGKRRSSI DGSEPAKTSLQTIGLVTTIVYEDAGKRRSSI DGSEPAKTSLQTIGLVTTIVYEDAGKRRSSI DGSEPAKTSLQTIGLVTTIVYEDAGKRRSSI DFFSLADTHLSDLPYTWGDRDSGGACVM FFFFSLADTHLSDLPYTWGDRDSGGACVM FFFFSLADTHLSDLPYTWGDRDSGGACVM FFFFSLADTHLSDLPYTWGDRDSGGACVM FFFFSSQCATTHARHHTQLFVAPLVENGL C HAMAGGVRPLRGLRALCRVLLFLSQFCILSGG ESTEIPPYVMKCPSNGLCSRLPADCIDCTTNFS CTYGRPVTPDCAVKPSVTCVDQDFSCKNFII NMTCRFCWQLPETDYBCTNSTSCMSVGKNFII NMTCRFCWQLPETDYBCTNSTCMSVCRCPRQ RYPANCTVRUDHVHCLGRRTFPSMLYCNWT GGYKWVYGLWLLRHIPRWGLGADRRYLGP VAGTASGKLFSFGGLGIWTLIDVLLIGVGYVG PADGSLYI    595	1		İ				LCTLAATHMLNVAVPIATYSVVQLRRQRPDF
GSFILSALPAVGWHDTSERPYTHGCRFIVAE    GLGFGVCFLLUVGGSVAMGVICTAIALFQTL     AVQVGRQADHRAFTVFTTVVEDAQGKRRSSI     DGSEPAKTSLQTTIGLVTTIVFTYDCLMGFPVL     GPFSLADTHLSDLPYTWORDSGGACVM     GPFSLADTHLSDLPYTWORDSGGACVM     GPFSLADTHLSDLPYTWORDSGGACVM     FFFEAESCSVPQAGVQRPDLGWLHAPPPGSC     HFPASASQVAGTTHARHHTQLIPAFLVENGL     C	1		•		*		EWNEGLCKVFVSTFYTLTLATCFSVTSLSYHR
GSFILSALPAVGWHDTSERPYTHGCRFIVAE    GLGFGVCFLLUVGGSVAMGVICTAIALFQTL     AVQVGRQADHRAFTVFTTVVEDAQGKRRSSI     DGSEPAKTSLQTTIGLVTTIVFTYDCLMGFPVL     GPFSLADTHLSDLPYTWORDSGGACVM     GPFSLADTHLSDLPYTWORDSGGACVM     GPFSLADTHLSDLPYTWORDSGGACVM     FFFEAESCSVPQAGVQRPDLGWLHAPPPGSC     HFPASASQVAGTTHARHHTQLIPAFLVENGL     C			ĺ				MWMVCWPVNYRLSNAKKQAGHTVMGIWM
AVQVGRQADHRAFTYPTITVYEDAGGKRRSSI   DGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL GPFSLADTHLSDLPYTWGDRDSGGACYM   GPFSLADTHLSDLPYTWGDRDSGGACYM   GPFSLADTHLSDLPYTWGDRDSGGACYM   FFFEASSGSVPQGVQRPDLGWLHAPPPVGSC   HFPASASQVAGTTHARHHTQLIFAFLVENGL C   GESTEIPPYWMKCPSNGLCSRLPADCIDCTTNFS   CTYGKPVTFDCAVKPSVTCVDQDFKSQKNPII   NMTCRFCWQLPFTDYBCTNSTSCMTVSCPRQ   RYPANCTVRQDHVHCLGNRTFPKMLYCNWT   GGYKWVYGLWLRHHFRWGLGADRFYLOF   VAGTASGKLFSFGGLGIWTLIDVLLIGVGYVG   PADGSLYI							GSFILSALPAVGWHDTSERFYTHGCRFIVAEI
AVQVGRQADHRAFTYPTITVYEDAGGKRRSSI   DGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL GPFSLADTHLSDLPYTWGDRDSGGACYM   GPFSLADTHLSDLPYTWGDRDSGGACYM   GPFSLADTHLSDLPYTWGDRDSGGACYM   FFFEASSGSVPQGVQRPDLGWLHAPPPVGSC   HFPASASQVAGTTHARHHTQLIFAFLVENGL C   GESTEIPPYWMKCPSNGLCSRLPADCIDCTTNFS   CTYGKPVTFDCAVKPSVTCVDQDFKSQKNPII   NMTCRFCWQLPFTDYBCTNSTSCMTVSCPRQ   RYPANCTVRQDHVHCLGNRTFPKMLYCNWT   GGYKWVYGLWLRHHFRWGLGADRFYLOF   VAGTASGKLFSFGGLGIWTLIDVLLIGVGYVG   PADGSLYI							GLGFGVCFLLLVGGSVAMGVICTAIALFOTL
DGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL					-		
1943   A   4506   2   193					٠.		
1943   A   4506   2   193				L			GPFSLADTHLSDLPYTWGDRDSGGACVM
HFPASASQVAGTTHARHHTQLIPVAFUL C	593	1943	Α	4506	2	193	FFFEAESCSVPQAGVORPDLGWLHAPPP\GSC
S94							HFPASASOVAGTTHARHHTOLIF\AFLVENGL
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KF\TRYNSVRPL\ATLSYASDLY\NGSQY\KSLV FEFDRDCDYFAIAGVTKKIKVYEYDTVIQDA VDIHYPENEMTCNSKISCISWSSYHKNLLASS DYEGTVILWDGFTGQRSKVYQEHEKRCWSV DFNLMDPKLLASGSDDAKVKLWSTNLDNSV ASIEAKANVCCVKFSPSSRYHLAFGCADHCV HYYDLRNIKQPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGKPAYCLRSFKGHIN EKNFVGLASNGDYIACGSENNSLYLYYKGLS KTLLTFKPDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTNKVLELV  597 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLLGSSDPYIS ASQVAEITSVRHHTWLIFCILGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP  598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF		j	1		ľ		
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VDIHYPENEMTCNSKISCISWSSYHKNLLASS DYEGTVILWDGFTGQRSKVYQEHEKRCWSV DFNLMDPKLLASGSDDAKVKLWSTNI.DNSV ASIEAKANVCCVKFSPSSRYHLAFGCADHCV HYYDLRNIKQPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGKPYCLRSFKGHIN EKNFV\GLASNGDYIACGSENNSLYLYYKGLS KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTNKVI.ELV  597 A 4518 536 824 RSLALSPGLECSGMISHCNLHLLGSSDPTS ASQVAEITSVRHHTWLIFCILGQMGFHHVGE QAGLELLTSWDPAILPSQSAGTIGMSPHAWPP 598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF		l				ļ	
DYEGTVILWDGFTGQRSKVYQEHEKRCWSV DFNLMDPKLLASGSDDAKVKLWSTNLDNSV ASIEAKANVCCVKFSPSSRYHLAFGCADHCV HYYDLRNTKQPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNYGKPYCLRSFKGHIN EKNFVGLASNGDYIACGSENNSLYLYYKGLS KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTI\KVLELV  597 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLGSSDPPTS ASQVAEITSVRHHTWLIFCILGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP  598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF	[ ]	İ	ĺ		1	ľ	
DFNLMDPKLLASGSDDAKVKLWSTNLDNSV ASIEAKANVCCVKFSPSSRYHLAFGCADHCV HYYDLRNTKQPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGKPYCLRSFKGHIN EKNFVGLASNGDYIACGSENNSLYLYYKGLS KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTI\KVLELV  597 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLGSSDPPTS ASQVAEITSVRHHTWLIFCILGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP  598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF		ļ	j		*		
ASIEAKANVCCVKFSPSSRYHLAFGCADHCV HYYDLRNTKQPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGKPYCLRSFKGHIN EKNFVGLASNGDYIACGSENNSLYLYYKGLS KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTI\KVLELV  597 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLLGSSDPPTS ASQVAEITSVRHHTWLIFCI\LGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP  598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF		ŀ					
HYYDLRNIKQPIMVFKGHRKAVSYAKFVSG EEIVSASTDSQLKLWNVGKPYCLRSFKGHIN EKNFVGLASNGDYIACGSENNSLYLYYKGLS KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTIKVLELV  597		l		1	1		
EEIVSASTDSQLKLWNVGKP\YCLRSFKGHIN EKNFVGLASNGDYIACGSENNSLYLYYKGLS KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTYKVLELV  597		l	J	İ	İ		
EKNFVGLASNGDYIACGSENNSLYLYYKGLS KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV CWRALPDGESNVLIAANS\QGTNKVLELV  597		l	İ		I		HYYDLRNTKQPIMVFKGHRKAVSYAKFVSG
S97 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLLGSSDPTIS ASQVAEITSVRHHTWLIFCILGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP 598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSF		•		j	I	ļ	EEIVSASTDSQLKLWNVGKP\YCLRSFKGHIN
S97 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLLGSSDPTIS ASQVAEITSVRHHTWLIFCILGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP 598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSF		1	- 1	- 1		]	EKNFV\GLASNGDYIACGSENNSLYLYYKGLS
597 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLLGSSDPPI'S ASQVAEITSVRHHTWLIFCILGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP 598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF		i	ļ	1	1	1	KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV
ASOVAEITSVRHHTWLIFCILGGMGFHHVGE QAGLELLTSWDPAILPSQSAGTIGMSPHAWPP 598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF	607	1045					
ASQVAEITSVRHHTWLIFCI\LGQMGFHHVGE QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP  598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF	397	1947	A	4518	536	824	RSLALSPGLECSGMISAHCNLHLLGSSDPPTS
598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF				1	1	1	ASQVAEITSVRHHTWLIFCILGOMGFHHVGE
598 1948 A 4524 1 384 FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF							QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP
TLGKLPRKTLSVKLMKNRDEVOAMIYDDGSS	598	1948	A	4524	1	384	FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF
						İ	TLGKLPRKTLSVKLMKNRDEVQAMIYDDGSS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, B=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  RREMQSQSVMLALRRGDAVWLLSHDHDG YGAYSNHGKYITFSGFLVYPDLAPAAPPGLG ASELL  MGOPAPYAEGPIQGGDAGELCKCDFLVFTSP
399	1545	A	4320	300		NPEAVCEAGTPAMFQTAWRQMESCSI/AQAG VQWRDPGSLHPPPLGFKRFSCLSLPSSWDYK HAPPHPANFCIFSRDQVSPCWPGWSRSLDLVI PPPWLPKVLGLQA
600	1950	A	4529	776	334	FFFETESCYVAQAGVQWCDLCSLQAPPPG\SS DPPASASRVAGTTGARHHTQLIFVFLVETGFH \MLARDGLKLLTSSDPPASASQSSWDYRREPP RLANFFVFLVETGSRYVAQAGVQWLFTGAIP LLISTGVLTCSVSDLGRFTPP
601	1951	A	4533	1460	403	HEVQESIHFLESEFSRGISDNYTLALITYALSS VGSPKAKEALNMLTWRAEQEGGMQFWVSSE SKLSDSWQPRSLDIEVAAYALLSHFLQFQTSE GIPIMRWLSRQRNSLGGFASTQDTTVALKALS EFAALMNTERTNIQVTVTGPSSPSPVKFLIDT HNRLLLQTAELADGTANGSV/SISANGFGFAI CQLNVVYNVKASGSSRRRRSIQNQEAFDLDV AVKENKDDLNHVDLNVCTSFSGPGRSGMAL MEVNLLSGFMVPSEAISLSETVKKVEYDHGK LNLYLDSVNETQFCVNIPAVRNFKVSNTQDA SVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSD VQRLPSL
602	1952	A	4540	1963	295	MRAPGRPALRPLPLPLLLLLSSPWGRAVPC VSGGLPKPANITFLSINMKNVLQWTPPEGLQG VKVTYTVQYFIYGQKKWLNKSECRNINRTYC DLSAEISDYEHQYYAKVKAIWGTKCSKWAE SGRFYPFLETQIGPPEVALITDEKSISVVLTAP EKWKRNPEDLPVSMQQIYSNLKYNVSVLNT KSNRTWSQCVTNHTLVLTWLEPNTLYCVHV ESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK IIFWYVLPISITVFLFSVMGYSIYRYIHVGKEK HPANLILIYGWEFDKRFFVPAÆKIVUNFIVTL NISDDSKISHQDMSLLGKSSDVSSLNDPQPSG NLRPPQEEEVKHLGYASHLMEIFCDSEENT\ EGTSFTQQESLSRTIPPDKTVIEYEYDVRTTDI CAGPEQELSLQEEVSTQGTLLESQAALAVL GPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEE EPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCE PSEGDGLGEEGLLSRLYEEPAPDRPPGENETY LMQFMEEWGLYVOMEN
603	.1953	A	4543	3	600	YSAVEFVEQASGISDWWNPALRKRMLSDSGL GMIAPYYEDSDLKDLSHSRVLQSPVSSEDHAI LQAVIAGDLMKLIESYKNGGSLLIQGPDHCSL LHYAAETGNGEIVKYILDHGPSELLDMADSE TGETALHKAACQRNRAVCQLLVDAGASLRK\ TDSKGKTPQERAQQA\GDPDLAA/YTIESRQN YKVIGHEDLETAV
604	1954	A	4548	3	938	QDNKVQNGSLHQKDTVHDNDFEPYLTGQAN QSNSYPSMSDPYLSSYYPPSIGFPYSLNEAPW STAGDPPIPYLTTYGQLSNGDHHFMHDAVFG QPGGLGNNIYQHRFNFFPENPAFSAWGTSGS QGQQTQSSAYGSSYTYPPSSLGGTVVDGQPG FHSDTLSKAPGMNSLEQGMVGLKIGDVSSSA VKTVGSVVSSVALTGVLSGNGGTNVNMPVS KPTSWAAIASKPAKPQPKMKTKSGPVMGGG LPPPPIKHNMDIGTWDNKGPVPKAPVPQQAP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	Į .	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	}	l	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine.
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ì		ł	į	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ľ	ĺ	l	Ì	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
<del> </del>	<u> </u>		<del> </del> -	504.00.00	<del> </del> -	SPOAAPOPOOVAOPLPAOPPALAOPOVOSPO
Ì	İ	İ	İ	ĺ	İ	OPPO
605	1955	A	4553	2	2304	ILLQEKRNCLLMQLEEATRLTSYLQSQLKSLC
003	1933	^	4555	*	2304	ASTLTVSSGSSRGSLASSRGSLASSRGSLSSVS
1			i	ļ	l	FTDIYGLPQYEKPDAEGSQLLRFDLIPFDSLGR
1			Ì			DAPFSEPPGPSGFHKQRRSLDTPQSLASLSSRS
1		i e				SLSSLSPPSSPLDTPFLPASRDSPLAQLADSCE
1		1		!		GPGLGALDRLRAHASAMGDEDLPGMAALQP
			i .		}	HGVPGDGEGPHERGPPPASAPVGGTVTLRED
		1				SAKRLERRARRISACLSDYSLASDSGVFEPLT
ľ	1	ł			1	KRNEDAEEPAYGDTASNGDPQIHVGLLRDSG
		i	1	! :		SECLLVHVLQLKNPAGLAVKEDCKVHIRVYL
				i		PPLDSGTPNTYCSKALEFQVPLVFNEVFRIPV
		1				HSSALTLKSLQLYVCSVTPQLQEELLGIAQIN
		ł				LADYDSLSEMQLRWHSVQVFTS\LNHQGRGR
						LGVQERAPPGTLHTPSPSPA/STDAVTVLLAR
		1				TTAQLQAVERELAEERAKLEYTEEEVLEMER
	,	1	}			KEEQAEAISERSWQADSVDSGCSNCTQTSPPY
]		<b>!</b>				PEPCCMGIDSILGHPFAAQAGPYSPEKFQPSPL
1		İ		• •		KVDKETNTEDLFLEEAASLVKERPSRRARGSP
1		}				FVRSGTIVRSQTFSPGARSQYVCRLYRSDSDS
						STLPRKSPFVRNTLERRTLRYKQSCRSSLAEL
		ł				MARTSLDLELDLQASRTRQRQLNEELCALRE
1		l	1			LRQRLEDAQLRGQTDLPPWVLRDERLRGLLR
						EAERQTRQTKLDYRHEQAAEKMLKKASKEI
						YQLRGQSHKEPIQVQTFREKIAFFTRPRINIPPL
		1		,		PADDV
606	1956	A	4555	3429	776	PGSGPGPAPFLAPVAAPVGGISFHLQIGLSREP
						VLLLQDSSGDYSLAHVREMACSIVDQKFPEC
[ [			l i			GFYGMYDKILLFRHDPTSENILQLVKAASDIQ
						EGDLIEVVLSASATFEDFQIRPHALFVHSYRA
						PAFCDHCGEMLWGLV\RQGLKCEGCGLNYH
1						KRCAFKIPNNCSGVRRRRLSNVSLTGVSTIRT
						SSAELSTSAPDEPLLQKSPSESFIGREKRSNSQ
						SYIGRPIHLDKILMSKVKVPHTFVIHSYTRPTV
						CQYCKKLLKGLFRQGLQCKDCRFNCHKRCA
						PKVPNNCLGEVTINGDLLSPGAESDVVMEEG
						SDDNDSERNSGLMDDMEEAMVQDAEMAMA
						ECQNDSGEMQDPDPDHEDANRTISPSTSNNIP
						LMRVVQSVKHTKRKSSTVMKEGWMVHYTS
						KDTLRKRHYWRLDSKCITLFQNDTGSRYYKE
						IPLSEILSLEPVKTSALIPNGANPHCFEITTANV
i I			·			VYYVGENVVNPSSPSPNNSVLTSGVGADVAR
[						MWEIAIQHALMPVIPKGSSVGTGTNLHRDISV
						MARINICULDENT/DIGLETAN/UEDDEAU COCORCI
i l						SISVSNCQIQENVDISTVYQIFPDEVLGSGQFGI
						VYGGKHRKTGRDVAIKIIDKLRFPTKQESQLR
1						NEVAILQNLHHPGVVNLECMFETPERVFVVM
1			ĺ	- 1		EKLHGDMLEMILSSEKGRLPEHITKFLITQILV
						ALRHLHFKNIVHCDLKPENVLLASADPFPQV
	. [					KLCDFGFARIIGEKSFRRSVVGTPAYLAPEVL
[		' I		i		RNKGYNRSLDMWSVGVIIYVSLSGTFPFNED
						EDIHDQIQNAAFMYPPNPWKEISHEAIDLINN
						LLQVKMRKRYSVDKTLSHPWLQDYQTWLDL
.				-		RELECKIGERYITHESDDLRWEKYAGEQGLQ
						YPTHLINPSASHSDTPETEETEMKALGERVSIL
607	1957	A	4563	1	4499	SRPWWLRASERPSAPSAMAKRSRGPGRRCLL
					l	ALVLFCAWGTLAVVAQKPGAGCPSRCLCFRT
				ł	ļ	TVRCMHLLLEAVPAVAPQTSILDLRFNRIREI
					ļ	QPGAFRRLRNLNTLLLNNNQIKRIPSGAFEDL
	ļ	- 1		1		ENLKYLYLYKNEIQSIDRQAFKGLASLEQLYL
						Z

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, B=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  HFNQIETLDPDSFQHLPKLERLFLHNNRTHL VPGTFNHLESMKRLRLDSNTLHCDCEILWLA DLLKTYAESGNAQAAAICEYPRRIQGRSVATI TPEELNCBRPRITSEPQDADVTSGNTVYFTCR AEGNPKPEIIWLRNNNELSMKTDSRLNLLDD GTLMIQNTOETDQGIYQCMAKNVAGEVKTQ EVTLRYFGSPARPTFVIQPQNTEVLVGESVTL ECSATGHPPPRISWTRGDRTPLPVDPRVNITPS GGLYIQNVVQGDSGEYACSATNNIDSVHATA FIIVQALPQFTVTPQDRVVIEGQTVDFQCEAK GNPPPVIAWTKGGSQLSVDRRHLVLSSGTLRI SGVALHDQGQYECQAVNIIGSQKVVAHLTVQ PRVTPVFASIPSDTTVEVGANVQLPCSSQGEP EPAITWNKDGVQVTESGKFHISPEGFLTINDV GPADAGRYECVARNTIGSASVSMVLSVNVPD VSRNGDPFVATSIVEAIATVDRAINSTRTHLF DSRPRSPNDLLALFRYPRDPYTVEQARAGEIF ERTLQLIQEHVQHGLMVDLNGTSYHYNDLVS PQYLNLIANLSGCTAHRRVNNCSDMCFHQKY RTHDGTCNNLQHPMWGASLTAFERLLKSVY ENGFNTPRGINPHRLYNGHALPMPRLVSTTLI GTETVTPDEQFTHMLMQWGQFLDHDLDSTV VALSQARFSDGQHCSNVCSNDPPCFSVMIPPN DSRARSGARCMFFYRSSPVCGSGMTSLLMNS VYPREQINQLTSYIDASNVYGSTEHEARSIRD LASHRGLLRQGIVQRSGKPLLPFATGPPTECM RDENESPIPCFLAGDHRANEQLGLTSMHTLW FREHNRIATELLKLNPHWDGDTIYYETRKIVG AEIQHITYQHWLPKILGEVGMRTLGEYHGYD PGINAGIFNAFAT\AAFRFGHTLVNPLLLPGLD ENFQPIAQDHLPLHKAFFSFFRIVNEGGIDPLL RGLFGVAGKMRVPSQLLNTELTERLFSMAHT VALDLAAINIQRGRDHGIPPYHDYRVYCNLS AAHTFEDLKNEIKNPEIREKLKRLYGSTLNID LFPALVVEDLVPGSRLGPTLMCLLSTQFKRLR DGDRLWYENPGVFSPAQLTQIKQTSLARILCD NADNITRVQSDVFRVAEFPHGYGSCDEIPRVD LRVWQDCCEDCRTRGQFNAFSYHFRGRRSLE FSYQEDKPTKKTRPRKIPSVGRQGEHLSNSTS AFSTRSDASG\TNDFQRVCSWEMQKTITDLR FGELCGUKSGRLGIDSEEDYYTPQKVDVPKAL
608	1958	A	4566	354	1135	PGACCPVCLQKRAEEKP
609	1959	A	4567	1	412	FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSH RARPRINLRNVIYSFAVTYCLNYISLAMSSTL KLSFHVLSGS
610	1960	A	4570	697	467	ECRGVISAH\CCTLCLPSSSDSASAF\RVARTT GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\N LVIRPPRPFKVLGLQA

SEQ ID	SEQ ID	Met	Lego	Deadistad	18.2.4.1.1	
NO: of	NO: of	hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1.00	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
			' ' '	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		peptide		/=possible nucleotide deletion. \=possible
1	1	1	ł	sequence	1	nucleotide insertion
611	1961	A	4571	25	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRT
		1			1	WNPNVPESPRIPAPRLPKRMSGAPTAGAALM
į	}	ŀ				LCAATAVLLSAQGGPVQSKSPRFASWDEMN
						VLAHGLLQLGQG\CANT\GAHPQSAERAGA\R
	İ		į			LSACGSACQGTEGSTDLPLAPESRVDPEVLHS
l	1	l	1			LQTQLKAQNSRIQQLFHKVAQQQRHLEKQHL
1		İ	1	[	ĺ	RIQHLQSQFGLLDHKHLDHEVAKPARRKRLP
ŀ		1			1	EMAQPVDPAHNVSRLHRLPRDCQELFQVGER
		•				QSGLFEIQPQGSPPFLVNCKMTSDGGWTVIQR
		1	1			RHDGSVDFNRPWEAYKAGFGDPHGEFWLGL
1		1	1	ļ	1	EKVHSITGDRNSRLAVQLRDWDGNAELLOFS
ļ			1			VHLGGEDTAYSLQLTAPVAGQLGATTVPPSG
		1		İ		LSVPFSTWDQDHDLRRDKNCAKSLSGGWWF
1	1			1		GTCSHSNLNGQYFRSIPQQRQKLKKGIFWKT
		L				WRGRYYPLQATTMLIQPMAAEAAS
612	1962	A	4575	162	3	FFFETESRSVAQAGVQWRDLSSLQPPPPG\SR
(12	10.00	<u> </u>	1			GSPASASPVAGITGTRHHRTRG
613	1963	Α	4584	687	321	PLAQRRPFLWVTVKTNGHIWGSSTYPHFWGS
l		J		j		SNS/PASASQVAGIPNARHQARIIFVFLVEPRF
		1				HHVGRAGLGFL/NLAICLPQHPKVLGLQACN
614	1064	<del>   </del>	4500			LNIKPHPAHKYISMIQFNVHFMCMSVHIYI
014	1964	A	4589	727	299	PGSAQSAQRGRGRRRARAGSATQITMYSFMG
		[				GGLFCAWVGTILLVVAMATDHWMQYRLSGS
				Ì		FAHQGLWRYCLGNKCYLQTDSIAYWNATRA
						FMILSALCAISGIIMGIMAF/GWVAVLMTFFA
615	1965	A	4590	2	414	GIFYMCAYRVHECRRLSTPR
0.5	1303	^	4390	4	414	TILPEKIQAWAQKQCPQSGEEAVALVVHLEK
		ĺ	1			ETGRLRQQVSSPVHREKHSPLGAAWEVADFQ
		•				PEQVETOPRAVSREEPGSLHSGHQEQLNRKR ERRPLPKNARPSPWVPALADEWNTLHOEVTT
						TRLPAGSQEPVKD
616	1966	A	4592	773	488	DFALVAQAGVQWHNLGSPQPLPPGFKRFSCL
			10,2	,,,	400	SLPSSWEYRCVPP/RLANFVFLVEMGFLHVGO
						AGLELPTSGDPPALASQSAGITGVTTVPSGPG
617	1967	В	4595	84	478	XRHGLREPLLERRCAAASSFQHSSSLGRELPY
			'''		170	DPVDTEGFGEGGDMQERFLFPEYILDPEPOPT
	1					REKQLQELQQQQEEEERQRQQRREERRQQNL
			1			RARSREHPVVGHPDPALPPSGVNCSGCGAEL
	]		1			HCQDAR*
618	1968	A	4596	2945	1188	ARSRNSARGVYGMCVDTLFLCFLEDLERNDG
						SAERPYFMCSTLKKPLARRCFPAIHAYKGVL
						MVGNETTYEDGHGSRKNITDLVEGAKKANG
						VLEARQLAMRIFEDYTVSWYWIIIGLVIAMA
	"					MSLLSIILLHLLAGIMGWVMIIMEI\SELGYRIF
					l	HCYMEYSRLRGEAGSDVSLVDLGFQTDFRV
						YLHLRQTWLAFMIILSILEVIIILLLIFLRKRILI
			1			AIALIKEASRAVGYVMCSLLYPLVTFFLLCLCI
			[		ľ	AYWASTAVFLSTSNEAVYKIFDDSPCPFTAKT
					l	CNPETFPSSNESRQCPNARCOFAFYGGESGYH
						RALLGLQIFNAFMFFWLANFVLALGQVTLAG
				- 1	1	AFASYYWALRKPDDLPAFPLFSAFGRALRYH
						TGSLAFGALILAIVQIIRVILEYLDORLKAAEN
						KPAKCLMTCLKCCFWCLEKFIKFLNRNAYIM
					1	IAIYGTNFCTSARNAFFLLMRNIIRVAVLDKV
				ļ		TDFLFLLGKLLIVGSVGILAFFFFTHRIRIVQDT
				. 1	l	APPLNYYWVPILTVIVGSYLIAHGFFSVYGMC
						VDTLFLCFLEDLERNDGSAERPYFMSSTLKKL
						LNKTNKKAAES
619	1969	A	4601	2	357	RTSVEPYILGEF/RKLSNNTKVVKTEYKATEY

: .		T = -				:
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ļ	ļ	)	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	ļ	Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ			peptide		/=possible nucleotide deletion, \=possible
		1	Ī	sequence		nucleotide insertion
				·		GLAYGHFSYEFSNHRDVVVDLQGWVTGNGK
	ł	l	}	. ·	1	GLIYLTDPQIHSVDQKVFTTNFGKRGIFYFFN
	l		į		,	NQHVECNEICHRLSLTRPSMEKPCKS
620	1970	A	4606	1	2415	MERLWGLFQRAQQLSPRSSQTVYQRVEGPR
		1		-	1	KGHLEEEEEDGEEGAETLAHFCPMELRGPEP
1	Į.		ļ	j	J	LGSRPROPNLIPWAAAGRRAAPYLVLTALLIF
	[		1		ļ	TGAFLLGYVAFRGSCQACGDSVLVVSEDVN
			1	ļ		YEPDLDFHQGRLYWSDLQAMFLQFLGEGRL
	i	i	ł	i	1	EDTIRQTSLRERVAGSAGMAALTQDIRAALS
		1				RQKLDHVWTDTHYVGLQFPDPAHPNTLHWV
	1	ļ		1	ł	
			1			DEAGKVGEQLPLEDPDVYCPYSAIGNVTGEL
			l	ļ		VYAHYGRPEDLQDLRARGVDPVGRLLLVRV
		•	1			GVISFAQKVTNAQDFGAQGVLIYPEPADFSQ
		1	1		ł	DPPKPSLSSQQAVYGHVHLGTGDPYTPGFPSF
	İ	l	1	i	i :	NQTQFPPVASSGLPSIPAQPISADIASRLLRKL
	1					KGPVAPQEWQGSLLGSPYHLGPGPRLRLVVN
		l	ł		ł	NHRTSTPINNIFGCIEGRSEPDHYVVIGAQRDA
		1	1 :		Į	WGPGAAKSAVGTAILLELVRTFSSMVSNGFR
	1	]	}			PRRSLLFISWDGGDFGSVGSTEWLEGYLSVL
	1	· .	1		ĺ	HLKAVVYVSLDNAVLGDDKFHAKTSPLLTSL
		l				IESVLKQVDSPNHSGQTLYEQVVFTN\PSWD\
	i :	ĺ	1			AEVIRPLPM\DSSAY\SFTAFVGVPAVEFSFME\
	i	Ì				DDQ\AYPFLHTKEDTYENLHKVLQGRLPAVA
	İ	1				QAVAQLAGQLLIRLSHDRLLPLDFGRYGDVV
			'		İ	LRHIGNLNEFSGDLKARGLTLQWVYSARGDY
		l	1	, :		IRAAEKLRQEIYSSEERDERLTRMYNVRIMRV
	•		İ	· ·	Ì	EFYFLSQYVSPADSPFRHIFMGRGDHTLGALL
		<b> </b>	1			DHLRLLRSNSSGTPGATSSTGFQ\ESRFRRQL\
	1		<b>i</b>		ĺ	ALL\TWDACKGAANALSGDVWNIDNNF
621	1971	A	4610	793	334	ISRVDDFVGSGIANVIIAVAIFSIPAFARLVRG\
021	1271	^	4010	133	224	1
	ļ	1				NTLVLKQQTFIESARSIGASDMTVLLRHILPGT
	J	1	1			GSSIVVFFTMRIGTSIISAASLSFLGLGAQPPTP
			1			EWGAMLNEARADMVIAPHVAVFPALAIFLTV
	1000	L				LAFNLLGDGLRDALDPKIKG
622	1972	A	4614	2.	820	LVYVMIAIFCIASAMSLYNCLAALIHKIPYGQ
	1					CTIACRGKNMEVRLIFLSGLCIAVAVVWAVF
	l	1	1			RNEDRWAWILQDILGIAFCLNLIKTLKLPNFK
		l				SCVILLGLLLYDVFFVFITPFITKNGESIMVEL
	ł	1				AAGPFGNNEKNDGNLVEATGQPSAPHEKLPV
		ļ				VIRVPKLIYFSVMSVCLMPVSILGFGDIIVPGL
		j				LIAYCRRFDVQTGSSYIYYVSV\TVAYAIGMIL
		1				TFVVLG\LMKKGQPALLYLVPCTLITA/CQFV
	<u></u>	l				AWETVREMKKFWERVTS
623	1973	Ā	4619	17	691	TLVSVVEFVRRADLTREDLAPSSVDSGQAGF
		1				GGCCESGLPNTMPSAFSVSSFPVSIPAVLTQT
	1	l	]		l	DWTEPWLMGLATFHALCVLLTCLSSRSYRLO
			1.			IGHFLCLVILVYCAEYINEAAAMNWRLFSKY
		1				QYFDSRGMFISIVFSAPLLVNAMIIVVMWVW
		1				KTLNVMTDLKNAQERRKEKKRRKED*GAA
		1				AAWSLRPSRPPSAAPSAAVCVAWASFOLTHG
		l	j .			LKNRCFI
624	1974	A	4622	164	668	
	17/4	ות	4022	104	000	VSCYTALQSIMNQPESANDPEPLCAVCGQAH
· · · · · ·					l	SLEENHFYSYPEEVDDDLICHICLQALLDPLD
U	137.				i .	TO COUNTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
024						TPCGHTYCTLCLTNFLVEKDFCPMDRKPLVL
024						QHCKKSSILVNKLLNKLLVTCPFREHCTQVL
						QHCKKSSILVNKLLNKLLVTCPFREHCTQVL QRCDLEHHFQTSQAWGTHL*SQLLGRLRQED
						QHCKKSSILVNKLLNKLLVTCPFREHCTQVL QRCDLEHHFQTSQAWGTHL*SQLLGRLRQED CLSPGVHHCSEV
625	1975	Α	4625	474	473	QHCKKSSILVNKLLNKLLVTCPFREHCTQVL QRCDLEHHFQTSQAWGTHL*SQLLGRLRQED

000 10	TOPOTE	1	1000	1 30 41		
SEQ II		Met		Predicted	Predicted end	Amino acid sequence (A=Alanine O=Cysteine,
NO: of		hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	-	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	
1			İ		İ	/-possible nucleotide deletion, \-possible
626	1976	<del>                                     </del>	4500	sequence		nucleotide insertion
020	1 19/0	A	4629	249	1 3	KLKGNECECYHCNVCIFLMIKK*GLFLC*IYFI
1	-	} .	·		1	LFFET*SHSFTRLECSGTISAHCSLQLQGSSNSP
		1				ASASQVAGIAGTHH
627	1977	Α	4635	1	301	FFFFETKPFFAPQAGGQGPSRGSLNPLPTGLK
			ŀ			QFSGLTLSRSGNNGPRPPPRVNFGILRGNGVP
1	ł	İ				PGGAG*PRPPDLRGPPGLAPPQGGNNGGDPP
	j	1			•	ARAYL
628	1978	I A	4648	: 1357	782	
020	1776	Ι^	4040	1337	/82	KLFSSQRLFGPHIQAINPSFLLLSFFPS*LLAMR
		1	ı	İ		TVGNNAFILVFLVYRIVLLLF*HV*PAYFQPSK
		1	1			NKTAKINCN*RPFLFLVCYLL*AELHIGIFIANF
		1				YDCIPNKLNEHLWPKLLQSLIFHVDFCGFLHK
		1				VFYICFTEFLLFLYFL*LFIIKVSCSII*CSTICVF
	1.	1	1	!	1	SYKSFAVIIFFVDNTRFFSFGF
629	1979	A	4660	18	999	HHELHTLELLQNPKEVLTRSEIQDVNYSLEAV
1	1	"	1.500		***	KAKAACODI WARMI ADEGMANI I 2000 144
		1				KVKTVCQIPLMKEMLKRFQVAVNLAEDTAH
	1	1				PKLVFSQEGRYVKNTASASSWPVFSSAWNYF
		1	Ì		ł	AGWRNPQKTAFVERFQHLSCVLGKNVFTSG
1		1	1		ł	KHYWEVESRDSLEVAVGVCREDVMGITDRS
						KMSPDVGIWAIYWSAAGYWPLIGFPGTPTQQ
1					j	EPALHRVGVYLDRGTGNVSFYSAVDGVHLH
			- 1			TFSCSSVSRLRPFFWLSPLASLVIPPVTDRK*G
1	i	1	1			FSSPDQNSFPVVQLRDTHPWALFCPSCLYPG
	1	ł	-			WSIFWVSLTVPFGICPLCASQEAVPWEVGLA
	1	i	•			NGDGTGNFPRRFWEIFL
630	1980	A	4669	2	358	
""	1500	1 ''	4007	2	330	FFFFFETESHSVAQAGMQWRNLGSLPAPPPGF
	1		1 1			TPFFCLSLLNGWDYRRPPPHLANFFVLLVETG
ł		l	1			FHDVGQDGLDLLTS*STPSASQSAEITGVSHC
						TRLKKIRFAKGHVEFFFESHVE
631	1981	A	4674	953	614	TPIRGTDDEHEECTVQEYSAGKNTCLRPGAV
	1	1	1			AHTCNPCTLGGRGRWIT*GSGVQDQPGPTWQ
1	-	ŀ				NPVFLERRPRALHSSPGLTTQRILWAQGLWV
ŀ	l	1	1			GAGSTGCSRGPRGEGVFREG
632	1982	A	4678	34	314	RSTHASGMISPSFGFMGHLLRLEFEILPSTPNP
		• •	1070	<b>3</b> T	314	*I DOVOCE A A COOL ICITI OFFCODDI IN CARCADO
			1 1			*LPSYQGEAAGSSLISHLQTFSPDLKGVYCTFP
633 ·	1002	1	14000	,	12/1	ASGLAPVPTHWTVSELSRSPVATATFC
1033	1983	A	4696	1	1365	RTLGMEGERRASQAPSSGLPAGGANGESPGG
	1	l				GAPFPGSSGSSALLQAEVLDLDEDEDDLEVFS
1	1	1	1 1	i	ļ	KDASLMDMNSFSPMMPTSPLSMINQIKFEDEP
1		1				DLKDLFITVDEPESHVTTIETFITYRIITKTSRG
1		]		1	.	EFDSSEFEVRRRYQDFLWLKGKLEEAHPTLII
1		I		i		PPLPEKFIVKGMVERFNDDFIETRRKALHKFL
		l				NRIADHPTLTFNEDFKIFLTAQAWELSSHKKO
1.		l		-		
	1	[		l		GPGLLSRMGQTVRAVASSMRGVKNRPEEFM
[		1		1		EMNNFIELFSQKINLIDKISQRIYKEEREYFDE
		l				MKEYGPIHILWSASEEDLVDTLKDVASCIDRC
1		[				CKATEKRMSGLSEALLPVVHEYVLYSEMLM
1		}	1 1	ŀ	•	GVMKRRDQIQAELDSKVEVLTYKKADTDLL
1						PEEIGKLEDKVECANNALKADWERWKQNM
	1		1		j	QNDIKLAFTDMAEENIHYYEQCLATWESFLT
Ī			1		]	SOTNLHLEEASEDKP
634	1984	A	4708	421	158	SYWVGEDYTYKFFEVILIDPFHKAIRRNPDTO
1 ,		)	""	721	130	DIW AUGUST TEATER THE ATTENTION TO THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE ATTENTION OF THE A
l			1 1	1		WISKAVYKHREMCGLTSTGRKSHGLEKDRM
626	1005		<b> </b>			FPHAIGGSCRAA*RRKTLQFPCYH
635	1985	Α	4709	42	341	YIKQPDAKERRRTVHWKKETESEASEITIPPST
				ł		PGVPQAPGHWEDYGRGDNFYLPH*DPGGIVL
				!		WNIFNRMPIARKNITDGEHHEYLIEVPRLFHT
L			[	ŀ		SED
636	1986	A	4721	2	351	EKPDHFFPEGTSFIHEPRRPN*GDLVHCLGGIS
1				-		DELLALATINOSI MELULIA GODINATA CON CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL D
			<del></del>			RSTTVTVA*LMQKLNLSMNDAYYIVIMKMSS

SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	}		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uciico				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	İ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
-	l	İ		peptide	Soquence	/=possible nucleotide deletion, \=possible
ì	l	l		sequence		nucleotide insertion
<b></b>	<del></del>		<del> </del>	Boquesico		ISPNFNSMDQPLDFQRTLGLRSPCYNRVPAQK
			1			MYFTTPSNHNAYQVDSVQST
637	1987	A	4726	664	253	NTGLTCSIQRKCGETQLYRREENRLILLLQDH
037	1507	^	1720	1 004	233	LKSESFQVLTLSPRLEFSGLISAHCNLRLPGSS
						DSSASSSRAAGITGVHHHAWLIFFFLVETGFL
				]		HAG*AGLELLTSGDPPASASRSAGITGVSHHA
				1	1	RPRETRFL
638	1988	A	4734	24	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDG
050	1,500	11	1754	۱	372	TLERGHWNNKMEFVLSVAGEIIGLGNVWRFP
	İ				•	YLCYKNGGGAFFIPYLVFLFTCGIPVFLLETAL
						GOYTSOGGVTAWRKICPIFEGIGYASOMIVIL
1	·					LNVYYIIVLAWALFYLFSSFTIDLPWGGCYHE
	1	1				WNTEHCMEFQKTNGSLNGTSENATSPVIEFW
639	1989	A	4743	1040	699	OGLTLLPRMECSATITAHCSLELPGSIDLPTSA
055	1707	1	1743	1040	022	S*VARTTGTHHHPWLILVLLL*TWGSYYVAQ
1				1		AGLELLGSSNLPAAMVSQSAQIIGHDHCAWA
(	ĺ			{	{	TSNHVLYTQEGLRRGKEG
610	1990	A	4771	527	2	GRIDCPHPATVLAQPIFIDACSVLGAYQGAQN
0.10	1990	Α	1772	327	-	WIRRRPCLPSGCLKMNREIGPLQHSLCCPGWS
İ						QTPGLKAILLRQPPK*LGLQMESHSCPPAWSA
1	ļ	į	ļ	į.	ł	MARSRLTATSASQVQAILLPQPPGTTDSCSPS
1		1	Ì	İ		PDHEOOPLSWVLPPPQKDMNPREQQVALGP
1	ĺ		-			QAAALPWAVWRNDCFPR
641	1991	A	4780	16	473	RPSSQCGGIPTGWKKGLAPELSSELSSPPLPAR
041	1991	A	4700	1.0	1/3	LQLAASPYFSPSWAECPQPVPAGTHATWCLA
1	ì	ļ	ľ	i	i	RVWARMTPPGPAGIPSHPLPPPPPERSVPIPSP
i			Ì			FPARDSGSRQGHSTDRYKHTDAPRDAHRRVP
1						QRDTDTGVHTGSGTHTHAHTPPEK
642	1992	A	4798	1	487	GYSFRCDIVDYSRSPTALRMARTCWLYYFSK
1 042	*//2	^	4/20	1 ^	} ~~/	FIELLDTIFFVLRKKNSQVTFLHVFHHTIMPW
				l		TWWFGVKFAAGGLGTFHALLNTAVHVVMY
	·	1				SYYGLSALGPAYQKYLWWKKYLTSLQLVQF
						VIVAIHISQFFFMEDCKYQFPVFACIIMSYSFM
1		l ·	Í	1	ĺ	FLLLFLH
643	1993	A	4799	2	391	LMAFIEMHISGSLVYLKIKTKIYSYFSMLNFLL
			11.5	1		QEIPLSEILRISSPRDFTNISQGSNPHCFEIITDT
1			İ			MVYFVGENNGDSSHNPVLAATGVGLDVAQS
ļ	}	Į	]	<b>!</b> .		WEKAIRQALMPVTPQASVCTSPGQGKDHSK
		1			1	Q*ASVCTSPGQGKDHSKQ
644	1994	A	4800	488	101	AYPLFAVHPVHTECVAGVVGRAYLLCALFFL
				1	1	LSFLGYCKAFRESNKEGAHSSTFWVLLSIFLG
		ļ			I	AVAMLCKEQGITVLVRAATWLGPAFSVCPFP
		1	1	(	1	SYKDIWGWPCLCGVLHAYIPLLV
645	1995	A	4805	458	126	LLWTTVLCQTPARPQSTMIHLGHILFLLLLPV
1	""	1			1	AAAQTTPGERSSLPAFYPGTSGSCSGCGSLSL
	ľ	ľ	1	ţ.	1	PLLAGLVAADAVASLLIVGAVFLCARPRRSP
		1		1		AQEDGKVYINMPGRG
646	1996	A	4817	47	1033	LQGDTWHLSFLSHFSRLHGGVPGRGLLEGNL
1	1	1	""	''		LQPQAPGHDMTSIPFPGDRLLQVDGVILCGLT
	]	1	j	j	1	HKQAVQCLKGPGQVARLVLERRVPRSTQQC
1	1	1		I		PSANDSMGDERTAVSLVTALPGRPSSCVSVT
	1	1	1	1		DGPKF*SSN*KRIANGLGFSFVQMEKESCSHL
		1		İ		KSDLVRIKRLFPGHPAEENGAIAAGDIILGRE
	1		1			WEGPRKASSSRCRGSWAMQLSVQAGPSFAS
	1	ł	1	ł	ŀ	YYPAAVEVLHLLRGAPQEVTLLLCRPPPGAL
		1			1	PELEQEWQTPELSADKEFTRATCTDSCTSPIL
	1	İ				GSRGQLGGTVPPQMQGKAWGLRPESSQKAIR
ļ		1	1			EGTMGAKTERDLGPVP
647	1997	TA T	4854	1044	335	PRVRGDWPLEKKKSNSNIHPIFSWCGSTDSKD

SEQ ID	SEQID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ı	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
i i				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	sequence	/=possible nucleotide deletion, \=possible
				sequence	1	nucleotide insertion
		$\vdash$	+	55425.65	<del> </del>	IVMPTYDLTDSVLETMGRVSLDMMSVQANT
ĺ	ĺ	Ì	1	Ì	į	GPPWESKNSTAVWRGRDSRKERLELVKLSRK
1		1	1	!		HPELIDAAFTNFFFFKHDENLYGPIVKHISFFD
	1	1	ł	i		FFKHKYQINIDGTVAAYRLPYLLVGDSVVLK
j	1		1	l	1	QDSIYYEHFYNELQPWKHYIPVKSNLSDLLEK
		j		j	j	LKWAKDHDEEAKKIAKAGQEFARNNLMGD
	1	1	İ	Ì	]	DIFCYYFQTFPRNMPIYK
648	1998	A	4867	2030	837	
		1	1.00	2030	1 657	AGMLPAVGSADEEEDPAEEDCPELVPMETTQ
l		1				SEEEEKSGLGAKIPVTIITGYLGAGKTTLLNYI
	İ	Ī				LTEQHSKRVAVILNEFGEGSALEKSLAVSQG
l	1		1		ŀ	GELYEEWLELRNGCLCCSVKDNGLRAIENLM
l		į.				QKKGKFDYILLETTGLADPGAVASMFWVDA
l						ELGSDIYLDGIITIVDSKYGLKHLAEEKPDGLI
		İ				NEATRQVALADAILINKTDLVPEEDVKKLRT
	1					TIRSINGLEQUILETQRSRVDLSNVLDLHAFDSL
		1	1 .			SGISLQKKLQHVPGTQPHLDQSIVTITFDVPG
						NAKEEHLNMFIQNLLWEKNVRNKDNHCMEV
	1		1 .			IRLKGLVSIKDKSQQVIVQGVHELYDLEETPV
		1				SWKDDTERTNRLVLLGRNLDKDILKQLFIAT
649	1999	A	4873	226	189	VTETEKQWTTHFKEDQVCT
		1.	10/3	220	107	DGVSLLLPKLGVQWAQYWAHWQPPLPGFKR
						FSCLSLRSSWD*KCAPPHPAFVFLVEMGFHRV
						GQAGLELRTSGDPPASASQSAGITGVSHLA*P
650	2000	A	4874	2	437	TSMPLLPFQRLCVYI
	1	1	1 40/4	-	437	FFFLRRSFAFVAQAGVQWCDLGSPQPLPPGF
:		ł				K*FSCLSLPSSWDYRHAPPPCPS*FLYF**RQG
						FTMLARLVLNS*PHDLPTSPSQSAEIKGVSHR
	i		1			CPASFYLFLKYYLEAKFCA*GECAPSAGVGA GYKRGHKSCLLINCVVQI
651	2001	A	4898	1701	771	DANGETTI ARIANDOSTUDBONA DEL CASTO
			1020	.,,,	′′′	DAWGPETRLARILNPDSFIEPRPGRLPELEATR
						PHMEPKASCPAAAPLMERKFHVLVGVTGSV
• •						AALKLPLLVSKLLDIPGLEVAVVTTERAKHFY SPQDIPVTLYSDADEWEMWKSRSDPVLHIDL
						DDMADI I I VADI DANTI CENAROSONA A TO
						RRWADLLLVAPLDANTLGKVASGICDNLLTC VMRAWDRSKPLLFCPAMNTAMWEHPITAQQ
	1		1			VDQLKAFGYVEIPCVAKKLVCGDEGLGAMA
			1 1			EVGTIVDKVKEVLFQHSGFQQS*PGISVMGVP
				1		LYSEWVQAKSVKMDVGKIGGYPHLLNGGPA
				l	l	LSLPRGQACSRLNWTEGPGLSFFQPGEAAA
652	2002	A	4927	1	611	FRGRQTSRPARGFSPWRPPGTMQEPSSGECPA
			-	-		SP*I PCASNRI AEGGI IEDGADI ADADADEDE
				ļ		SP*LPCASNRLAFGGLIFPCAPLVPYPAPFSPLL PAFSCAPRPRAHTHSRTHPSAPLVPKPSSRAR
						GQSPIPSRASSPSCSWAQVPGVALARCAGVC
				1	- 1	KPGDSWRVAACISGRCCSRGRRRGSGPRNPE
					l	QSFRGAWGPSFWGSWKSQRELSAGGAQAWP
				İ	J	LLGSAGSGLRGEA
653	2003	A	4965	2	283	FFFFI*DGVSLCHPGWNAVARSWLTATSASR
				-		VOAVOCEDI DOGULIVE INTERNATIONALIA
.					1	VQAVSCFRLPSSWDYRHATMPG*FF*YF**R
654	2004	A	4968	3 ,	437	WGFTH_AILVLNS*PQVICPPWPPKVLTLQA
			""	• '		RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGD
1					]	IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW
					ļ	DPERDPGCRVQVSRGPRFGEQKTPGLQGCLP
	ĺ			- 1	ł	PPCLTHLAAASCVVVWCGRWKRDSAECQCD
655	2005	A	4983	201	397	HSCSAVSQQEDRCRSSSCS
		••	1703	201	J71	MNNNTTCIQPSMISSMALPIIYILLCIVGVFGN
656	2006	Ā	4988	332	150	TLSQWIFLTKIGKKTSTHIYLSHLVTANLLVC
		"	+700	332	159	LVHKDMYREFFEEEAQASNKHVTRCLTSLVI
657	2007	В	5008	120	165	REVHIKTMR*HFLPIRLEKNKNNIKD
001	2001	ا م	2000	129	465	MAGMKTASGDYIDSSWELRVFVGEEDPEAES

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NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	uou	in in	mucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	uence	(	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	dence	l	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	İ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	İ	l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i	1				Seducince	/=possible nucleotide deletion, \=possible
	Ì	i	l'	peptide	1	nucleotide insertion
		ļ	ļ	sequence		VTLRVTGESHIGGVLLKIVEQINRKQDWSDH
	1	1				AIWWEQKRQWLLQTHWTLDKYGILADARLF
ļ		1				FGPQHRPVILRLPNRRALRLX*
	0000	<del>  </del>	5016		292	FFFFKETESHSVTQAGVQWHDLGSLQPPPPGF
658	2008	A	5017	1	192	KRFSCLSLLSSWDYRCAPPHPANFVFLVETGF
		1				HHVAQAGLKLLTL*SANLGLSTSLPIPLFILLS
		<del> </del>		1.5	330	RGHGGKSLTGGTPGNWGDGLLVSEDWSHLIF
659	2009	Α	5018	17	338	T*NSLVSPVLGKWSPCLQGPGLSAVHTWPWL
İ		i	1		1	1 T 1
		J			ļ	MAACWAVHVKTHMRPGLAVLPRLVLNSWS
						*AILLWPPKALGLQA
660	2010	Α	5028	2	310	SRVDDFVGERRGGCDECLCGHRGLRAVPLG
l	1	}				HPGHLCLQPPGGPA*FLDYCRGCCPHPVPGST
1	1		İ		ì	AGSCPROKKTTPGPTVLCVCSFWIYQRGEPH
	<u> </u>		L		<u> </u>	HRTGARWNH
661	2011	A	5050	752	431	RQSCSSTQAKVQWFHYGPLQSQPPGLKQSSQ
	1				[	LSLPNSRDHRHVPPRLAIFSFAETGSPYFAQAS
ļ	}	1			j	LELLGSSHPPTSASQSARITGVSHRAWPLK*F
	J	1		<u> </u>		NLNQYQTLTMN
662	2012	Α	5054	48	103	ELNNGPFQMPLCNGGNLAVTGSWADRSPLH
1	1			1	1	EAASQGRLLALRTLLSQGYNVNAVTLDHVTP
			1	1	1	LHEACLGDHVACARTLLEAGANVNAITIDGV
Í	1	1	1	1	1	TPLFNACSQGSPSCAELLLEYGAQAQLESCLP
1	1	1			i	SPTHEGASKGHHECLDILISWGIDVDQEIPHSG
		1	1			TPLYVACMAQQFHCIWNLIYAGAGVRKGKY
1		1		1	l	WDTPLPGAGHQSTQKLE*LFAMVEIWQ
663	2013	Α	5066	951	580	VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK
İ		1			1	ADLPEGVAVSGPSPAEFCRKHRLPAPVPFSCA
		l .	ł			GPAEPSTTIFTQLATMAAFPHLVHAELHPSSF
ľ	1					WLRGLLGVYGAAVAAVLSFSLYRVLVKSQ
664	2014	Α	5071	550	1	LSFIEVLSMEQVNKTVYREFVVLGFSSLARLQ
1		1	1			QLLFVIFLLYLFTLGTNAIIISTIVLDRALHTP
	i	1	1	]		MYFFLAILSCSEICYTFVIVPKMLVDLLSQKK
1	1	1.				TISFLGCAIQMFSFLFFGSSHSFLLAAMGYDR
	1		1			YMAICNPLRYSVLMGHGVCMGLMAAAWAC
}		l				GFTVSLVTTSLVFHLPFHSSNQHE
665	2015	A	5074	496	692	QQYHNTGSAGHHAHCQVGHSPHVHYPSGCG
	Į.		1			PL*IQRGLPSFNSLEGHSLKDSGHEESVQLDSE
	1					HDVQRSLYCDTAVNDVLNTSVTSMGSQMPD
		1	1		1	HDQNEGFHCREECRILGHSDRCWMPRNPMPI
	1	]			ŀ	RSKSPEHVRNIIALSIEATAADVEAYDDCGPT
1	1	ł		l	1	KRTFATFGKDVSDHPAEERPTLKGKRTVDVT
		1			1	ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL
İ	·			1		PTKPSVSYEIVDPGITARRC
666	2016	A	5080	408	248	IMLLSTSS*VYFQSSTKDSHFFLFDFQKTGPPL
1		1		1	1	VGPKAQLSGLQLQPCLYKRR
667	2017	A	5081	129	247	DLTNSHFFLFDFQKTGPPLGGPKAQFSSLQLQ
1 ***		1		1	1	PCVY*RR
668	2018	A	5086	852	233	NIKSNDRWVQIKTAYKYFF*KNGDNYNWVF
***	1 2010	1.	1 300		1	RALPTTFADIENLKYLLFTRDASQPFYLGHTV
1	1			1	1	IFGDLEYVTVEGGIVLSRELMKRLNRLLDNSE
			1	1	1	TCADOSVIWKLSEDKQLAICLKYAGVHAENA
1	1	1	į	1	1	EDYEGRDVFNTKPIAQLIEEALSNNPQQVVEG
	1	1		j		CCSDMAJTFNGLTPQKMEVMMYGLYRLRAF
	1	1		1	1	GHYFNDTLVFLPPVGSEND
669	2019	A	5101	+1	329	PGRPTRPPLLTLLAHVSPEPAGPSCDSLAOPG
009	2019	A	10101	1.	323	ASGV*VOHDSHPPLLCGSQCLSEPVPGSHGPP
		1	1	1		RGCOHEAAPCPRGPGSDGLHHASAACASLPP
1	1	1				SPILPVLLPELGPL
COD	7000	<del>                                     </del>	2100	-	547	DAWGNRCAVGAAPRLIHLHLCCTPADPSRKP
670	2020	A	5102	3	J41	DATIONACA TORAL ADILIDIDOCTI ADI BARI

	1 050 10		- 484			
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	}	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ŀ		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł		peptide	1	/=possible nucleotide deletion, \=possible
			L	sequence	İ	nucleotide insertion
					!	DEL*NMNGRVDYLVTEERINLTRGPSGLCFNT
	1		1	1		VGGTDQQYVSNDSGIYVSRIKENGAAALDGR
		ł	ł			LQEGDKILSVNGQDLKNLLHQDAVDLFRNA
		1	İ			GYAVSLRVQHRLQVQNGPIGHRGEGDPSGIPI
		1				FMVLVPVFALTMVAAWAFMRYRQQL
671	2021	A	5105	672	400	RDGREELCLQQEPTLPSRICSSAPLLYFLFICPF
				***	'''	VLLLLLISLLCLYWKARKLSTLRSNTRKEKA
		!				LWVDLKEAGGVTTNRMED*EEDECN
672	2022	A	5148	72	314	
0,2	2022	1.	3140	'2	314	IIYFSYNIFLKITELLNDVERLKQALNGLSQLT
	1	ľ	1	Ì		YTSGNPTKRQSQLIDTLQHQVKSLEQQLAVS
673	2023	A	5152	210	225	NQAHGALQEYVLAPCS
0/3	2023	A	3132	210	335	REILCSRIGRLNIV*MSLFPNLTCRLNAIPIKIPA
674	0004	ļ.,	51.50			NHFVEVT
0/4	2024	Α.	5153	3	2953	LTEDQPFDILQKSLQEANITEQTLAEEAYLDA
						SIGSSQQFAQAQLHPSSSASFTQASNVSNYSG
	ł					QTLQPIGVTHVPVGASFASNTVGVQHGFMQH
						VGISVPSQHLSNSSQISGSGQIQLIGSFGNHPS
						MMTINNLDGSQIILKGSGQQAPSNVSGGLLV
						HRQTPNGNSLFGNSSSSPVAQPVTVPFNSTNF
	ļ '					QTSLPVHNIIIQRGLAPNSNKVPINIQPKPIQM
						GQQNTYNVNNLGIQQHHVQQGISFASASSPQ
			}	·		GSVVGPHMSVNIVNQQNTRKPVTSQAVSSTG
						GSIVIHSPMGQPHAPQSQFLIPTSLSVSSNSVH
						HVQTINGQLLQTQPSQLISGQVASEHVMLNR
						NSSNMLRTNQPYTGPMLNNQNTAVHLVSGO
	İ		l i			TFAASGSPVIANHASPQLVGGQMPLQQASPT
						VLHLSPGQSSVSQGRPGFATMPSVTSMSGPSR
	١٠					FPAVSSASTAHPSLGSAVQSGSSGSNFTGDOL
	1					TQPNRTPVPVSVSHRLPVSSSKSTSTFSNTPGT
			'			GTQQQFFCQAQKKCLNQTSPISAPKTTDGLR
						QAQIPGLLSTTLPGQDSGSKVISASLGTAQPQ
						QEKVVGSSPGHPAVQVESHSGGQKRPAAKQ
	ļ					LTKGAFILQQLQRDQAHTVTPDKSHFRSLSD
						AVQRLLSYHVCQGSMPTEEDLRKVDNEFETV
						ATQLLKRTQAMLNKYRCLLLEDAMRINPPAE
						MVMIDRMFNQEERASLSRDKRLALVDPEGFO
						ADFCCSFKLDKAAHETQFGRSDQHGSKASSS
-						LQPPAKAQGRDRAKTGVTEPMNHDOFHLVP
						NHIVVSAEGNISKKTECLGRALKFDKVGLVO
		' I				YQSTSEEKASRREPLKASQCSPGPEGHRKTSS
						RSDHGTESKLSSILADSHLEMTCNNSFQDKSL
						RNSPKNEVLHTDIMKGSGEPQPDLQLTKSLET
				ĺ	l	TFKNILELKKAGRQPQSDPTVSGSVELDFPNF
				Í		SPMASQENCLEKFIPDHSEGVVETDSILEAAV
75.5		· ·				NSILEC
675	2025	A	5154	599	1880	LKKMEPFSCDTFVALPPATVDNRIIFGKNSDR
					i	LYDEVQEVVYFPAVVHDNLGERLKCTYIEID
						QVPETYAVVLSRPAWLWGAEMGANEHGVCI
				.		GNEAVWGREEVCDEEALLGMDLVRLGLERA
						DTAEKALNVIVDLLEKYGQGGNCTEGRMVF
-					l	SYHNSFLIADRNEAWILETAGKYWAAEKVQE
(				.	ſ	GVRNISNQLSITTKIAREHPDMRNYAKRKGW
		,			ļ	WDGKKEFDFAAAYSYLDTAKMMTSSGRYCE
						GYKLLNKHKGNITFETMMEILRDKPSGINME
						GEFLTTASMVFILPQDSSLPCIHFFTGTPDPER
1						SVFKPFIFVPHISQLLDTSSPTFELEDLVKKKS
					j	HFKPDRRHPLYQKHQQALEVVNNNEEKAKI
						ALDER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
						MLDNMRKLEKELFREMESILQNKHLDVEKIV NLFPQCTKDEIQIYQSNLSVKVSS

SEQ ID NO: of nucl- cotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence		09/496 914	correspondi ng to first amino acid residue of peptide sequence	to last amino acid residue of peptide sequence	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
676	2026	A	5155	2	306	FFFLRRSLALSPRPDCGLQWRNLGSLQAPPPG FTPFSCLSLPSSWDYRRPPPRPANFLYF**RRG FTLLARMVSIS*PHDPPASASQSAGITGVSHRA RPT
677	2027	A	5167	97	740	FFHSVDLLALEQSKTFYKPDWFDIVESEVKCC KEAVCVIDMSSFTEFEITSTGDQALEVLQYLF SNDLDVPVGHIVHTGMLNEGGGYENDCSIAR LNKRSFFMISPTDQQVHCWAWLKKIMPKDS NLLLEDVTWKYTALNLIGPRAVDVLSELSYA PMTPDHFPSLFCKEMSVGYANGIRVMSMTHT GEPGFMLYIPIEYRWGFTMLSTLVSNS
678	2028	A	5183	1919	2018	PALCRLRDDMTVCVADFGLSKKIYSGDYYRQ GRIAKMPVKWIAIESLADRVYTSKSDVWAFG VTMWEIATRGMTPYPGVQNHEMYDYLLHG HRLKQPEDCLDELCKI**SPQSP
679	2029	A	5190	39	499	RESQVKHFKMRKIDLCLSSEGSEVILATSSDE KHPPENIIDGNPETFWTTTGMFPQEFIICFHKH VRIERLVIQSYFVQTLKIEKSTSKEPVDFEQWI EKDLVHTEGQLQNEEIVAHDGSATYLRFIIVS AFDHFASVHSVSAEGTVVSNLSS
680	2030	A	5204	541	92	EILAVLKLACGDISLNALALMVATAVLTLAPL LLICLSYLFILSAILRVPSAAGRCKAFSTCSAH RTVVVVFYGTISFMYFKPKAKDPNVDKTVAL FYGVVTPSLNPIIYSLRNAEVKAAVLTLLRGG LLSRKASHCYCCPLPLSAGIG
681	2031	A	5207	10	247	VPDNGDVTKLPVCSTLVEETSLTVSEAMEQSI KNESPLPGTLAHTCNTSTLGGRGRWIT*GREF DTSMANMVKPCLYRK
682	2032	A	5210	2	231	FFFETESYSITQAGVQWPNLSSLKTLPPGFK*F SCLSLPSSWDYRCLPPCPANFCIFSRNGVLPC WPGWSRTPDLS
683	2033	A	5218	85	402	CPSVSGLIKSDLRRHNINIGITNVDVKAVSNIF MIILLRSMYRINVKPYFFI*LFFSRVNC*SVIIG YARCYTFLIF*LFL*IPADSPTDQEPKTVMLSK QSESAI
684	2034	A	5220	1	194	NLMKEMQNLNSENHKTWEEYKDTK*IMSYF YG*ALNVIKMAVLPKLMYRFSATLVKIPQHL TDS
685	2035	A	5228	260	440	LHSQDGNSDPRKPQGEMSAHAFPVQTCGEED QKKTPQVPINFTELSKCS*S*KIMSGERE
686	2036	A	5239	79	508	GGEAAARAAKLSSPRPHRVGRRERGVGGMS AFSEAALEKKLSELSNSQQSVQTLSLWLIHHR KHSRPIVTVWERELRKAKPNRKLTFLYLAND VIQNSKRKGPEFTKDFAPVIVEAFKHVSSETD ESCKKHLGRVLSIWEERS
687	2037	A	5244	1	428	MAAVVAATALKGRGARNARVLRGILAGATA NKASHNRTRALQSHSSPEGKEEPEPLSPELEYI PRKRGKNPMKAVGLAWAIGFPCGILLFILTKR EVDKDRVKQMKARQNMRLSNTGEYESQRFR ASSQSAPSPDVGSGVQT
688	2038	A	5249	1	1407	LQQTEDKSLLNQGSSSEEVAGSSQKMGQPGP SGDSDLATALHRLSLRRQNYLSEKQFFAEEW QRKIQVLADQKEGVSGCVIPTESLASLCTTQS EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY HWQQLAQPNLGTILDPRPGVITKGFTQLPGD AIYHISDLEEDEEEGITFQVQQPLEVEEKLSTS KPVTGIFLPPITSAGGPVTVATANPGKCLSCT NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS GSSSSNTAVNSPALAYRLSIGESITNRRDSTTT

SEQ I	D   SEQ ID	Met	SEQ	Predicted	Predicted end	Amino celd
NO: o					nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence		09/496	correspondi		M=Methionine, N=Asparagine, P=Proline,
uence		i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
[			ĺ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
İ	- {	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		1		peptide	•	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
ļ	1				Ţ	FSSTMSLAKLLQERGISAKVYHSPISENPLQPL
1	Í		1	1	1	PKSLAIPSTPPNSPSHSPCPSPLPFEPRVHLSEN
			· ·			FLASRPAETFLQEMYGLRPSRNPPDVGQLKM
		}			i	NLVDRLKRLGIARVVKNPGAQENGRCQEAEI
			1			GPQKPDSAVYLNSGSSLLGGLRRNQSLPVIM
600		<del> </del>			<u>.l.</u>	GSFAAPVCTSSPKMGVLKED
689	2039	A	5254	2	2621	LSLFGSRALGRSGARAMAKAKKVGARRKAS
,	ł	}		J	]	GAPAGARGGPAKANSNPFEVKVNRQKFQILG
				l		RKTRHDVGLPGVSRARALRKRTQTLLKEYKE
		i			1	RDKSNVFRDKRFGEYNSNMSPEEKMMKRFA
1	1 .	1		l		LEQQRHHEKKSIYNLNEDEELTHYGOSLADIE
}		1		ĺ		KHNDIVDSDSDAEDRGTLSGELTAAHFGGGG
4						GLLHKKTQQEGEEREKPKSRKELIERLIAKSK
i	1	1				QEKRERQAQREDALELTEKLDODWKEIOTLI
1	-	1	1	1.	ļ	SHKTPKSENRDKKEKPKPDAYDMMVRELGE
1			1.	i		EMKAQPSNRMKTEAELAKEEOEHLRKLEAE
						RLRRMLGKDEDENVKKPKHMSADDLNDGFV
		1	1		i	LDKDDRRLLSYKDGKMNVEEDVQEEQSKEA
1	1	l	1	ľ	ļ	SDPESNEEEGDSSGGEDTEESDSPDSHLDLES
1		2				NVESEEENEKPAKEQRQTPGKGLISGKERAG
		l	1 !			KATRDELPYTFAAPESYEELRSLLLGRSMEEQ
		i				LLVVERIQKCNHPSLAEGNKAKLEKLFGFLLE
1		ł	1 1			YVGDLATDDPPDLTVIDKLVVHLYHLCQMFP
1	1	l				ESASDAIKFYLRDAMHEMEEMIETKGRAALP
						GLDVLIYLKITGLLFPTSDFWHPVVTPALVCL
1	1		1			SQLLTKCPILSLQDVVKGLFVCCLFLEYVALS QRFIPELINFLLGILYIATPNKASQGSTLVHPFR
	i		1 1			ALGKNSELLVVSAREDVATWQQSSLSLRWA
}		!	1	1		SRLRAPTSTEANHIRLSCLAVGLALLKRCVLM
		}				YGSLPSFHAIMGPLRALLTDHLADCSHPQELQ
		i .	1 1	i		ELCOSTLTEMESQKQLCRPLTCEKSKPVPLKL
	i .		1			FTPRLVKVLEFGRKQGSSKEEQERKRLIHKHK
	1		] ]	1		REFKGAVREIRKDNQFLARMQLSEIMERDAE
690	10010					RKRKVKQLFNSLATQEGEWKALKRKKFKK
090	2040	A	5261	1 .	304	FFFFVFLVETGFHHVGQAGLELLTSGDPPTW
l	1		łł			ASQSAGITGVSHCSWPVIYVLSTLLHAVRNVI
					j	FKRTFPLKSSSFLSYDKEIFPILIVLKFYLVTLT
691	2041					SFVK
1 051	2041	A	5270	3	158	NCHTTHCTANWVIILPGTPPGWKIDGPAAAL
692	2042		5000			EVLSSFFFFFLKFSYKPONIV
1	2042	A	5282	56	1268	GMEPVGCCGECRGSSVDPRSTFVLSNLAEVV
1	)					ERVLTFLPAKALLRVACVCRLWRECVRRVLR
					ſ	THRSVTWISAGLAEAGHLEGHCLVRVVAREL
	1			- 1	ł	ENVRILPHTVLYMADSETFISLEECRGHKRAR
		.	'	l	ļ	KRTSMETALALEKLFPKQCQVLGIVTPGIVVT
l				1		PMGSGSNRPQEIEIGESGFALLFPOIEGIK IOPF
				1	f	HFIKDPKNLTLERHQLTEVGLLDNPELRVVLV
	1 1	İ		1	1	FGYNCCKVGASNYLQQVVSTFSDMNIILAGG
				ŀ		QVDNLSSLTSEKNPLDIDASGVVGLSFSGHRI
		J		į	İ	QSATVLLNEDVSDEKTAEAAMQRLKAANIPE
		l		ſ	İ	HNTIGFMFACVGRGFQYYRAKGNVEADAFR
		1	1	}		KFFPSVPLFGFFGNGEIGCDRIVTGNFILRKCN
693	2043	A	5301	362	507	EVKDDDLFHSYTTIMALIHLGSSK
					501	EEIKERFGPGLVIYWYGFIQELDCNRERGILLK
694	2044	A	5310	<del></del>	204	ACFPINIVILCHSIA
				- 1		RVLTAINHTLKENLRKFYKGKKDKPLDLRPK
		1		1	1	KTRAMRRRLNMHEENLKTKKQHRKERLYPL RKYAAKA
695	2045	Ā	5315	125		
	<u>-</u>					ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	[	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine. K=Lysine, L=Leucine.
cotide	seq-	ļ	USSN	location	corresponding	
seq-	uence		09/496 914	correspondi ng to first	to last amino acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	}	į		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide	Sednettce	/=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
<b>!</b>	-			Sequence		TGSGKEEGPAPCKQMKLEAAGGPSALNFDSP
	İ					SSLFESLISPIKTETFFKEFWEQKPLLIQRDDPA
						LATYYGSLFKLTDLKSLCSRGMYYGRDVNV
ŀ						CRCVNGKKKVLNKDGKAHFLOLRKDFDOKR
						ATIOFHOPORFKDELWRIOEKLECYFGSLVGS
						NVYITPAGSOGLPPHYDDVEVFILOLEGEKH
						WRLYHPTVPLAREYSVEAEERIGRPVHEFML
[	1		i			KPGDLLYFPRGTIHQADTPAGLAHSTHVTIST
1	ļ					YONNSWGDFLLDTISGLVFDTAKEDVELRTG
						IPROLLLOVESTTVATRRLSGFLRTLADRLEG
	Ì					TKELLSSDMKKDFIMHRLPPYSAGDGAELSTP
						GGKLPRLDSVVRLQFKDHIVLTVLPDQDQSD
l .	1			}		ETQEKMVYIYHSLKNSRETHMMGNEEETEFH
						GLRFPLSHLDALKQIWNSPAISVKDLKLTTDE
	·					EKESLVLSLWTECLIQVV
696	2046	A	5318	1476	742	LMKXYLEAAELGEISDIHTKLLRLSSSQGTIET
l .	}	ł				SLQDIDSRLSPGGSLADAWAHQEGTHPKDRN
j	] .				]	VEKLQVLLNCMTEIYYQFKKDKAERRLAYN
						EEQIHKFDKQKLYYHATKAMTHFTDECVKK
İ						YEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDI
ł	1					EEEVSKYQEYTNELQETLPQKMFTASSGIKHT
1						MTPIYPSSNTLVEMTLGMKKLKEEMEGVVKE
						LAENNHILESGGSLTMDGGLRNVDCL
697	2047	A	5320	244	478	LDYNFFLFEMTFGLVSQAGVQWHDLGSLQPP
1	ł					PPGFKQFSCLSLPSSWDYRHLPPHLANFSREG
698	2048	A	5324	266	714	VSPSWPGWSRTPDFR LPIRKSLRSVRSGFPTSQSPITRNLDGTASGSC
098	2040	Α	J324	200	/14	LAKTVTGSLFRINVGLRGLVAGGIIGALLGTP
j	1	1				VGGLLMAFQKYSGETVQERKQKDRKALHEL
i						KLEEWKGRLQVTEHLPEKIESSLQEDEPENDA
ŀ						KKIEALLNLPRNPSVIDKQDKD
699	2049	A	5334	699	277	RPHGHLVCISSSAGLSGVNGLADYCASKFAA
				***		FGFAESVFVETFVQKQKGIKTTIVCPFPIKTGM
1					İ	FEGCTTGCPSLLPILEPKYAVEKIVEAILQEKM
						YLYMPKLLYFMMFLKSFLPLKTGLLIADYLGI
	1					LHAMDGFADQKK
700	2050	A	5344	3	614	PTAEEMSSLTPESSPELAKRSWFGNFISLDKEE
						QIFLVLKDKPLSSIKADIVHAFLSIPSLSHSVLS
<b>!</b>						QTSFRAEYKASGGPSVFQKPVRFQVDISSSEG
		l				PEPSPRRDGSGGGGIYSVTFTLISGPSRRFKRV
	l	İ				VETIQAQLLSTHDQPSVQALADEKNGAQTRP
1	1					AGAPPRSLQPPPGRPDPELSSSPRRGPPKDKK
		L				LLATNGTPL
701	2051	Α	5346	3	1383	HASVLFCRVMAASKTQGAVARMQEDRDGSC
1		l ·				STVGGVGYGDSKDCILEPLSLPESPGGTTTLE
						GSPSVPCIFCEEHFPVAEQDKLLKHMITEHKIV
	[		,	ł		IADVKLVADFQRYILYWRKRFTEQPITDFCSV
1				1		IRINSTAPFEEQENYFLLCDVLPEDRILREELQ
1		}		1		KQRLREILEQQQQERNDTNFHGVCMFCNEEF
	1					LGNRSVILNHMAREHAFNIGLPDNIVNCNEFL
1						CTLQKKLDNLQCLYCEKTFRDKNTLKDHMR
1	1	1				KKQHRKINPKNREYDRFYVINYLELGKSWEE
		1				VQLEDDRELLDHQEDDWSDWEEHPASAVCL
						FCEKQAETIEKLYVHMEDAHEFDLLKIKSELG
1						LNFYQQVKLVNFIRRQVHQCRCYGCHVKFKS
ľ	1	ŀ				KADLRTHMEETKHTSLLPDRKTWDQLEYYFP
						TYENDTILLWTLSDSESDLTAQEQNENVPIISE DTSKLYALKQSSILNQLLL
702	2052	A	5356	2502	1540	MAAATRGCRPWGSLLGLLGLVSAAAAAWD
L / 42	1 2002	14	3330	2502	1 10 70	INTERNATIONAL INCOMPORTATION ASSAURANTAIN

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E-Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Scrine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LASLRCTLGAFCECDFRPDLPGLECDLACHL AGQHLAKALVVKALKAFVRDPAPTKPLVLSL HGWTGTGKSYVSSLLAHYLFQGGLRSPRVH HFSPVLHFPHPSHERYKKDLKSWVQGNLTA CGRSLFLFDEMDKMPPGLMEVLRPFLGSSWV VYGTNYRKAIFIFISNTGGEQINQVALEAWRS RRDREBILLQELEPVISRAVLDNPHHGFSNSGI
		İ				MEERLLDAVVPFLPLQRIIIIVRHCVLNELAQL GLEPRDEVVQAVLDSTTFFPEDEQLFSSNGCK
703	2053	A	5380	278	657	TVASRIAFFL  LFLQKLRMKTBEEARTHTEIEMFLRKEQQKL EERLEFWMEKYDKDTEMKQNELNALKATKA SDLAHLQDLAKMIREYEQVIIEDRIEKERSKK KVKQDLLELKSVIKLQAWWRGTMIRREIGGF KM
704	2054	A	5381	1	1003	FRGRAVKMAAVVEVEVGGGAAGERELDEV DMSDLSPEEQWRVEHARMHAKHRGHEAMH AEMVLILIATLVVAQLLLVQWKQRHPRSYN MVTLFQMWVVPLYFTVKLHWWRFLVIWILF SAVTAFVTFRATRKPLVQTTPRLVYKWFLLIY KISYATGIVGYMAVMFTLFGLNLLFKIKPEDA MDFGISLLFYGLYYGVLERDFAEMCADYMA STIGFYSESGMPTKHLSDSVCAVCGQQIFVDV SEEGIIENTYRLSCNHVFHEFCIRGWCIVGKK QTCPYCKEKVDLKRMFSNPWERPHVMYGQL LDWLRYLVAWQPVIIGVVQGINYILGLE
705	2055	A	5396	3	675	TYDROPLQLATRAGOPLDINMAGEPKPYRPKP GNKRPLSALYRLESKEPFLSVGGYVFDYDYY RDDFYNRLFDYHGRVPPPPRAVIPLKRPRVA VTTTRRGKGVFSMKGGSRSTASGSTGSKLKS DELQTIKKELTQIKTKIDSVLGRLDKIEKQQK AEAEAQKKLLEESLVLIQEECVSEIADHSTEEP AEGGPDADGEEMTDGIEEAFDEDGGHELFLQ IK
706	2056	A	5410	2	98	GRVGLNLEGRGCSEPKWRHCTPTWATEQDSI S
707	2057	A	5415	6	287	PFKLTPSFLSHAFSSGQERKVFIELNHIKKCNT VRGVFVLEEFGNYTILLLGLDSHGSNSNLGAP
708	2058	A	5423	3	291	EEGLGAGRKRTSVEKSGGAGVTRKKRDP SSSNPLGSPSTLWKLCSFPVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTTEVTVTLTABSTASILVSVERBETJOVE
709	2059	A	5424	679	347	GCTIFKTVTLTARSTASLLKSVRPRTHQKE RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK
710	2060	A	5442	1073	559	GESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPTIPSSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ
711	2061	A	5449	1	319	GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD LYRDIPELQGF
712	2062	A	5499	91	749	RPTPGHGDFWMQPLTKDAGMSLSSVTLASAL QVRGEALSEEEIWSLLFLAAEQLLEDLRNDSS DYVVCPWSALLSAAGSLSFQGRVSHIEAAPF

						· · · · · · · · · · · · · · · · · · ·
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence .	ł	İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1	•	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ĺ	1		peptide		/=possible nucleotide deletion, \=possible
	· ·	1		sequence		nucleotide insertion
						KAPELLQGQSEDEQPDASQMHVYSLGMTLY
	1	ľ			1	WSAGFHVPPHQPLQLCEPLHSILLTMCEDQPH
						RRCTLQSVLEACRVHEKEVSVYPAPAGLHIR
					1	RLVGLVLGTISEVSREPCFSSSSCWSCVAIKI
713	2063	A	5506	22	478	VEELILVSRLDPHLHTPMYFFLAHLSFLDLSFT
	1	1	1	]		TSSIPQLLYNLNGCDKTISYMGCAIQLFLFLGL
		Į	1			GGVECLLLAVMAYDRCVAICKPLHYMVIMN
	l	İ	1		ľ	PRLCRGLVSVTWGCGVANSLAMSPVTLRLPR
	İ			ļ	1	CGHHEVDHFLCEMPALIRMACISTV
714	2064	A	5514	25	220	AIRPYWCENNIIGIGKLSTADGKAFADPEVLR
/ 14	2004	^	3314	23	1 220	RLTSSVSCALDEAAAALTRMRAESTANAGQS
	1	l	1	1	1	DK
71.5	2055	<del>  </del>		<del> </del>	010	
715	2065	Α	5526	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAM
	!		1	[	1	GRTALFHHSGGSSGYESLRRDSEATGSASSAP
)	j .	]	ļ	j	ļ	DSMSESGAASPGARTRSLKSPKKRATGLQRR
		1		l .	l	RLIPAPLPDTTALGRKPSLPGQWVDLPPPLAG
	1	1		1		SLKEPFEIKVYEIDDVERLQRPRPTPREAPTQG
						LACVSTRLRLAERRQQRLREVQAKHKHLCEE
1						LAETQGRLMLEPGRWLEQFEVDPELEPESAE
ĺ	ł	i	ł	i	1	YLAALERATAALEQCVNLCKAHVMMVTCFD
1	ł	}			1	ISVAASAAIPGPQEVDV
716	2066	A	5529	458	790	SPGYGENKFTVTSXNIAVPLCEMNKIYSYYSD
	1					SSSSERTMDLVLEMCNTNSIHWCGISGRQLG
		i				KLHPSSSLCLALTLLSSVQGLQSISGLRLTDTF
			1		1	LKRTYEYDDIAQVCV
717	2067	A	5531	3	460	NSEDLLKYFNPESWOEDLDNMYLDTPRYRG
' ' '			1 222.	-		RSYHDRKSKVDLDRLNDDAKRYSCTPRNYS
1	į	1	į			VNIRBELKLANVVFFPRCLLVQRCGGNCGCG
ŀ						TVNWRSCTCNSGKTVKKYHEVLOFEPGHIKR
ł	1	1	1	l		RGRAKTMALVDIQLDHHERCDCICSSRPPR
718	2068	A	5586	311	88	AVLKNMAPMTALGLLDLHILNLILFLSAGEDF
/10	2008	Ι^	3300	311	00	TSVVSEIMMYILLVFLTLWLLIEMIYCYRKVS
L		<u> </u>		<u></u>		KAEEAAQENA
719	2069	A	5598	1	330	KNCANEAVVQKILDRVLSRYDVRLRPNFGSM
f		l		1		LATNSTRGLNEDELMAHGQEKDSSSESEDSC
l	1	i	1		1	PPSPGCSFTEGFSFDLLNPDYVPKVDKWSRFL
L	<u></u>	<u> </u>	<u> </u>	<u></u>	<u> </u>	FPLAFGLFNIVAAERC
720	2070	A	5628	798	148	LPPAQIPEAWLLLANVVVVLILVPLKDRLIDP
<b> </b>	1	1		1	1	LLLRCKLLPSALQKMALGMFFGFTSVIVAGV
l	1	İ	1			LEMERLHYIHHNETVSQQIGEVLYNAAPLSIW
	1		İ			WQIPQYLLIGISEIFASIPGLEFAYSEAPRSMQG
				1	1	AIMGIFFCLSGVGSLLGSSLVALLSLPGGWLH
	]	1	1			CPKDFGNINNCRMDLYFFLLAGIQAVTALLF
			1	1	<u> </u>	VWIAGRYERASQGPASHSRFSRDRG
721	2071	A	5632	146	536	MSALIVRKLRSAELTLFSELPTVLGANVNAA
'	'	1	"""	1	300	KLHETALHHAAKVKNVDLIEMLIEFGGNIYA
ŀ		1				RDNRGKKPSDYTWSSSAPAKCFEYYEKTPLT
l			1		1	LSOLCRVNLRKATGVRGLEKIAKLNIPPRLID
1		]	1	ļ	1	YLSYN
700	2000	<del> </del>	8/20	12	3000	
722	2072	A	5638	3	3806	CPSLDIRSEVAELRQLENCSVVEGHLQILLMF
1			1	1		TATGEDFRGLSFPRLTQVTDYLLLFRVYGLES
1			1	1		LRDLFPNLAVIRGTRLFLGYALVIFEMPHLRD
1			1	1		VALPALGAVLRGAVRVEKNQELCHLSTIDW
			1.	l		GLLQPAPGANHIVGNKLGEECADVCPGVLGA
		1		1		AGEPCAKTTFSGHTDYRCWTSSHCQRVCPCP
			1	1		HGMACTARGECCHTECLGGCSQPEDPRACV
	1	1	1		1	ACRHLYFQGACLWACPPGTYQYESWRCVTA
!						ERCASLHSVPGRASTFGIHQGSCLAQCPSGFT
1	1					RNSSSIFCHKCEGLCPKECKVGTKTIDSIQAA
				<del></del>		

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
иепсе		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1	~ `	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l		peptide	Schactico	/=possible nucleotide deletion, \=possible
]	1	l	1	sequence		nucleotide insertion
	<del> </del>		<del> </del>	SCAUCITO		QDLVGCTHVEGSLILNLRQGYNLEPQLQHSL
ĺ	i	Ì	İ	İ	İ	
					ĺ	GLVETITGFLKIKHSFALVSLGFFKNLKLIRGD
		ł	1	İ		AMVDGNYTLYVLDNQNLQQLGSWVAAGLTI
		1		1	ļ	PVGKIYFAFNPRLCLEHIYRLEEVTGTRGRQN
1			ŀ		1	KAEINPRINGDRAACQTRILRFVSNVTEADRI
1				ŀ		LLRWERYEPLEARDLLSFIVYYKESPFQNATE
1	1		]	ļ		HVGPDACGTQSWNLLDVELPLSRTQEPGVTL
1		i		1		ASLKPWTQYAVFVRAITLTTEEDSPHQGAQS
1		1		ļ	1	PIVYLRTLPAAPTVPQDVISTSNSSSHLLVRW
						KPPTQRNGNLTYYLVLWQRLAEDGDLYLND
· ·		i	1	ŀ		YCHRGLRLPTSNNDPRFDGEDGDPEAEMESD
	1			1		CCPCQHPPPGQVLPPLEAQEASFQKKFENFLH
	1					NAITIPISPWKVTSINKSPORDSGRHRRAAGPL
1	1 .					RLGGNSSDFEIQEDKVPRERAVLSGLRHFTEY
1						RIDIHACNHAAHTVGCSAATFVFARTMPHRE
1						ADGIPGKVAWEASSKNSVLLRWLEPPDPNGL
1		I				ILKYEIKYRRLGEEATVLCVSRLRYAKFGGV
1		!	ļ			HLALLPPGNYSARVRATSLAGNGSWTDSVAF
	1					YILGPEEEDAGGLHVLLTATPVGLTLLIVLAA
						LGFFYGKKRNRTLYASVNPEYFSASDMYVPD
						EWEVPREQISIRELGQGSFGMVYEGLARGLE
1		1				AGEESTPVALKTVNELASPRECIEFLKEASVM
1						KAFKCHHVVRLLGVVSQGQPTLVIMELMTR
						GDLKSHLRSLRPEAENNPGLPQPALGEMIQM
1	}					AGEIADGMAYLAANKFVHRDLAARNCMVSQ
						DFTVKIGDFGMTRDVYETDYYRKGGKGLLP
1						VRWMAPESLKDGIFTTHSDVWSFGVVLWEIV
						TLAEQPYQGLSNEQVLKFVMDGGVLEELEGC
						PLQLQELMSRCWQPNPRLRPSFTHILDSIQEEL
1						RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSP
723	2072		5.550		-	TPRDCSPQNGGPGH
123	2073	A	5672	1	216	LAWIDNILPEKEKKETDKKRKKKGAHEDCD
			·			EEPQFPPPSVIKIPMESVQSDPQNGIHCIARKR
70.4			-5504	72		SSSWSYSL
724	2074	A	5704	4235	940	ARGRRSRPVWAASWGGRGRPAARRRPRGLA
1	1					ATMGFELDRFDGDVDPDLKCALCHKVLEDP
				1		LTTPCGHVFCAGCVLPWVVQEGSCPARCRGR
				ļ		LSAKELNHVLPLKRLILKLDIKCAYATRGCGR
						VVKLQQLPEHLERCDFAPARCRHAGCGQVLL
				ĺ	1	RRDVEAHMRDACDARPVGRCQEGCGLPLTH
	'				1	GEQRAGGHCCARALRAHNGALQARLGALHK
				-		ALKKEALRAGKREKSLVAQLAAAQLELQMT
1			1	i	ł	ALRYQKKFTEYSARLDSLSRCVAAPPGGKGE
1			ł	İ	ļ	ETKSLTLVLIIRDSGSLGFNIIGGRPSVDNIIDG
i			ŀ			SSSEGIFVSKIVDSGPAAKEGGLQIHDRIIEVN
					ļ	GRDLSRATHDQAVEAFKTAKEPIVVQVLRRT
			ļ			PRTKMFTPPSESQLVDTGTQTDITFEHIMALT
1		ŀ	İ	ļ		KMSSPSPPVLDPYLLPEEHPSAHEYYDPNDYI
1		1				GDIHQEMDREELELEEVDLYRMNSQDKLGLT
1			i	1		VCYRTDDEDDIGIYISEIDPNSIAAKDGRIREG
1		ļ		Ì		DRIIQINGIEVQNREEAVALLTSEENKNFSLLI
		1	İ	ľ	1	ARAELQLDEGWMDDDRNDFLDDLHMDMLE
		l	1		1	EQHHQAMQFTASVLQQKKHDEDGGTTDTAT
		l	ļ	- 1	I	ILSNQHEKDSGVGRTDESTRNDESSEQENNG
]			ŀ	i		DDATASSNPLAGQRKLTCSQDTLGSGDLPFS
1		1	j	ļ	ľ	NESFISADCTDADYLGIPVDECERFRELLELK
		1	j	İ		CQVKSATPYGLYYPSGPLDAGKSDPESVDKE
			į	ļ		LELLNEELRSIELECLSIVRAHKMQQLKEQYR
1			}	1	ļ	ESWMLHNSGFRNYNTSIDVRRHELSDITELPE
<u></u>	]	į	1	- 1	İ	KSDKDSSSAYNTGESCRSTPLTLEISPDNSLRR

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			000			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	İ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	scq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	İ		}	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	-		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
İ				peptide		/-possible nucleotide deletion, \-possible
1		ŀ		sequence		nucleotide insertion
						AAEGISCPSSEGAVGTTEAYGPASKNLLSITE
	1				]	DPEVGTPTYSPSLKELDPNQPLESKERRASDG
		]			ŧ	SRSPTPSOKLGSAYLPSYHHSPYKHAHIPAHA
		İ				OHYOSYMOLIQOKSAVEYAQSQMSLVSMCK
•			1			DLSSPTPSEPRMEWKVKIRSDGTRYITKRPVR
1	l	l	1	: i		DRLLRERALKIREERSGMTTDDDAVSEMKM
ļ		•		,		GRYWSKEERKQHLVKAKEQRRRREFMMQSR
Ì						LDCLKEQQAADDRKEMNILELSHKKMMKKR
	1			ĺ	1	NKKIFDNWMTIQELLTHGTKSPDGTRVYNSF
ĺ	1	1				1
		<u> </u>	L		1.550	LSVTTV
725	2075	Α	5707	3	1770	QISTEVSEAPVANDKPKTLVVKVQKKAADLP
		1		1	1	DRDTWKGRFDFLMSCVGYAIGLGNVWRFPY
	1	1	ļ		Ì	LCGKNGGGAFLIPYFLTLIFAGVPLFLLECSLG
1	1	ĺ		1	ſ	QYTSIGGLGVWKLAPMFKGVGLAAAVLSFW
1	1	İ			· ·	LNIYYIVIISWAIYYLYNSFTTTLPWKQCDNP
		1		ĺ	1	WNTDRCFSNYSMVNTTNMTSAVVEFWERN
		1	1		I	MHQMTDGLDKPGQIRWPLAITLAIAWILVYF
	1	1		1	1	CIWKGVGWTGKVVYFSATYPYIMLIILFFRGV
						TLPGAKEGILFYITPNFRKLSDSEVWLDAATQ
1		l .	1.			IFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVC
1	ļ	ŀ			ł	CINSCTSMFAGFVIFSIVGFMAHVTKRSIADV
	1	Į.	1		l	AASGPGLAFLAYPEAVTQLPISPLWAILFFSM
	1				1	LLMLGIDSQFCTVEGFITALVDEYPRLLRNRR
1.						ELFIAAVCIISYLIGLSNITQGGIYVFKLFDYYS
ł	1			İ		ASGMSLLFLVFFECVSISWFYGVNRFYDNIQE
ł	ì					MVGSRPCIWWKLCWSFFTPIIVAGVFIFSAVQ
ł						MTPLTMGNYVFPKWGQGVGWLMALSSMVL
						IPGYMAYMFLTLKGSLKQRIQVMVQPSEDIV
1						
	1	ļ.,	I	1	400	RPENGPEQPQAGSSTSKEAYI
726	2076	Α	5711	156	423	PRRDPGRTPELRGSAPRKTGANMPVRRGHVA
	ı			ł	1	PQNTFLGTIRKFEGQNKKFIIANARVQNCAII
	1		<u> </u>	<u></u>		YCNDGFCEMTGFSRPDVMQKPCTCD
727	2077	A	5716	3	274	HASEYFFKLCSFQVFLSFPLATIVIDVGLVVIP
		ł			1	LVKSPNVHYVYVLLLVLSGLLFYIPLIHFKIRL
			L	<u> </u>		AWFEKMTCYLQLLFNICLPDVSEE
728	2078	Α	5737	1899	649	IQASRASPYPRVKVDFALSCHEDLLAPISEPIE
1	1	1	1	ļ	1	WKYHSPEEEISLGPACWLWDFLRRSQQAGFL
	1.	1	1	]		LPLSGGVDSAATACLIYSMCCQVCEAVRSGN
}			1	1	}	EEVLADVRTIVNQISYTPQDPRDLCGRILTTC
			1	l	,	YMASKNSSQETCTRARELAQQIGSHHISLNID
1	1					PAVKAVMGIFSLVTGKSPLFAAHGGSSRENL
Ì		1			1	ALQNVQARIRMVLAYLFAQLSLWSRGVHGG
	1	1		1	1	LLVLGSANVDESLLGYLTKYDCSSADINPIGG
	1	1		1		ISKTDLRAFVOFCIORFOLPALQSILLAPATAE
	]	1	1	1		LEPLADGQVSQTDEEDMGMTYAELSVYGKL
1	1	1	1	1	}	
1		1		1		RKVAKMGPYSMFCKLLGMWRHICTPRQVAD
	1	l	İ			KVKRFFSKYSMNRHKMTTLTPAYHAENYSPE
1		ı	1	1	1	DNRFDLRPFLYNTSWPWQFRCIENQVLQLER
	<u> </u>	<u>L</u>	<u></u>		<u> </u>	AEPQSLDGVD
729	2079	A	5741	1	5976	PGCAARLSRARAPGPGAAGAGRKRLADPGPP
1	1	1	1			PASRRLRAPGSRPRLAPCTRRAAQPAHARMA
1	1	1	1	1	1	PRAAGGAPLSARAAAASPPPFQTPPRCPVPLL
1		1	1	1	1	LLLLLGAARAGALEIQRRFPSPTPTNNFALDG
1	1	1	1	I	1	AAGTVYLAAVNRLYQLSGANLSLEAEAAVG
	1	l	1	1	1	PVPDSPLCHAPQLPQASCEHPRRLTDNYNKIL
	1	1	1		1	QLDPGQGLVVVCGSIYQGFCQLRRRGNISAV
		1	1	1	1	AVRFPPAAPPAEPVTVFPSMLNVAANHPNAS
		1	1		1	TVGLVLPPAAGAGGSRLLVGATYTGYGSSFF
		1	1			PRNRSLEDHRFENTPEIAIRSLDTRGDLAKLFT
L		<u> </u>	1	1	<u></u>	L VALOPEDILY, EN LEIVINGED I KODEWELL

SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1.00	in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	ĺ	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	•	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		l		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
	1		[ ·	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/-possible nucleotide deletion, \-possible
	1	•		sequence		nucleotide insertion
	Ţ	<u> </u>	<u> </u>		<u> </u>	FDLNPSDDNILKIKQGAKEQHKLGFVSAFLKP
İ	-	l	Ì	}		SDPPPGAQSYAYLALNSEARAGDKESQARSL
				i		LARICLPHGAGGDAKKLTESYIQLGLQCAGG
1	İ	1	l	ľ		AGRGDLYSRLVSVFPARERLFAVFERPQGSPA
· ·	1	ŀ		ļ		ARAAPAALCAFRFADVRAAIRAARTACFVEP
	1				1	APDVVAVLDSVVQGTGPACERKLNIQLQPEQ
}	]	ļ				LDCGAAHLQHPLSILQPLKATPVFRAPGLTSV
1						AVASVNNYTAVFLGTVNGRLLKINLNESMQ
						VVSRRVVTVAYGEPVHHVMQFDPADSGYLY
1						LMTSHQMARVKVAACNVHSTCGDCVGAAD
		1		:   		AYCGWCALETRCTLQQDCTNSSQQHFWTSA
						SEGPSRCPAMTVLPSEIDVRQEYPGMILQISGS
						LPSLSGMEMACDYGNNIRTVARVPGPAFGHQ
			]			IAYCNLLPRDQFPPFPPNQDHVTVEMSVRVN
		ľ		į .		GRNIVKANFTIYDCSRTAQVYPHTACTSCLSA
	1	1				QWPCFWCSQQHSCVSNQSRCEASPNPTSPQD
	1	l				CPRTLLSPLAPVPTGGSQNILVPLANTAFFQG AALECSFGLEEIFEAVWVNESVVRCDQVVLH
		1	1			TTRKSQVFPLSLQLKGRPARFLDSPEPMTVM
		1				VYNCAMGSPDCSQCLGREDLGHLCMWSDGC
1		ŀ	]			RLRGPLQPMAGTCPAPEIRAIEPLSGPLDGGT
		i				LLTIRGRNLGRRLSDVAHGVWIGGVACEPLP
						DRYTVSEEIVCVTGPAPGPLSGVVTVNASKE
	İ					GKSRDRFSYVLPLVHSLEPTMGPKAGGTRITI
			]			HGNDLHVGSELQVLVNDTDPCTELMRTDTSI
			1			ACTMPEGALPAPVPVCVRFERRGCVHGNLTF
						WYMQNPVITAISPRRSPVSGGRTITVAGERFH
						MVQNVSMAVHHIGREPTLCKVLNSTLITCPSP
1						GALSNASAPVDFFINGRAYADEVAVAEELLD
						PEEAQRGSRFRLDYLPNPQFSTAKREKWIKH
						HPGEPLTLVIHVSTKGAGKEQDSLGLQSHEY
				i		RVKIGQVSCDIQIVSDRIIHCSVNESLGAAVGQ
1	1					LPITIQVGNFNQTIATLQLGGSETAIIVSIVICSV
						LLLLSVVALFVFCTKSRRAERYWQKTLLQME
1			]			EMESQIREEIRKGFAELQTDMTDLTKELNRSQ GIPFLEYKHFVTRTFFPKCSSLYEERYVLPSQT
İ	1					
					Į	LNSQGSSQAQETHPLLGEWKIPESCRPNMEE GISLFSSLLDNKHFLIVFVHALEQQKDFAVRD
				ł	ļ	RCSLASLLTIALHGKLEYYTSIMKELLVDLID
					!	ASAAKNPKLMLRRTESVVEKMLTNWMSICM
						YSCLRETVGEPFFLLLCAIKQQINKGSIDAITG
			1		ļ	KARYTLNEEWLLRENIEAKPRNLNVSFQGCG
						MDSLSVRAMDTDTLTQVKEKILEAFCKNVPY
						SQWPRAEDVDLEWFASSTQSYILRDLDDTSV
			ĺ			VEDGRKKLNTLAHYKIPEGASLAMSLIDKKD
1	1 1	- 1		1	.	NTLGRVKDLDTEKYFHLVLPTDELAEPKKSH
i						RQSHRKKVLPEIYLTRLLSTKGTLQKFLDDLF
İ	]	1		l		KAILSIREDKPPLAVKYFFDFLEEOAEKRGISD
					. 1	PDTLHIWKTNSLPLRFWVNILKNPOFVFDIDK
1			ŀ		1	TDHIDACLSVIAQAFIDACSISDLOLGKDSPTN
1		ļ	l	I	İ	KLLYAKEIPEYRKIVQRYYKQIQDMTPLSEQE
			j	ļ	l	MNAHLAEESRKYQNEFNTNVAMAEIYKYAK
1	] ]		ŀ	1		RYRPQIMAALEANPTARRTQLQHKFEQVVAL
730	2000	<del>-                                    </del>	- F744		900	MEDNIYECYSEA
130	2080	A	5744	3	292	QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ
		ļ			- 1	VANGKGNQRNMGSPQPSLLAFERNLELQIMG
		1	.		l	LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT
731	2081	A	5747	<del></del>	100	LKD
131	2001	^	3/4/	1	382	FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC
L			1			FRVDEVNWITWNTNVGIINEDPGNCEGVKRT

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		i	į	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ì	ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/=possible nucleotide deletion, \=possible
	L			sequence		nucleotide insertion
		İ	ł	l	ł	LSFSLRSSRVSGRHWKNFALVPLLREASARD
						RQSAQPEEVYLRQFSGSLKPEDAEVFKSPAAS
-2:	-	<u> </u>		155		GEK AQAESSTVASPEATAGPLCTRIPNVPPPTPIRP
732	2082	A	5753	198	3	PGKLQAQLPCPSPVRFTSARIPPASRPQTKS
	0000		5754	2	2223	AAGPPGLEAEGRAPESAGPGPGGDAAETPGL
733	2083	Α	3/34	4	2223	PPAHSGTLMMAFRDVTVQIANQNISVSSSTAL
			İ		[	SVANCLGAQTVQAPAEPAAGKAEQGETSGR
		1				EAPEAPAVGREDASAEDSCAEAGASGAADG
j	1		}	ļ		ATAPKTEEEEEEEETAEVGRGAEAEAGDLEQ
		1	1		1	LNRTSTSTKSAKSGSEASASASKDALQAMILS
	1					LPRYHCENPASCKSPTLSTDTLRKRLYRIGLN
		ŀ			,	LFNINPDKGIQFLISRGFIPDTPIGVAHFLLQRK
į	1	j		]	]	GLSRQMIGEFLGNSKKQFNRDVLDCVVDEM
ĺ				1	}	DFSSMELDEALRKFQAHIRVQGEAQKVERLIE
		1	1			AFSQRYCMCNPEVVQQFHNPDTIFILAFAIILL
		1		Į		NTDMYSPNIKPDRKMMLEDFIRNLRGVDDG
1					l '	ADIPRELVVGIYERIQQKELKSNEDHVTYVTK
ĺ	ĺ			Í	į.	VEKSIVGMKTVLSVPHRRLVCCSRLFEVTDV
1				1		NKLQKQAAHQREVFLFNDLLVILKLCPKKKS
İ		l				SSTYTFCKSVGLLGMQFQLFENEYYSHGITLV
	ł					TPLSGSEKKQVLHFCALGSDEMQKFVEDLKE
İ	ł	ì		Ì	1	SIAEVTELEQIRIEWELEKQQGTKTLSFKPCGA QGDPQSKQGSPTAKREAALRERPAESTVEVSI
ì						HNRLOTSOHNSGLGAERGAPVPPPDLQPSPPR
	1	1	1		1	QQTPPLPPPPTPPGTLVQCQQIVKVIVLDKPC
						LARMEPLLSQALSCYTSSSSDSCGSTPLGGPG
l	l .	l	ł	İ		SPVKVTHOPPLPPPPPPYNHPHQFCPPGSLLH
		ŀ			1	GHRYSSGSRSLV
734	2084	A	5788	8	362	SSVMGDLVGQGLEEQIVARDENSWLIDGGTP
		1		_		IDDVMRVLDIDEFPQSGNYETIGGFMMFMLR
1		1	1			KIPKRTDSVKFAGYKFEVVDIDNYRIDQLLVT
						RIDSKATALSPKLPDAKDKEESVA
735	2085	A	5827	1	1257	MVFSAVLTAFHTGTSNTTFVVYENTYMNITL
		İ				PPPFQHPDLSPLLRYSFETMAPTGLSSLTVNST
	i	j		1		AVPTTPAAFKSLNLPLQITLSAIMIFILFVSFLG
	1		1	ļ		NLVVCLMVYQKAAMRSAINILLASLAFADM
	Ī	1		1		LLAVLNMPFALVTILTTRWIFGKFFCRVSAMF
1		1				FWLFVIEGVAILLIISIDRFLIIVQRQDKLNPYR
	Į.	1				AKVLIAVSWATSFCVAFPLAVGNPDLQIPSRA
	1	1	1	1		PQCVFGYTTNPGYQAYVILISLISFFIPFLVILY SFMGILNTLRHNALRIHSYPEGICLSQASKLGL
]				1		MGLQRPFQMSIDMGFKTRAFTTILILFAVFIVC
]	1	i				WAPPTTYSLVATFSKHFYYQHNFFEISTWLL
	1	]		1		WLCYLKSALNPLIYYWRIKKFHDACLDMMP
1	1	1	1	[		KSFKFLPQLPGHTKRRIRPSAVYVCGEHRTVV
736	2086	+	5870	3	268	FTRSDELARHYRTHTGEKRFSCPLCPKQFSRS
130	2000	^	30/0	"	200	DHLTKHARRHPTYHPDMIEYRGRRRTPRIDPP
	1	1	1			LTSEVESSASGSGPGPAPSFTTCL
737	2087	l <sub>A</sub>	5871	2	521	LTWPOLFLETLPELLHMSRPAEDGPSPGALVR
131	2007	1~	7071	1	32.	RSSSLGYISKAEEYFLLKSRSDLMFEKQSERH
		l		1	1	GLARRLTTARRPPASSEQAQQELFNELKPAV
				1	1	DGANFIVNHMRDONNYNEEKDSWNRVART
		1	1	1	1	VDRLCLFVVTPVMVVGTAWIFLQGVYNQPPP
		1		1		QPFPGDPYSYNVQDKRFI
738	2088	A	5881	1	1160	LVVTAITAILAFPNEYTRMSTSELISELFNDCG
		1		1		LLDSSKLCDYENRFNTSKGGELPDRPAGVGV
1		]		}	1	YSAMWQLALTLILKIVITIFTFGMKIPSGLFIPS
•	1			1	l .	MAVGAIAGRLLGVGMEQLAYYHQEWTVFNS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-	.	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
Ī	l			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	1	/=possible nucleotide deletion, \=possible
			l	sequence	ľ	nucleotide insertion
						WCSQGADCITPGLYAMVGAAACLGGVTRMT
İ		İ	Ϊ	Ì	İ	VSLVVIMFELTGGLEYIVPLMAAAMTSKWVA
		ł	} .		1 .	DALGREGIYDAHIRLNGYPFLEAKEEFAHKTL
1						AMDVMKPRRNDPLLTVLTQDSMTVEDVETII
		1				SETTYSGFPVVVSRESQRLVGFVLRRDLIISIE
1 !		l		i	1	NARKKQDGVVSTSIIYFTEHSPPLPPYTPPTLK
1						LRNILDLSPFTVTDLTPMEIVVDIFRKLGLRQC
						LVTHNGRLLGIITKKDVLKHIAQMANQDPDSI LFN
739	2089	A	5892	2	916	TLQLAASVPFFAISLISWWLPESARWLIINGKP
		]	]			DQALQELRKVARINGHKEAKNLTIEVLMSSV
]					1	KEEVASAKEPRSVLDLFCVPVLRWRSCAMLV
						VNFSLLISYYGLVFDLQSLGRDIFLLQALFGA
]						VDFLGRATTALLLSFLGRRTIQAGSQAMAGL
1						AILANMLVPQDLQTLRVVFAVLGKGCFGISL
						TCLTIYKAELFPTPVRMTADGILHTVGRLGA
]				i	į ·	MMGPLILMSRQALPLLPPLLYGVISIASSLVVI
1 1						FFLPETQGLPLPDTIQDLESQKSTAAQGNRQE
740	2090	A	5900	2	426	AFTVESTSLLEIVALHGAL
'	2000	^	3300	2	420	RPIKTLGIGFHFSVDGVHFLTQREVQNLWKE
1					ĺ	NLIILDTAKKHGYEVVDTFTTTMGRYKEFLQG KCGCHFHEVVKSKLSKEYNFIKMKRSRNHIM
}			ļ	l	į ,	GRYFSNQSKLQQGTVTNFRSPYHVRGPINQV
		i	1			CSEILLSRMCANKRTM
741	2091	A	5910	3	412	RMPESTLLIICENGYILEAPLPTIKQEEDDHDV
		ŀ				VSYEIKDMCIKCFHFSSVKSKILRLIEIEKRER
		i				QRELKEKIREERRNKLAAEMGEDGEKEFOEE
		- [	[	1	1	EEEKEEEEEEEPLPEIFIPSTPSPILCGFYSEPG
742	2092	_	-			KFWV
/42	2092	A	5936	1	482	MGCRLLCCVVFCLLQAGPLDTAVSQTPKYLV
	ĺ	- 1	1	1		TQMGNDKSIKCEQNLGHDTMYWYKQDSKK
	I	1			-	FLKIMFSYNNKELIINETVPNRFSPKSPDKAHL
		- 1			i	NLHINSLELGDSAVYFCASSQDTALQSHCIPV
	i		ľ	- 1	İ	HKPPGSARKLQGSVCTCTQGSSLHSLMASDG VPVC
743	2093	A	5938	1	1566	MNSFFGTPAASWCLLESDVSSAPDKEAGRER
	1					RALSVQQRGGPAWSGSLEWSRQSAGDRRRL
1		- 1				GLSRQTAKSSWSRSRDRTCCCRRAWWILVPA
1	1	1			1	ADRARRERFIMNEKWDTNSSENWHPIWNVN
1			- 1	i		DTKHHLYSDINITYVNYYLHOPOVAAIFIISYF
	1		ĺ		1	LIFFLCMMGNTVVCFIVMRNKHMHTVTNLFI
1	1	1	1	J	[	LNLAISDLLVGIFCMPITLLDNIIAGWPFGNTM
1					1	CKISGLVQGISVAASVFTLVAIAVDRFQCVVY
	İ	Ì	ŀ	1		PFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLII
	İ	- 1				VQEEKYYRVRLNSQNKTSPVYWCREDWPNQ
1	1	- 1	]	i		EMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLF
	ĺ	- 1	ľ	İ	l	RAAVPHTGRKNQEQWHVVSRKKQKIIKMLLI VALLFILSWLPLWTLMMLSDYADLSPNELQII
		- 1		1		NIYIYPFAHWLAFGNSSVNPIIYGFFNENFRRG
				į	1	FQEAFQLQLCQKRAKPMEAYALKAKSHVLIN
	- 1	- 1	1	1	1	TSNQLVQESTFQNPHGETLLYRKSAEKPQQE
					_	LVMEELKETINSSEI
744	2094	A	5966	149	327	SHVCVSHYAGSSGCPAGAGAGAVALGISAVA
716						LYDYQGGRLGVARGAWYMEAPDIROGDM
745 2	2095	Α :	5970 4	413	856	GAPHTDWAWAPTPMSGLGSGRGROGTLASS
	1		[		1	PLSLPLLLAGVTGILATELFDOMARPAACMV
1		ľ	-	•		CGALMWIMLILVGLGFPFIMEALSHPLYVPFI.
1	ļ	- 1	1	1	1	GVCVCGAIYTGLFLPETKGKTFQEISKELHRL NFPRRAQGPTWRSLEVIQSTEL

000 to	SEO ID	Non	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID		Met	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide			location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ĺ	09/496	correspondi		O=Glutamine, R=Arginine, S=Serine,
uence		l	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		!	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		residue of	sequence	Y=1yrosine, X=Unknown, *=stop codon,
		1	l	peptide	1	/=possible nucleotide deletion, \=possible
	ľ	i	ì	sequence		nucleotide insertion
746	2096	A	5971	3	1343	AQTARRIIGLELDTEGHRLFVAFSGCIVYLPLS
	1	İ	ļ			RCARHGACQRSCLASQDPYCGWHSSRGCVDI
i		Į.	1			RGSGGTDVDQAGNQESMEHGDCQDGATGSQ
i	j	1	Ī		[	SGPGDSAYGVRRDLPPASASRSVPIPLLLASV
l	ł		1			AAAFALGASVSGLLVSCACRRAHRRRGKDIE
			1			TPGLPRPLSLRSLARLHGGGPEPPPPSKDGDA
}		1	1	1	l	VQTPQLYTTFLPPPEGVPPPELACLPTPESTPE
		1		!		LPVKHLRAAGDPWEWNQNRNNAKEGPGRSR
			1		1	
1		1	1	į		GGHAAGGPAPRVLVRPPPPGCPGQAVEVTTL
ļ		l	1			EELLRYLHGPQPPRKGAEPPAPLTSRALPPEP
1		ł	J		j	APALLGGPSPRPHECASPLRLDVPPEGRCASA
I	1					PARPALSAPAPRLGVGGGRRLPFSGHRAPPAL
l	ļ	1	1	<u> </u>		I.TRVPSGGPSRYSGGPGKHLLYLGRPEGYRG
		1	1	į		RALKRVDVEKPQLSLKPPLVGPSSRQAVPNG
]	1	į.	ļ	i	1	GRFNF
747	2097	A	5998	2	754	DHASLPCSWNHRFDVETRHVFIGDHSGQVTI
/4/	209/	A	2276		'37	LKLEQENCTLVTTFRGHTGGVTALCWDPVQ
		Į.	1	ļ	'	RVLFSGSSDHSVIMWDIGGRKGTATELQGHN
1		1	1	ļ	ł	DRVQALSYAQHTRQLISCGGDGGIVVWNMD
1		1	1	:	ļ	DRVQALSYAQHIRQLISCUGDUGIVVWNIVD
(	1	ſ	1			VERQETPEWLDSDSCQKCDQPFFWNFKQMW
			1		1	DSKKIGLRQHHCRKCGKAVCGKCSSKRSSIPL
1		1			i	MGFEFEVRVCDSCHEAITDEERAPTATFHDSK
1	1	1	1		ļ	HNIVHVHFDATRGWLLTSGTDKVIKLWDMT
	ŀ	1			1	PVVS
748	2098	A	6001	2	747	AMVFGGVVPYVPQYRDIRRTQNADGFSTYV
/ 70	2050	1 **	0001	-	' ' '	CLVLLVANILRILFWFGRRFESPLLWQSAIMIL
į	İ	1		1		TMLLMLKLCTEVRVANELNARRRSFTAADS
j	1	1	}		j	KDEEVKVAPRRSFLDFDPHHFWQWSSFSDYV
	1	1	ì		ł	OCVLAFTGVAGYITYLSIDSALFVETLGFLAV
İ	1	1				LTEAMLGYPQLYRNHRHQSTEGMSIKMVLM
1	1	1	}		1	WTSGDAFKTAYFLLKGAPLQFSVCGLLQVLV
1	1		1		1	WISGDARKIA IFLLKUAPLUFS VCOLLUVL V
<u> </u>		İ		<u> </u>		DLAILGQAYAFARHPQKPAPHAVHPTGTKAL
749	2099	Α	6002	2	447	GRPDRSELVRMHILEETFAEPSLQATQMKLK
	1	i		1	I	RARLADDLNEKIAQRPGPMELVEKNILPVDSS
		1		İ		VKEAIIGVGKEDYPHTQGDFSFDEDSSDALSP
}		1	ł	}		DQPASQESQGSAASPSEPKVSESPSPVTTNTP
1	1	1			1	AQFASVSPTVPEFLKTPPTAD
750	2100	A	6004	2	427	LLTQAMLVLPHRPQWFTPGPRLQAQGPCQEG
'30	2100	[ n	0004	"	127	WRWELRLRNYVPEDEDLNKRRVPQAKPDAV
1		1	1	1	1	QEKVKEQLEAAKPEPVIEEVDLAKLAPRKPD
1	1	İ	1	1		WDLKRDVAKKLEKLLKRTQRAIAELIRERLK
1		1	1		1	
				<u> </u>		GQEDSLDSAVDAATEHKTC
751	2101	A	6007	33	1280	TDQAKVDNQPEKLVRSAEDVSTVPTQPDNPF
		1	1	1	1	SIIPDKLKRMSKSVPAFLQDESDDRETDTASE
		1	1		1	SSYQLSRHKKSPSSLTNLSSSSGMTSLSSVSGS
1	1	1	1	1		VMSVYSGDFGNLEVKGNIQFAIEYVESLKEL
1	1					HVFVAQCKDLAAADVKKQRSDPYVKAYLLP
1	1	1	1	1		DKGKMGKKKTLVVKKTLNPVYNEILRYKIEK
	1	1	1			QILKTQKLNLSIWHRDTFKRNSFLGEVELDLE
1	1			1		TWDWDNKQNKQLRWYPLKRKTAPVALEAE
i	1	1		i		I WDWDINGINGULA I FUNKLIAF VALEAE
1			1	1 '		NRGEMKLALQYVPEPVPGKKLPTTGEVHIWV
	Ī		1	i		KECLDLPLLRGSHLNSFVKCTILPDTSRKSRQ
	1		1	1	1	KTRAVGKTTNPIFNHTMVYDGFRPEDLMEAC
	1		i			VELTVWDHYKLTNQFLGGLRIGFGTGKSYGT
	1			1		EVDWMDSTSEEVALWEKMVNSPNTWIEATL
	1	ļ	1		1	PLRMLLIAKISK
750	12102	A	6028	108	1283	KEIFSPFELISVKPLCLLLGVTCSQSMAFEELL
752	2102	A	0028	100	1205	SQVGGLGRFQMLHLVFILPSLMLLIPHILLENF
1		1	1	1		AAAIPGHRCWVHMLDNNTGSGNETGILSEDA
ł	1	1	1	1	!	WATE OUT A LIMITOR LIMITOR OF TATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PA

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				:		LLRISIPLDSNLRPEKCRRFVHPQWQLLHLNG THSTSEADTEPCVDGWVYDQSYFPSTIVTKW DLVCDYQSLKSVVQFLLLTGMLVGGIIGGHV SDRFGRRFILRWGLLQLAITDTCAAFAPTFPV YCVLRFLAGFSSMIIISNNSLPITEWIRPNSKAL VVILSSGALNIGQIILGGLAYVFRDWQTLHVV ASVPFFVFFLLSRWLVESARWLIITNKLDEGL KALRKVARTNGIKNAEETLNIEVVRSTMQEE LDAAQTKTTVWDLFRNPSMRKRICILVFLRK KNLKEKA
753	2103	A	6043	1	1470	DSFESILRLIFEIHHSGEKGDIVVFLACEQDIEK VCETVYQGSNLNPDLGELVVVPLYPKEKCSL FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN SVRFVIDVGVERRKVYNPRIRANSLVMQPISQ SQAEIRKQILGSSSSGKFFCLYTEEFASKDMTP LKPAEMQEANLTSMVLFMKRIDIAGLGHCDF MNRPAPESLMQALEDLDYLAALDNDGNLSE FGIIMSEFPLDPQLSKSILASCEFDCVDEVLTIA AMVTAPNCFSHVPHGAEEAALTCWKTFLHPE GDHFTLISIYKAYQDTTLNSSSEYCVEKWCRD YFLNCSALRMADVIRAELLEIKRIELPYAEPA FGSKENTLNIKKALLSGYFMQIARDVDGSGN YLMLTHKQVAQLHPLSGYSITKMPEWVLF HKFSISENNYIRITSEISPELFMQLVPQYYFSNL PPSESKDILQQVVDHLSPVSTMNKEQQMCET CPETEQRCTLQ
754	2104	A	6055	2	394	YYALHHWPFPDLLCQTTGAIFQMNMYGSCIF LMLINVDRYAAIVHPLRLRHLRRPRVARLLC LGVWALILVFAVPAARVHRPSRCRYRDLEVR LCFESFSDELWKGRLLPLVLLAEALGFLLPLA AVVYSS
755	2105	A	6059	3	1795	LGLGSGTLLSVSEYKKKYREHVLQLHARVKE RNARSVKITKRPTKLLIAPESAAPEBALGPAEE PEPGRARRSDTHTFNRLFRRDEEGRRPLTVVL QGPAGIGKTMAAKKILYDWAAGKLYQGQVD FAFFMPCGELLERPGTRSLADLILDQCPDRGA PVPQMLAQPQRLLFILDGADELPALGGPEAAP CTDPFEAASGARVLGGLLSKALLPTALLLVTT RAAAPGRLQGRLCSPQCAEVRGFSDKDKKK YFYKFFRDERRAERAYRFVKENETLFALCFV PFVCWIVCTVLRQQLELGRDLSRTSKTTTSVY LLFITSVLSSAPVADGPRLQGDLRNLCRLARE GVLGRRAQFAEKELEQLELRGSKVQTLFLSK KELPGVLETEVTYQFIDQSFQEFLAALSYLLE DGGVPRTAAGGVGTLLRGDAQPHSHLVLTT RFLFGLLSAERMRDIERHFGCMVSERVKQEA LRWVQGQGQGCPGVAPEVTEGAKGLEDTEE PEEEEEGEEPNYPLELLYCLYETQEDAFVRQA LCRFPELALQRVRFCRMDVAVLSYCVRCCPA GQALRLISCRLVAAQEKKKKSLGKRLQASLG GG
756	2106		6060	12	436	SGRPTRPAKPTGQGMGRFMLTLVCQGSIMMS ARDLIMNNLTELQPGLFHHLRFLEELRLSGNH LSHIPGQAFSGLYSLKILMLHNNQLGGIPAQA LWELPSLQSLRLDANLISLVPERSFEGLSSLRH LWLDDNALTEIPS
757	2107	A	6063	54	419	ITPLGLGAADMCAFPWLLLLLLQEGSQRRL WRWCGSEEVVAVLQESISLPLEIPPDEEVENII WSSHKSLATVVPGKEGHPATIMVTNPHYQG

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ĺ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	1		914	ng to first amino acid	acid residue of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	l l	peptide	sequence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
<del></del>	<del> </del>		<del></del>	Doquence		QILTMLLRSLQQPSASWPRDCSSSCSW
758	2108	A	6066	125	438	IGISCPATIFVPMFSHSLIGIGEEYQLPYYNMV
		··	1.	1	100	PSDPSYEDMREVVCVKRLRPIVSNRWNSDEC
	ĺ	1	1	İ	1	LRAVLKLMSECWAHNPASRLTALRIKKTLAK
					İ	MVESQDVKI
759	2109	Α	6072	3	650	PGRRFRPAALEERAMEKLREKVPFQNRGKGT
	1			1	l	LSSIPNNSDTRKATETTSLSSKPEYVNPDFRW
•					İ	SKDPSSKSGNLLETSEVGWTSNPEELDPIRLA
			1			LLGKSGLSCQVGSATSHPVSCQEPIDEDQRISP
						KDKSTAGREFSGQVSHQTTSENQCTPIPSSTV
		}			}	HSSVADMQNMPAAVHALLTQPSLSAAPFAQ
		1				RYLGTLPSTGSTTLPQCHAGNATVW
760	2110	A	6077	3	730	PLRLTLMEEVLLLGLKDREGYTSFWNDCISSG
			ļ			LRGCMLIELPLRGRLQLEACGMRRKSLLTRK
	İ	1	ĺ			VICKSDAPTGDVLLDEALKHVKETQPPETVQ
		l			1	NWIELLSGETWNPLKLHYQLRNVRERLAKNL
						VEKGVLTTEKQNFLLFDMTTHPLTNNNIKQR LIKKVOEAVLDKWVNDPHRMDRRLLALIYL
	1	1				AHASDVLENAFAPLLDEQYDLATKRVRQLLD
		ļ	1		1 .	LDPEVECLKANTNEVLWAVVAAFTK
761	2111	A	6078	833	390	IVSFHLSGFKKFVRPFSFLSVHGLQVDEYHSV
701	2111	^	0078	033	1 390	HOKLSADMADHSNLIRSLLVGAEDARLMRD
			1	ļ	J	MKTMKSRYMELYDLNRDLLNGYKIRWNNH
		i	]			TELLGNLKAVNQAIQRAGRLRVGKPKNQVIT
	İ					ACRDAIRSNNINTLFKIMRVGTASS
762	2112	A	6079	2	2686	KKAITCGEKEKQDLIKSLAMLKDGFRTDRGS
		1	ĺ	[		HSDLWSSSSSLESSSFPLPKQYLDVSSQTDISG
			[	l	1	SFGINSNNQLAEKVRLRLRYEEAKRRIANLKI
				1		QLAKLDSEAWPGVLDSERDRLILINEKEELLK
						EMRFISPRKWTQGEVEQLEMARKRLEKDLQ
		1	1	1		AARDTQSKALTERLKLNSKRNQLVRELEEAT
			1	1		RQVATLHSQLKSLSSSMQSLSSGSSPGSLTSSR
			İ	1		GSLVASSLDSSTSASFTDLYYDPFEQLDSELQ
			1	1		SKVEFLLLEGATGFRPSGCITTIHEDEVAKTQ KAEGGGRLQALRSLSGTPKSMTSLSPRSSLSS
						PSPPCSPLMADPLLAGDAFLNSLEFEDPELSA
		1			l	TLCELSLGNSAQERYRLEEPGTEGKQLGQAV
		1		1		NTAQGCGLKVACVSAAVSDESVAGDSGVYE
Ì				1		ASVQRLGASEAAAFDSDESEAVGATRIQIALK
			ì	1		YDEKNKQFAILIIQLSNLSALLQQQDQKVNIR
	}		Į.	1		VAVLPCSESTTCLFRTRPLDASDTLVFNEVFW
					İ	VSMSYPALHQKTLRVDVCTTDRSHLEECLGG
	ļ	1		}	1	AQISLAEVCRSGERSTRWYNLLSYKYLKKQS
		1	1	l		RELKPVGVMAPASGPASTDAVSALLEQTAVE
		1		1		LEKRQEGRSSTQTLEDSWRYEETSENEAVAE
				1		EEEEEVEEEEGEEDVFTEKASPDMDGYPALK
٠.		1	1	1		VDKETNTETPAPSPTVVRPKDRRVGTPSQGPF
		1	1	1		LRGSTIIRSKTFSPGPQSQYVCRLNRSDSDSST
		1	1	!		LSKKPPFVRNSLERRSVRMKRPSPPPQPSSVK
		1		1		SLRSERLIRTSLDLELDLQATRTWHSQLTQEIS
	1	1	1	ļ	`	VLKELKEQLEQAKSHGEKELPQWLREDERFR
		1	1	1		LLLRMLEKRMDRAEHMGELQTDKMMRAAA
		1				KDVHRLRGQSCKEPPEVQSFREKMAFFTRPR
7.70	1	ļ	1.000	<del> </del>	1.550	MNIPALSADDV
763	2113	A	6082	3	1558	PHPIRFSKLCVSFNNQEYNQFCVIEEASKANE
ł		1	1		Ī	VLENLTQGKMCLVPGKTRKLLFKFVAKTED
		1		1		VGKKIEITSVDLALGNETGRCVVLNWQGGGG DAASSQEALQAARSFKRRPKLPDNEVHWGSII
l	1			1	ţ	IOASTMIISRVPNISVHLLHEPPALTNEMYCLV
<b>i</b>	1	j	1	1	1	I MUSTIMIENT LINEAL MISAUPPLEAFTHEMITCPA

## PCT/US01/03800

SEO ID	SEQ ID	T 1/-4	, Lee	Dung!	T 8 10 : 1 - 2	
NO: of	NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine O=Cysteine,
nucl-	peptide	1100	in NO.	nucleotide	location	D-Aspartic Acid, E-Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		i	Ì	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	-	/=possible nucleotide deletion, \=possible
	<del>                                     </del>	-	ļ	sequence	<del> </del>	nucleotide insertion
i	i	i	i		i	VTVQSHEKTQIRDVKLTAGLKPGQDANLTQK
1		ŀ			1	THVTLHGTELCDESYPALLTDIPVGDLHPGEQ
1 .	ł	į	1		1	LEKMLYVRCGTVGSRMFLVYVSYLINTTVEE KEIVCKCHKDETVTIETVFPFDVAVKFVSTKF
					ļ	EHLERVYADIPFLLMTDLLSASPWALTIVSSE
		l				LHLAPSMTTVDQLESQVDNVILQTGESASECF
		ļ			1	CLQCPSLGNIEGGVATGHYIISWKRTSAMENI
1		ļ			j	PIITTVITLPHVIVENIPLHVNADLPSFGRVRES
ĺ		ļ				LPVKYHLQNKTDLVQDVEISVEPSDAFMFSG
						LKQIRLRILPGTEQEMLYNFYPLMAGYQQLPS
	ļ	1				LNINLLRFPNFTNQLLRRFIPTSIFVKPQGRLM
764	2114	A	6093	1	1422	DDTSIAAA
1		<b>'`</b>	600,5	•	1422	AAADLANSNAGAAVGRKAGPRSPPSAPAPAP PPPAPAPPTLGNNHQESPGWRCCRPTLRERN
						ALMFNNELMADVHFVVGPPGATRTVPAHKY
						VLAVGSSVFYAMFYGDLAEVKSEIHIPDVEPA
			]			AFLILLKYMYSDEIDLEADTVLATLYAAKKYI
			i i			VPALAKACVNFLETSLEAKNACVLLSQSRLF
						EEPELTQRCWEVIDAQAEMALRSEGFCEIDR ·
]						QTLEIIVTREALNTKEAVVFEAVLNWAEAEC
			,	1		KRQGLPITPRNKRHVLGRALYLVRIPTMTLEE
			l			FANGAAQSDILTLEETHSIFLWYTATNKPRLD
						FPLTKRKGLAPQRCHRFQSSAYRSNQWRYRG RCDSIQFAVDRRVFIAGLGLYGSSSGKAEYSV
] .						KIELKRLGVVLAQNLTKFMSDGSSNTFPVWF
}			ĺ			EHPVQVEQDTFYTASAVLDGSELSYFGQEGM
						TEVQCGKVAFQFQCSSDSTNGTGVQGGQIPE
768	2115		4000			LIFYA
765	2115	Α .	6099	1	1150	SGFTHYAIYDFIVKGSCFCNVHADQCIPVHGF
		- 1	Ì			RPVKAPGTFHMVHGKCMCKHNTAGSHCQH
					,	CAPLYNDRPWEAADGKTGAPNECRTCKCNG
]	Ì	I				HADTCHFDVNVWEASGNRSGGVCDDCQHN TEGQYCQRCKPGFYRDLRRPFSAPDACKPCS
		-				CHPVGSAVLPANSVTFCDPSNGDCPCKPGVA
1						GRRCDRCMVGYWGFGDYGCRPCDCAGSCD
						PITGDCISSHTDIDWYHEVPDFRPVHNKSEPP
		}			j	WEWEDAQGFSALLHSGKCECKEOTLGNAKA
]	i	l	1	ł	1	FCGMKYSYVLKIKILSAHDKGTHVEVNVKIK
	ŀ	ļ	.		1	KVLKSTKLKIFRGKRTLYPESWTDRGCTCPIL
			1		İ	NPGLEYLVAGHEDIRTGKLIVNMKSFVQHWK
766	2116	A	6103	2	384	PSLGRKVMDILKRECK MTAAATATW FEGVI EVERGEL OLUMPING
"		-		-	204	MTAAATATVLKEGVLEKRSGGLLQLWKRKR CVLTERGLQLFEAKGTGGRPKELSFARIKAVE
	1			İ	1	CVESTGRHIYFTLVTEGGGEIDFRCPLEDPGW
	l					NAQITLGLVKFKNQQAIQTVRARQSLGTGTL
					ł	VS
767	2117	A	6106	ı	542	SGSSHASDGSGFQELRICSEDQTPLIAGMCSLP
			ŀ		į	MARYYIIKYADQKALYTRDGQLLVGDPVAD
					İ	NCCAEKICTLPNRGLDRTKVPIFLGIOGGSRC
			}		ł	LACVETEEGPSLQLEDVNIEELYKGGEEATRF
	ĺ		l		- 1	TFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQ
768	2118	A	6109	3	292	PVQLTKESEPSARTKFYFEQSW
			3107	-	272	FILQAVLQLSSQEARYKAFĞTCVSHIGAILAF YTPSVISSVMHRVARCAAPHVHILLANFYLLF
					ļ	PPMVNPIIYGVKTKQIRDSLGSIPEKGCVNRE
769	2119	A	6110	1	711	RHEPSCSNGVASTKSKQNHSKYPAPSSSSSSS
	1		1		· -	SSSSSSPSSVNYSESNSTDSTKSQHHSSTSNQ
			j		i	ETSDSEMEMEAEHYPNGVLGSMSTRIVNGAY
	L					KHEDLQTDESSMDDRHPRRQLCGGNQAATE

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F-Phenylalanine, G-Glycine, H-Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	· ·		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ł	İ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		i	1	peptide	1	/-possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
						RILLFGRELQALSEQLGREYGKNLAHTEMLQD
	l		1	İ	ĺ	AFSLLAYSDPWSCPVGQQLDPIQREPVCAAL
			1			NSAILESQNLPKQPPLMLALGQASECLRLMA
<u> </u>		<u> </u>		<u> </u>	550	RAGLGSCSFARVDDYLH
770	2120	A	6125	2	570	YFGLNLHVQHLGNNVFLLQTLFGAVILLANC
			ļ		ļ	VAPWALKYMNRRASQMLLMFLLAICLLAIIF
Ì			1	1	İ	VPQEMQMLREVLATLGLGASALANTLAFAH GNEVIPTIIRARAMGINATFANIAGALAPLMM
1		İ			}	ILSVYSPPLPWIIYGVFPFISGFAFLLLPETRNK
l	1		ŀ			PLFDTIQDEKNERKDPREPKQEDPRVEVTQF
221	2121	A	(126	909	353	RSFVLDTASAICNYNAHYKNHPKYWCRGYF
771	2121	A	6126	303	ددد	RDYCNIIAFSPNSTNHVALRDTGNQLIVTMSC
	1	1			j	LTKEDTGWYWCGIORDFARDDMDFTELIVT
ĺ		ľ	ĺ	Ī	1	DDKGTLANDFWSGKDLSGNKTRSCKAPKVV
						RKADRSRTSILIICILITGLGIISVISHLTKRRRS
1 .		l	1	l	1	QRNRRVGNTLKPFSRVLTPKEMAPTEQM
772	2122	A	6148	7	810	FVLGILALSHTISPFMNKFFPASFPNRQYQLLF
//2	2122	A	0146	l '	1 810	TOGSGENKEEINYEFDTKDLVCLGLSSIVGV
1		l	l .			WYLLRKHWIANNLFGLAFSLNGVELLHLNN
-		1	ſ			VSTGCILLGGLFIYDVFWVFGTNVMVTVAKS
1		1	1	j		FEAPIKLVFPODLLEKGLEANNFAMLGLGDV
ł			1			VIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF
1		ļ	1	l	1	GLGLTIFIMHIFKHAQPALLYLVPACIGFPVLV
1		1		i		ALAKGEVTEMFSYEESNPKDPAAVTESKEGT
l			ļ			EASASKGLEKKEK
773	2123	A	6161	3	1088	COPMLVTRKNHPKLLLRRTESVAEKMLTNW
1		1	5151	1	1	FTFLLYKFLKESAGEPLFMLYCAIKHQMEKG
1					ļ	PIDAITGEARYSLSEDKLIRHLIDYKTLTLNCV
i		1			1	NPENENAPEVPVKGLDCDTGTQAKEKLLDA
	1	ŀ		ł		AYKGVPYSQRPKAADMDLEWRQGRMARIIL
ſ	•	1	[		[	QDEDVTTKIDNDWKRLNTLAHYQVTDGSSV
	}		1			ALVPKQTSAYNISNSSTFTKSLSRYESMLRTA
1	,	1	ļ	1		SSPDSLRSRTPMITPDLESGTKLWHLVKNHDH
ł	į	1	ŀ	1	1	LDQREGDRGSKMVSEIYLTRLLATKGTLQKF
	1 '	1			1	VDDLFETIFSTAHRGSALPLAIKYMFDFLDEQ
1					1	ADKHQIHDADVRHTWKSNCLPLRFWVNVIK
	<u>L</u> .	L	<u> </u>			NPQFVFDIHKNSITDACLSVV
774	2124	A	6163	860	125	KTAVKKRNLNPVFNETLRYSVPQAELQGRVL
1					1	SLSVWHRESLGRNIFLGEVEVPLDTWDWGSE
	1	i	1		1	PTWLPLQPRVPPSPDDLPSRGLLALSLKYVPA
1	j .	1	1	I	Į.	GSEGAGLPPSGELHFWVKEARDLLPLRAGSL
	ļ	ŀ	1			DTYVQCFVLPDDSRASRQRTRVVRRSLSPVF
			1		1	NHTMVYDGFGPADLRQACAELSLWDHGALA
			1	,	j	NRQLGGTRLSLGTGSSYGLQVPWMDSTPEEK
				<u> </u>		QLWQALLEQPCEWVDGLLPLRTNLAPRT
775	2125	Α	6191	2	392	ARGIGSLGRDHSGSGGGTGMAGAWVRKAAD
1	1	}	1	ļ		YVRSKDFRDYLMSTHFWGPVANWGLPIAAIT
	1	1		1		DMK\KSPEIISRRMTFAL*CYSLTFVRFAHYVQ
1.	1	1	1	<b>1</b> .	İ	PWNWLMLGCHTAVDFDQLISSMPCISHGMT
<u>                                     </u>	<u> </u>	<u> </u>	<u> </u>		L	ASASAL
776	2126	A	6217	1	827	FRGYWGVREAFTDASWSGGLGPGKPGMKIT
J	]			1 .	1	RQKHAKKHLGFFRNNFGVREPYQILLDGTFC
1	1	1				QAALRGRIQLREQLPRYLMGETQLCTTRCVL
				1		KELETLGKDLYGAKLIAQKCQVRNCPHFKNA
						VSGSECLLSMVEEGNPHHYFVATQDQNLSVK
ł	1		1	ł	1	VKKKPGVPLMFIIQNTMVLDKPSPKTIAFVKA
	1					VESG/RLSQCMRKKVSNISKRNRV**KTLNRG
1	1	1				RRKKRKKISGPNPLSCLKKKKKAPDTQSSASE KKRKRKRIRNRSNPKVLSEKQNAEGE
		T .	1	1	1	I KARAKKIKIKONTA Y LÖKKUNAKUK

SEQ ID	SEQ ID	Met	SEQ	Predicted	18.0.0	
NO: of		hod	ID NO:		Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
nucl-	peptide	nou .	in in	beginning nucleotide	nucleotide location	D-Aspartic Acid, E-Glutamic Acid,
eotide	seq-		USSN	location	corresponding	F-Phenylalanine, G-Glycine, H-Histidine,
seq-	uence	ļ.	09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence		ŀ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
		i	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	peptide	Sequence	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
777	2127	A	6236	1038	1402	YYQISSLPSIVGNGIFLWLLICIFLAKQGGSRL*
i	i	i	1	1	1	FQPFGRPRGGGHLRSGVLGQPGQHGETP/SFF
		1			1	YNSKISPALWGPPVIPSALGGEAGKSL*PRRQ
į		1	1			RFQRGGIAPLPSRVRGRAKLFLKKK
778	2128	A	6237	422	913	ASFFHHHRGAFLLLLAIPGS*GQDQSLIHWSN
ł			1		713	AVSNAD\LLDLK\N*LDH\LEEKMPL\EVKVVP
		i	1			PQVL\SEPN*RSGGCFSAPSFEVPPWTGEVKP/
1	i	ŀ				SPQRDGGALG\QGPLGIPSDSILALLKKQT*RA
İ	1	ļ				LLNWPLGSLRRSSCFGGQDGQDLKPRSGLGC
		ł				NSFRYRR
779	2129	A	6249	420	36	ARAPSPSFSVRDVELSDPARERGEMPVAVGP
1		{			50	YGQSQPSCFDRVKMGFVMGCAVGMAAGAL
j		1				FGTFSCLSSILVSSSG/SGMRGRELMGGIGKTM
		l				MQSGGTFGTFMAIGMGIRC*PWLPTTSVPSH
						OSOPMY
780	2130	A	6263	415	1380	RIMRMCDRGIQMLITTVGAFAAFSLMTIAVG
				123	1500	
1		i				TDYWLYSRGVCRTKSTSDNETSRKNEEVMT
	1	1				HSGLWRTCCLEGAFRGVCKKIDHFPEDADYE
1	1	l	1			QDTAEYLLRAVRASSVFPILSVTLLFFGGLCV
1			1 1			AASEFHRSRHNVILSAGIFFVSAGLSNIIGIIVYI
		l	1 1			S\ANAGRTPGQR\DSKKSYSYGWSF/YFSGAFS
			1 1			FIIGR/IIC*GVGLPWHIYIEKHQQLRAKSHSEF LKKSTFARLPPYRYRFRRRSSSRSTEPRSRDLS
İ	1	ļ				PISKGFHTIPSTDISMFTLSRDPSKITMGTLLNS
	1					DRDHAFLQFHNSTPKEFKESLHNNPANRRTT
	1	ĺ	1 1			PV PV
781	2131	A	6274	832	318	RIIKVKDLKQTLAIKTAYPRCKCLVEMDQIFH
ł					310	LQVKQKQLACLCTWQARDPDCPPSTKVVL/L
[		· ·	1 1			VGPGMGCMVALFQDSIAWSNKSMPSSLSAIS
1	1		1 1			QSPCQVQAPEGPSSFHLPTLSFTTCLSWQGGD
İ			1 1			LEFLGDLKGCSELKNFQELITQSALVHPKADV
					l	WWYCGRPLLGTLPSN
782	2132	A	6281	1324	393	WISLPSSLLCRKNGSSAEDDRR\GEPSAEEAEG
1						EREDWGIGSA*SVGAVSKVPSARF*RTYPS\E
}			] [			DEEEVTHQKSSSSDSNSEEHRKKKTSRSRNK
i						KKRKNKSSKRKHRKYSDSDSNSESDTNSDSD
			1 1			DDKKRVKAKKKKKKKKKKKKKKKKKKKKKK
						ESSDSSCKDSEEDLSEATWMEQPNVADTMDL
1			]	ŀ		IGPEAPIIHTSQDEKPLKYGHALLPGEGAAMA
1	]					EYVKAGKRIPRRGEIGLTSEEIGSFECSGYVM
	į l					SGSRHRRMEAVRLRKENQIYSADEKRALASF
L				]		NQEERRKRESKILASFREMVHKKTKGKDDK
783	2133	A	6305	201	1032	WDDYPQGALRREAAEGLHFLGPPGRVRGQ
1	[					LRGITGPAWYCHSPSHSLLSAFCHLPTPSRCP
				:		AMARPPVPGSVVVPNWHES/RRGQGVPGLHS
				1		AQEPPAGVWAA*AASAAAA\LSIDTASYKIFV
				1	1	SGKSGVGKTALVAKLAGLEVPVVHHETTGIO
					İ	TTVVFWPAKLQASSRVVMFRFEFWDCGESA
1	1 1			Į	!	LKKFDHMLLACMENTDAFLFLFSFTDRASFE
1	1 1			ĺ	:	DLPGQLARIAGEAPGVVRMVIGSKFDQYMHT
L_					į	DVPERDLTAFRQAWELPLLRVKSVPGRRLG
784	2134	A	6308	86	96	GSSPDPASLITMKNQDKKNGAAKQSNPKSSP
1	] ]		'			GQPEAGPEGAQERPSQAAPAVEAEGPGSSQA
	į į			1	[	PRKPEGAQARTAQSGALRDVSEELSRQLEDIL
1				l		STYCVDNNQGPGEDGAQGEPAEPEDAEKSR
						TYVARNGEPEPTPVVNGEKEPSKGDPNTEEIR
				ļ	l	QSDEVGDRDHRRPQEKKKAKGLGKEITLLM
1				1	ļ	QTLNTLSTPEEKLAALCKKYAELLEEHRNSQ
L	1 1					KQMKLLQKKQSQLVQEKDHLRGEHSKAVLA
						ATAVVEUS AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACT

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nuclcotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F-Phenylalanine, G-Glycine, H-Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
1	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ĺ			acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1		914	ng to first		
ł	Í	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	ł	i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	'	1		peptide	ŀ	/=possible nucleotide deletion, \=possible
1	Į	}	1	sequence	ł	nucleotide insertion
			<del> </del>	-		RSKLESLCRELQRHNRSLKEEGVQRAREEEE
1	ł	1		1	ł	KRKEVTSHFQVTLNDIQLQMEQHNERNSKLR
	[	İ		1	İ	
)	j.	l	1	1	1	QENMELAERLKKLIEQYELREEHIDKVFKHK
1		İ			}	DLQQQLVDAKLQQAQEMLKEAEERHQREKD
į.	l .		1		į	FLLKEAVESQRMCELMKQQETHLKQQLALY
l	i				1	TEKFEEFQNTLSKSSEVFTTFKQEMEKMTKKI
ŀ			1	ł	1	KKLEKETIMYRSRWESSNKALLEMAEEKTV
1						RDKELEGLQVKIQRLEKLCRALQT/GAQ*PVR
	1	1		1		GORWGSHRTSAVRIFS
	<u> </u>	<u> </u>				
785	2135	Α	6319	1493	889	SPQGPLLRSVSPVSAGASSVTPGGAQPGVTTT
1	1	l	1	j	Į.	PPSLVAVAPAPGSAAGPAAGWQ*HAGCR/WT
Í	1				1	KLPWSWGMRPMKIFFSEEYRSISTRISHDAL*
Į.				1	1	EKCTOPAKPLSMIR\TGSSVSPG/PLVKWNWT
1	1	1		1	1	RREFRNSGTRVVSSCCGMSCMYSFLGHCSV/S
1	1	1		1		ODLPLVHVDVGWQPPLGPTVGLRPGLLPLHD
1	1	1	ĺ		1	
	<u> </u>	<u> </u>				TTPCQKLVVDDLDWA
786	2136	Α	6320	551	135	RWLPVAECDSSCVGCTGEGPGNCKECISGYA
1	1	1	i	1		REHGQCADVDECSLAEKTCVRKNENCYNTP
ì	1	1		1		GSYVCVCPDGFEET/RRCLCAAGRG*SHRRRK
1	1	1	1	ł		PDTAALPRRPVMCRTYPLNYSEGCPVENVAL
1		ł				RMPSPAVDSGGERLPAL
L		<del> </del>	5000	1600	007	DYVLTAELHRQRSPGVSFGLSVFNLMNAIMG
787	2137	A	6330	1693	227	
1	1.	ł	1	ł	ł	SGILGLAYVMANTGVFGFSFLLLTVALLASYS
1	l		1	j		VHLLLSMCIQTAYLGP*TNYFMVLPAH*LTCL
	ļ	1			,	PLIEFLQSL*NSL\*AVTSYEDLGLFAFGLPGKL
ļ	1	ļ	1			VVAGTIIIQNIGAMSSYLLIIKTELPAAIAEFLT
1	1	1				GDYSRYWYLDGQTLLIIICVGIVFPLALLPKIG
j	J	)	]	}	j	FLGYTSSLSFFFMMFFALVVIIKKWSIPCPLTL
	1	1			1	NYVEKGFQISNVTDDCKPKLFHFSKESAYALP
	1			1	ļ ·	
1			i	1	<b>[</b>	TMAFSFLCHTSILPTYCELQSPSKKRMQNVTN
1		1		İ	j	TAIALSFLIYFISALFGYLTFYD/GTTKAQRGE
1	1	1				VTCHRIKDKVESELLKG***IP*SHDVVVMT\V
ł	ı		ļ.	I	ł	KLCILFAVLL\TVPLIHFPARKAVTMMFFSNFP
1		1	1			FSWIRHFLITLALNIIIVLLAIYVPDIRNVFGVV
J	1	1	1	J	1	GASTSTCLIFIFPGLFYLKLSREDFLSWKKLGV
		i	1	ì	l	
		1			1	GCFC/LLSFKTSILRNSLSVYIILPASRKSIYFKI
788	2138	A	6351	1	6622	PRSLCFSLWAEAAVLADGGLRRRRLLRGTM
1	1		ı	1	j.	SASFVPNGASLEDCHCNLFCLADLTGIKWKK
1	1	1	1		1	YVWQGPTSAPILFPVTEEDPILSSFSRCLKADV
l	1	1	1		1	LG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLF
1	1		1	1	1	TMTYQKKKMECGRMDFPMNAVLCFSKAVH
1		1	1		1	NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN
	1 .	Į.	1		1	KSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY
1	1	1	1	1	1	
1	1	1		1	1	LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQ
				1	1	AFKMSDSATKKLIGEWKQFYPISCCLKEMSE
1	1	ı	1	1	1	EKQEDMDWEDDSLAAVEVLVAGVRMIYPAC
1		ı	1		1	FVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPAS
1	1	1	1	1	1	TRDPAMSSVTLTPPTSPEEVQTVDPQSVQKW
	1	1		1	1	VKFSSVSDGFNSDSTSHHGGKIPRKLANHVV
1		1	1			AVEOUA OPOLIZIONE L'OUTOURI MYTANIA A
1	1	1	i		1	DRVWQECNMNRAQNKRKYSASSGGLCEEAT
1	1	1	1	1	1	AAKVASWDFVEATQRTNCSCLRHKNLKSRN
1	1	1		1		AGQQGQAPSLGQQQQILPKHKTNEKQEKSEK
		1	1			POKRPLTPFHHRVSVSDDVGMD\ADS\ASQRL
1	1	1	1	1	1	V\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTE
1		1	1 '		1	MANSPQPPPLSPIPCDVVDEGVTKTPSTPQS
	1	1	1	1		MULTOI GLI LOI HII CDAADOOA LIVITOILO
1	1	1		1		QHFYQMPTPDPLVPSKPMEDRIDSLSQSFPPQ
1		,	1	1		YQEAVEPTVYVGTAVNLEEDEANIAWKYYK
	1	i	1			FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESV
	1		1	}		TSVTELMVQCKKPLKVSDELVQQYQIKNQCL
1	i	1	1	1		SALASDAEOEPKIDPYAFVEGDEEFLFPDKKD
•		1	1		1	

SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino cold regrees (A. Alester C. C.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide	iiou	in in	nucleotide	location	
cotide	sed-	1	USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ì	09/496	correspondi	to last amino	
uence	donoc	ł	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
			314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	<b>[</b>			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
İ		ŀ		peptide	sequence	/=possible nucleotide deletion, \=possible
	ŀ	}		sequence	į	
<b>—</b>	+		+	sequence	<del>                                     </del>	nucleotide insertion
i	ì	i	i	İ	İ	RONSERRAGKKHK VEDGTSSVTVL SHEEDA
İ		1	i	Í		MSLFSPSIKQDAPRPTSHARPPSTSLIYDSDLA
1			Í	1	Í	VSYTDLDNLFNSDEDELTPGSKRSANGSDDK
1						ASCKESKTGNLDPLSCISTADLHKMYPTPPSL
İ						EQHIMGFSPMNMNNKEYGSMDTTPGGTVLE
1		1				GNSSSIGAQFKIEVDEGFCSPKPSEIKDFSYVY
1						KPENCQIL VGCSMFAPLKTLPSQYLPLIKLPEE
						CIYRQSWTVGKLELLSSGPSMPFIKEGDGSNM
1					ļ.	DQEYGTAYTPQTHTSCGMPPSSAPPSNSGAGI
1		ł			ł	LPSPSTPRFPTPRTPRTPRTPRGAGGPASAQGS
1					İ	VKYENSDLYSPASTPSTCRPLNSVEPATVPSIP
	]	1			1	EAHSLYVNLILSESVMNLFKDCNSDSCCICVC
1	I	l				NMNIKGADVGVYIPDPTQEAQYRCTCGFSAV
					1	MNRKFGNNSGLFFEDELDIIGRNTDCGKEAE
1		1			1	KRFEALRATSAEHVNGGLKESEKLSDDLILLL
						QDQCTNLFSPFGAADQDPFPKSGVISNWVRV
						EERDCCNDCYLALEHGRQFMDNMSGGKVDE
	1	l .	Í 1		[	ALVKSSCLHPWSKRNDVSMQCSQDILRMLLS
1		ŀ		*	i	LQPVLQDAIQKKRTVRPWGVQGPLTWQQFH
						KMAGRGSYGTDESPEPLPIPTFLLGYDYDYLV
						LSPFALPYWERLMLEPYGSQRDIAYVVLCPE
				•		NEALLNGAKSFFRDLTAIYESCRLGQHRPVSR
			1			LLTDGIMRVGSTASKKLSEKLVAEWFSQAAD
1						GNNEAFSKLKLYAQVCRYDLGPYLASLPLDS
1		1	1 1			SLLSQPNLVAPTSQSLITPPQMTNTGNANTPS.
1	1					ATLASAASSTMTVTSGVAISTSVATANSTLTT
1			1			ASTSSSSSNLNSGVSSNKLPSFPPFGSMNSNA
						AGSMSTQANTVQSGQLGGQQTSALQTAGISG
ŀ						ESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH
				j		AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTL
1						GLLRCFLEMVQTLPPHIKSTVSVQIIPCQYLLQ
						PVKHEDREIYPQHLKSLAFSAFTQCRRPLPTS
	1 1		1			TNVKTLTGFGPGLAMETALRSPDRPECIRLYA
			ŀ			PPFILAPVKDKQTELGETFGEAGQKYNVLFV
						GYCLSHDQRWILASCTDLYGELLETCIINIDVP
	'					NRARRKKSSARKFGLQKLWEWCLGLVQMSS
				j		LPWRVVIGRLGRIGHGELKDWSCLLSRRNLQ
				Ì		SLSKRLKDMCRMCGISAADSPSILSACLVAM
1						EPQGSFVIMPDSVSTGSVFGRSTTLNMQTSQL
1	.					NTPQDTSCTHILVFPTSASVQVASATYTTENL
		İ		i		DLAFNPNNDGADGMGIFDLLDTGDDLDPDII
			1			NILPASPTGSPVHSPGSHYPHGGDAGKGQSTD
1				. [	-	RLLSTEPHEEVPNILQQPLALGYFVSTAKAGP
1					-	LPDWFWSACPQAQYQCPLFLKASLHLHVPSV
1	·			İ		QSDELLHSKHSHPLDSNQTSDVLRFVLEQYN
1 :				j	· • • • • • • • • • • • • • • • • • • •	ALSWLTCDPATQDRRSCLPIHFVVLNQLYNFI
789	2139	A	6250		2000	MNML
705	2137	м	6359	1	2002	TGTLTEDGLDVMGVVPLKGQAFLPLVPEPRR
				ļ		LPVGPLLRALATCHALSRLQDTPVGDPMDLK
						MVESTGWVLEEEPAADSAFGTQVLAVMRPP
				ļ		LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM
				ļ		SVVVAWPGATQPEAYVKGSPELVAGLCNPET
					Î	VPTDFAQMLQSYTAAGYRVVALASKPLPSVP
		l	1	1	ŀ	SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP
		- 1		l		QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA
			- 1	ŀ	l	RGCGMVAPQEHLIIVHATHPERGQPASLEFLP
			İ	ŀ	İ	MESPTAVNGVKDPDQAASYTVEPDPRSRHLA
				j	1	LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP
		ļ	1	- ]	ļ	EQKTELVCELQKLQYCVGMCGDGANDCGAL
		l		1		KAADVGISLSQAEASVVSPFTSSMASIECVPM

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alainine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
401150	[		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	ľ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	i		Sequence	/=possible nucleotide deletion, \=possible
	1	Ì		peptide	1	
	}	l		sequence		nucleotide insertion
						VIREGRCSLDTSFSVFKYMALYSLTQFISVLIL
	ì		į.		ĺ	YTINTNLGDLQFLAIDLVITTTVAVLMSRTGP
			1	ŀ		ALVLGRVRPPGALLSVPVLSSLLLQMVLVTG
	1	1				VQLGGYFLTLAQPWFVPLNRTVAAPDNLPNY
	1	İ			İ	ENTVVFSLSSFOYLILAAAVSKGAPFR\RPLTN
•						
			į.	ļ		NVPFLLASAL*SSVLVVLVLSPGLLHGPLALR
			1	1	}	NITDTGFKLLLVGLVTLNFVGGLHAGERARP
	1	1 .			j	VPPRLPAPPPAQAG\SKKRFKQLERELAEQPW
	í	i '			[	PPLPAGPLR
500	0140	-	(200	76	1050	SSAGSARKLOVMALAARLWRLLPFRRGAAP
790	2140	A	6380	76	1059	
	1	1	1		l	GSRLPAGTSGSRGHCGPCRFRGFEVMGNPGT
	i	1			ì	FKRGLLLSALSYLGFETYQVISQAAVVHATA
l		1	1	1	1	KVEEILEQADYLYESGETEKLYQLLTQYKESE
		1		1		DAELLWRLARASRDVAQLSRTSEEEKKLLVY
	J.	1	1	1	1	EALEYAKRA/L/EKNESSFASHKWYAICLSDV
	1	1		1	Í	GDYEGIKAKIANAYIIKEHFEKAIELNPKDATS
	1	1	1		ŀ	<b>.</b>
	1	1			1	IHLMGIWCYTFAEMPWYQRRIA*NACLQLPP
ļ						*FPPYEKALG\YFHRAEQVDPNFYSKNLLLLG
			1			KTYLKLHNKKLAAFWLMKAKDYPAHTEED
		1	1	1 .		KQIQTEAAQLLTSFSEKN
791	2141	A	6434	3	1460	IALLIVDGLAWDDQGGLALLHISPSKLIL*QDS
/91	2141	I A	0434	3	1400	SGMS/YVMVRCTITRAFFKSLLCHICQYSIGPQ
				· '		SGMS/IVMVRCIIIRAFFRSLLCHICQISIGIQ
	1		1	ļ		*VT\CPGQDACKE*KSTAN*GG*RE**PQVLFF
ļ	1		i			AFLSNPAVKFGRMSKKQRDSLYAEVQKHQQ
<u> </u>	Į		i	I		RLOEOROOGSGEAEALARVYSSSISNGLSNLN
1	.		1	l		NETSGTYANGSVIDLPKSEGYYNVVSGQPSP
	1	ł	1		1	DOSGLDMT\GIKQIKQEPIYDLTSVPNLFTY\SS
1	1	1	1			FNNGOLAPGIT\MTEIDRIAQNIKSHLETCQY
i	1	1	1			
		ľ		1		TMEELHQLAWQTHTYEEIKAYQSKSREALW
ŀ	1					QQCAIQITHAIQYVVEFAKRITGFMELCQNDQ
		1				ILLLKSGCLEVVLVRMCRAFNPLNNTVLFEG
1	1.		1	1	Į	KYGGMOMFKALGSDDLVNEAFDFAKNLCSL
1	ľ		I	İ	1	OLTEEEIALFSSAVLISPDRAWLIEPRKVQKLQ
						1 3
	1	1				EKIYFALQHVIQKNHLDDETLAKLIAKIPTITA
1	1	1		1	ļ	VCNLHGEKLQVFKQSHPEIVNTLFPPLYKELF
	i	1	1			NPDCATACK
792	2142	A	6440	92	781	SRGTFRCFCRDFFPCFSNMRLFLWNAVLTLFV
٠	1	1	1	1	1	TSLIGALIPEPEVKIEVLQKPFICHRKTKGGDL
	1	1	1	I		MLVHYEGYLEKDGSLFHSTHKHNNGQPIWFT
1	1	1	i	Į.		
		1	l	1		LGILEALKGWGPGA*K/DMCVGEKRKLIIPPA
1	1	1	1	1	1	LGYGKEGKGKIPPESTLIFNIDLLEIRNGPRSH
}	1	1	1			ESFQEMDLNDDWKLSKDEVKAYLKKEFEKH
	1	1		1		GAVVNESHHDALVEDIFDKEDEDKDGFISAR
	1.	1	1		1	EFTYKHDEL
-	+	1	+ 2442	2201	160	PRLKRLVVTEEDGGARPEALGKIAPRTPAELG
793	2143	A	6446	3201	152	
		1	1	1	ſ	ARADQELVTALMCDLRRPAAGGMMDLAYV
1	1	1	1		1	CEWEKWSKSTHCPSVPLACAWSCRNLIAFTM
1	1	1	1	1	l	DLRSDDQDLTRMIHILDTEHPWDLHSIPSEHH
1			1		1	EAITC\LEWDQSGFPGFLFSRWPTGQIK\CWS
1		1	1 .	1	1	MGVSTLA\NSWE\SSVGSL\VEGGPHLWALS\
	1	1	1		1	
1	l	1	1	1	1	WLH\NGVKLALHVEKSGASSFGEKFSR\VKFS
1	ı		l	1	1	P\SLTLF\GGNAMEGWIAVTVSGLVTVSLLQ\P
1	1				1	SGQVL\TST\ESLCRLRARVALADIAFTGGGNI
1	1		i			VVATADGSSA\SPVQFYKVCVSVVSEKCRIDT
1	1		1		1	
		1	1		1	DILPSLFMRCTTDLNRKDKFPAITHLKFLARD
ľ	1	ł	1 '	Ī	1 .	MSEQVLLCASSQTSSIVECWSLRKEGLPVNNI
ŀ	1	1	1		1	FQQISPVVGDKQPTILKWRILSATNDLDRVSA
1	1	1	I	1.	1	VALPKLPISLTNTDLKVASDTQFYPGLGLAL
i	1	]	1	ŀ	1	AFHDGSVHIVHRLSLQTMAVFYSSAAPRPVD
1	1	1	1	1	1	EPAMKRPRTAGPAVHLKAMQLSWTSLALVG
Į.	1	1	ı	1	1	ELWADICLY LOT VATIFFY WAS A TOPUT A A

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IDSHGKLSVALRLSPSMGHPLEVGLATRHTLFT LEYCMVTGYDWWDILLHVQPSMVQSLVEKL HEEYTRQTAALQQVLSTRILAMKASLCKLSP CTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNT PDKSPGDRLTEICTKITDVDIDKVMINLKTEEF VLDMNTLQALQQLLQWVGDFVLYLLASLPN QPCPTSEPCPTSEPSPTSEPSSP*SLC\G SLLRPGHSFLRDGTSLGMLRELMVVIRIWGLL KPSCLPVYTATSDTQDSMSLLFRLLTKLWICC RDEGPASEPDEALVDECCLLPSQLLIPSLDWL PASDGLVSRLQPKQPLRLQFGRAPTLPGSAAT LQLDGLARAPGQPKIDHLRRLHIGACPTEEC KACTRCGCVTMLKSPNRTTAVKQWEQRWIK NC/LVRWALVAGAPQLPLSPAAPQLLLSYPSA APEPGCCKSHRSPWTLLGAVNLSPPCRAVEG RGPDACVTSRASEEAPAFVQLGPQSTHHSPRT PRSLDHLHPEDRP
794	2144	A	6490	418	585	NGDKADLENESCRAQVLMPVVPALWEAEGG
795	2145	A	6499	395	1027	GSIEPRDLRLQ*AVITPL\TPAWVTQ KLLWLPPHSEQKRSPLYHPQGPSGTTPSAP\FS SHSPPPSLLQA\PSIAAFLRTHGHISASGPLRMP FPH\H*NAFLLVFPGQRSQLTS\PSHYLCREVFP DHHHLCRLSLESSPLFHHRVLFCVPKQNVN STRAQIFCLFVHIVGCRCINTFPLHLFRLHLWL HFLQIPLCKKNKSVKLGKTVVGRGCQSAAGS DTRVRAAVGAPGLPVEPLV
796	2146	A	6503	68	936	HSALLTHSSFCVFTLCQDFFTYSSMSEEVTYA DLQFQNSSEMEKIPEIGKFGEKAPPAPSHVWR PAALFLTLLCLLLLIGLGVLASMFHVTLKIEM KKMNKLQNISEELQRNISLQLMSNMNISNKIR NLSTTLQTIATKLCRELYSKEQEHKCKPCPRR WIWHKDSCYFLSDDVQTWQESKMACAAQN ASLLKINNKNALEFIKSQSRSYDYWLGLSPEE DSYYSWYESG*YNQIPSAWVIRNAPDLNNMY CGYINRLYVQYYHCTYKQRMICEKMANPVQ LGSTYFREA
797	2147	A	6507	1	881	PGSTHASARSQVPRSAGEAAPHSRRPPGLLPH APRAASAQLEERMRDPHPGMTLQEGDCRGS QTVSLTMGTADSDEMAPEAPQHTHIDVHIHQ ESALAKLLLTCCSALRPRATQARGSSRLLVAS WVMQIVLGILSAVLGGFFYIRDYTLLVTSGA AIWTGAVAVLAGAAAFIYEKRGGTYWALLR TLLALAAFSTAIAALKLWNEDFRYGYSYYNS ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM DMLKALFRTLQAMLLGVWILLLLASLTPLWL /SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG STHASARSQVPRSAGEAAPHSRRPPGLLPHAP RAASAQLEERMRDPHPGMTLQEGDCRGSQT VSLTMGTADSDEMAPEAPQHTHIDVHIHQES ALAKLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI WTGAVAVLAGAAAFIYEKRGGTYWALLRTL LALAAFSTAIAALKLWNEDFRYGYSYYNSAC RISSSSDWNTPAPTQSPEEVRRLHLCTSFMDM LKALFRTLQAMLLGVWILLLASLTFLWLYC WRMFPTKGVSP
798	2148	A	6528	912		VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAP RFLVAFAYWNHYLSCTSPCSCYRPLCRLNFG LNVVENLALLVLTYVSSSEDF/TWVPG*GRSG

NO: of nucle cotide cotide cotide cotide cotide cotide sequence	SEO ID		l Mar	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucleotide sequence  in SSN 09/496 914 in got first amino acid residue of peptide sequence  nucleotide sequence  in SSN 09/496 914 in got first amino acid residue of peptide sequence  sequence  nucleotide location corresponding to last amino acid residue of peptide sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence		SEQ ID	Met				
ectide sequence under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under under un		1	1100				
sequence    Sequence   09/496		1 * *	l				
uence  914		1 -					
amino acid residue of peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	•			914		acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide deletion, \=possible nucleotide insertion  EVFPEGTGLPLPHSDLPTSWCGHSLQCGS FPPAHENAFIVFIASSLGHMILITCILWRIJ HTVSQE\DGLSLAGAPRQPRRKSRTSVLRI MVRWELSSNGNPGRGVLGLGLGLGNKLI GQNLGL*HCVWVWETGE*KRWRLQMC GVASRRQ*VRNSVRGLVCHNSSAPPMYM SPTVFGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIVVILAAPACAPFIDR*\ REIRPSP*ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINPISFFSALAVYFRHNM EAGVYTIFALLEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF FFFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQT\HGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGGRQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPIPPTAPATPTTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE						of peptide	T=Threonine, V=Valine, W=Tryptophan,
sequence nucleotide insertion  EVFPEGTGLPLPHSDLPTSWCGHSLQCGS  FPPAIHENAFIVFIASSLGHMLLTCILWRLT  HTVSQE\DGLSLAGAPRQPRRKSRTSVLRI  MVRWELSSNGNPGRGVLGLGLGLGNKLI  GQ\NLGL*HCVWVVWETGE*KRWRLQMC  GVASRRQ*VRNSVRGLVCHNSSAPPMYM  SPTVFGGGVGG*LHVTFILHPPEVEAAGIP  GPSLPQRQGREIIIVVILAAPACAPTFIDR*\  REIRPSP*ELGLRGEPTLSYPASCRVIRQPII  RKSYSWKQRLFIINFISFFSALAVYFRHNM  EAGVYTIFAILEYTVVLTNMAFHMTAWW  GNKELLITSQPEEKRF  799 2149 A 6529 1 874 FPFFQRINFIEHSGSVSLLALACDLGWCEL  CCLVQGGGDLVDVVQTNHGEDEAGGDT  DEARCKESQQEAQENLREDLCLESFAKDI  QIIEGSERREHEETTKQAALDGEPLGGGQ  VHLHPSKEQQGQEGGERQRGARTHHWR  EKGRRVRLRPPSGKLRADQPVRKLGGPTI  ELPGLQPHAPTPHTA/PATPTYSPAPDTPN  RWKCPLPVEPRTRQLCRERTRKACPPKPE				1	residue of		Y=Tyrosine, X=Unknown, *=Stop codon,
EVFPEGTGLPLPHSDLPTSWCGHSLQCGS FPPAIHENAFIVFIASSLGHMLLTCILWRLT HTVSQE\DGLSLAGAPRQPRRKSRTSVLRI MVRWELSSNGNPGRGVLGLGLGLGNKLI GQNLGL*HCVWVWETGE*KRWRLQMC GVASRRQ*VRNSVRGLVCHNSSAPPMYM SPTVFGGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIIVVILAAPACAPFHDR*Y REIRPSP*ELGLRGEPTLSYPASCRVIRQPI RKSYSWKQRLFIINFISFFSALAVYFRHNM EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 PPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETTTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTAPATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE		1		1	peptide	_	
FPPAIHENAFIVFIASSLGHMLLTCILWRLT HTVSQE\DGLSLAGAPRQPRRKSRTSVLRI MVRWELSSNGNPGRGVLGL.GL.GL.GNKLI GQNLGL*HCVWVWETGE*KRWRLQMC GVASRRQ*VRNSVRGLVCHNSSAPPMYM SPTVFGGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIIVVILAAPACAPFIIDR*\ RERPSP**ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINFISFFSALAVYFRHNM EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 PPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETTTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTAPATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE					sequence		nucleotide insertion
HTVSQE\DGLSLAGAPRQPRRKSRTSVLRI MVRWELSSNGNPGRGVLGLGLGLGNKLI GQNLGL*HCVWVVWETGF*KRWRLQMC GVASRRQ*VRNSVRGLVCHNSSAPPMYM SPTVFGGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIVVILAAPACAPFHDR*Y REIRPSP*ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINFISFFSALAVYFRHNM EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 Å 6529 1 874 FPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETTTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE							EVFPEGTGLPLPHSDLPTSWCGHSLQCGSQSS
MVRWELSSNGNPGRGVLGLGLGLGNKLI GQNLGL*HCVWVVWETGE*KRWRLQMC GVASRRQ*VRNSVRGLVCHNSSAPPMYM SPTVFGGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIVVILAAPACAPFHDR*T REIRPSP*ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINFISFFSALAVYFRHNM EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 Å 6529 1 874 FFFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETTTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE			į .	į	ł		FPPAIHENAFIVFIASSLGHMLLTCILWRLTKK
GQNLGL*HCVWVVWETGE*KRWRLQMC GVASRRQ*VRNSVRGLVCHNSSAPPMYM SPTVFGGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIIVVILAAPACAPIPIDR*V REIRPSP*ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINPISFFSALAVYFRHNM EAGVYTIFAILEYTVVLINMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 PPFFQRINFIEHSGSVSLLALACDLGWCEI CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE							
GVASRRQ*VRNSVRGLVCHNSSAPPMYM SPTVFGGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIIVVILAAPACAPIPIDR*\ REIRPSP*ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINFISFFSALAVYFRHNN EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 PFFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRVVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE			İ	1		ĺ	
SPTVFGGGVGG*LHVTFILHPPEVEAAGIP GPSLPQRQGREIIIVVILAAPACAPTFIDR*\ REIRPSP*ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINFISFFSALAVYFRHIN EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 FPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRVVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE			1	}	1	J	
GPSLPQRQGREIIIVVILAAPACAPFHDR*T REIRPSP*ELGLRGEPTLSYPASCRVIRQPII RKSYSWKQRLFIINFISFFSALAVYFRHNN EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLTISQPEEKRF  799 2149 A 6529 1 874 FPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQGGGGRQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE			ĺ		[		
REIRPSP*ELGLRGEPTLSYPASCRVIRQFII RKSYSWKQRLFIINFISFFSALAVYFRHNM EAGVYTIFAILEYTVVLINMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 FPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE				1	1		
RKSYSWKQRLFIINFISFFSALAVYFRHNM EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 PFFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTAPATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE							
EAGVYTIFAILEYTVVLTNMAFHMTAWW GNKELLITSQPEEKRF  799 2149 A 6529 1 874 PPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTAPATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE				ł		[	
GNKELLITSQPEEKRF  799 2149 A 6529 1 874 FPFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE		1		1			
799 2149 A 6529 1 874 FFFFQRINFIEHSGSVSLLALACDLGWCEL CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRVVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE				İ	ł		
CCLVQGGGDLVDVVQTNHGEDEAGGDT DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE		24.10	<u> </u>	(500			
DEARCKESQQEAQENLREDLCLESFAKDI QIIEGSEREHEETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR BKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE	799	2149	) <b>^</b>	6529	j 1	0/4	
QIIEGSEREHETRTKQAALDGEPLGGGQ VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE		1	1	]		·.	
VHLHPSKEQQGQEGGERQRGARTHHWR EKGRRVRLRPPSGKLRADQPVRKLGGPT ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE			]	1			
EKGRRVRLRPPSGKLRADQPVRKLGGPTI ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE							
ELPGLQPHAPTPHTA/PATPTYSPAPDTPN RWKCPLPVEPRTRQLCRERTRKACPPKPE						1	
RWKCPLPVEPRTRQLCRERTRKACPPKPR				1	1		
		]					
			İ		i	Ì	GLPGDPTGPVTHHAPPVSPTGASGQERRAEP
GAVSYAHASATK					!	1	1
800 2150 A 6544 2 662 SAQRWAAVAGRWGCRLLALLLLVPGPG	800	2150	A	6544	2	662	SAQRWAAVAGRWGCRLLALLLLVPGPGGAS
			1			<u> </u>	EITFELPDNAKQCFYEDIAQGTKCTLEFQVITG
GHYDVDCRLEDPDGKVLYKEMKKQYDS							GHYDVDCRLEDPDGKVLYKEMKKQYDSFTF
TASKNGTYKFCFSNE\FSTFTHKTVYFDFC					}	1	TASKNGTYKFCFSNE\FSTFTHKTVYFDFQVG
		ļ	1		l	1	E\THLCFLVR/DRVSALTQMESACVSIHEALKS
					l		VIDYQTHFRLREAQGRSRAEDLNTRVAYWSV
		<u> </u>		<u> </u>		,	GEALILLVVSIGQVFLLKSFFSDKRTTTTRVGS
	801	2151	A	6556	1	1319	TPCMECIKGEGLREPQNLSGSQREPQTEGSM
						1	DGWRRMPRWGLLLLLWGSCTFGLPTDTTTF
						1	KRIFLKRMPSIRESLKERGVDMARLGPEWSQP
							MKRLTLGNTTSSVILTNYMDTQYYGEIGIGTP
			i	1		-	POTFKVVFDTGSSNVWVPSSKCSRLYTACVY
			·			İ	HKLFDASDSSSYKHNGTELTLRYSTGTVSGFL SQDIITVGGITVTQMFGEVTEMPALPFMLAEF
							DGVVGMGFIEQAIGRVTPIFDNIISQGVLKED
		1			{	ĺ	VFSFYYNRDSENSQSLGGQIVLGGSDPQHYE
GNEHYINI IKTGVWOIOMKGVSVGSSTI		1	1				GNFHYINLIKTGVWQIQMKGVSVGSSTLLCE
			1			ļ	DGCLALVDTGASYISGSTSSIEKLMEALGAKE
		1	1		l	į	KRLFDYVVKCNEGPTLPPTFLFLLGGKDTPLT
				}	1		SADYLFQESYSSKKLSTLAIHAMYIPPPTGPTL
VALGATFVIRKFYTEFDRGNNPHGFALAR		]				1	,
	802	2152	A	6567	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSL
1 3 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1		1	1	1	1	1	LAVVVLLALPVAWGQCNAPEW\LPFARPTNL
			[				TDEFEFPIGTYLNYECRPGYSGRPFSIICLKNS
	•	]				,	VWTGAKDRCRRKSCRNPPDPVNGMVHVIKG
		1					IQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIW
		1					DNETPICDRIPCGLPPTITNGDFISTNRENFHY
GSVVTYRCNPGSGGRKVFELVGEPSIYCI		1	1				GSVVTYRCNPGSGGRKVFELVGEPSIYCTSND
DQVGIWSGPAPQCIIPNKCTPPNVENGILV					1		DQVGIWSGPAPQCIIPNKCTPPNVENGILVSD
			I		1		NRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA
							LNKWEPELPSCSRVCQPPPDVLHAERTQRDK
			1	1			DNFSPGQEVFYSCEPGYDLRGAASMRCTPQG
DWSPAAPTCEVKSCDDFMGQLLNGRVLI		1	1	1	1		DWSPAAPTCEVKSCDDFMGQLLNGRVLFPV
			1				NLQLGAKVDFVCDEGFQLKGSSASYCVLAG
					Ì		MESLWNSSVPVCEQIFCPSPPVIPNGRHTGKP
LEVFPFGKAVNYTCDPHPDRGTSFDLIGE			1	1	1	I	I I EVEDECE AUDIVECTORUDO CECEDI ICECTID
			}				
FAKLKTQTNASDFPIGTSLKYECRPEYYG							CTSDPQGNGVWSSPAPRCGILGHCQAPDHFL

	SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
	nucl-	peptide		in	nucleotide	location	F-Phenylalanine, G-Glycine, H-Histidine,
1	cotide seq-	seq- uence		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
1	uence	uence		09/496 914	ng to first	to last amino acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
					amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		İ		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
		]			peptide		/=possible nucleotide deletion, \=possible
t				<del> </del> -	sequence		nucleotide insertion SITCLDNLVWSSPKDVCKPKSCKTPPDDVNG
į		İ	ĺ	İ	Ì	İ	MVHVITDIQVGSRINYSCTTGHRLIGHSSAECI
Ì							LSGNAAHWSTKPPICQRIPCGLPPTIANGDFIS
-		ĺ					TNRENFHYGSVVTYRCNPGSGGRKVFELVGE
-	:	ļ		}			PSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNV ENGILVSDNRSLFSLNEVVEFRCQPGFVMKGP
-							RRVKCQALNKWEPELPSCSRVCQPPPDVLHA
							ERTQRDKDNFSPGQEVFYSCEPGYDLRGAAS
						1	MRCTPQGDWSPAAPTCEVKSCDDFMGOLLN
			1			İ	GRVLFPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNG
			İ				RHTGKPLEVFPFGKAVNYTCDPHPDRGTSFD
	ĺ			1 1		i	LIGESTIRCTSDPOGNGVWSSPAPRCGILGHC
					ľ		QAPDHFLFAKLKTQTNASDFPIGTSLKYECRP
							EYYGRPFSITCLDNLVWSSPKDVCKRKSCKTP PDPVNGMVHVITDIQVGSRINYSCTTGHRLIG
					•		HSSAECILSGNTAHWSTKPPICQRIPCGLPPTI
			ļ				ANGDFISTNRENFHYGSVVTYRCNLGSRGRK
1	Ì		j :			]	VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN
	ľ					İ	KCTPPNVENGILVSDNRSLFSLNEVVEFRCOP GFVMKGPRRVKCQALNKWEPELPSCSRVCQ
	J						PPPEILHGEHTPSHQDNFSPGOEVFYSCEPGY
ı	i					1	DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF
							LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN
	- 1						PPAILNGRHTGTPSGDIPYGKEISYTCDPHPDR
1	1			ŀ			GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE
							LSVRAGHCKTPEQFPFASPTIPINDFEFPVGTS
							LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEPFNGMVHINTDTQFGSTVNYSC
	-					j ,	NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII
1							SCEPPPTISNGDFYSNNRTSFHNGTVVTYOCH
1							TGPDGEQLFELVGERSIYCTSKDDQVGVWSS
	1	l					PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH
			l				CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY
							SCEPSYDLRGAASLHCTPOGDWSPEAPRCTV
			- 1	- 1			KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC
İ				İ			EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT
l							CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS
			•	ŀ			SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL
		}		1.	·	Ţ	YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH
		}					YGDYVTLKCEDGYTLEGSPWSOCOADDRWD
		}				1	PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI
]				•			ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP
8	03	2153	A	6574	2	3233	RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL
		1	1	- 1	1	1	LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY
1				1		[	PWSWA\RVGPAVELALAQVKARPDLLPGWT
	1			Ì		1	VRTVLGSSENALGVCSDTAAPLAAVDLKWE
		-		ļ		İ	HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF
		-	İ	1	1	٠, ا	VAALHRRLGWERQALMLYAYRPGDEEHCFF
	1	İ	1			}	LVEGLFMRVRDRLNITVDHLEFAEDDLSHVT
	1	i					
	1				İ	Ī	RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVEELI DIEGOSLOGGOGDA PRID DIV
						· ·	RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGQDVSARQAFQAAKIITYKDPDNPEYL

			686		CK CCC	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	целсе	}	09/496	correspondi	to last amino	
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
1		i		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
<b>)</b> ,		]		residue of	sequence	Y=1 yrosine, X=Unknown, *-Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
i		_		sequence		nucleotide insertion
		1			}	DGLLLYIQAVTETLAHGGTVTDGENITQRMW
1				Ì	Í	NRSFQGVTGYLKIDSSGDRETDFSLWDMDPE
ļ	Ì					NGAFRVVLNYNGTSQELVAVSGRKLNWPLG
j	]	Ì	<b> </b>			YPPPDIPKCGFDNEDPACNQDHLSTLEVLALV
1	İ			ĺ	İ	GSLSLLGILIVSFFTYRKMQLEKELASELWRVR
1	ļ	}			·	WEDVEPSSLERHLRSAGSRLTLSGRGSNYGSL
	1		ļ	1		LTTEGQFQVFAKTAYYKGNLVAVKRVNRKR
	1	}	1	1		IELTRKVLFELKHMRDVQNEHLTRFVGACTD
ļ.	}			l	ł	PPNICILTEYCPRGSLQDILENESITLDWMFRY
ł						SLTNDIVKGMLFLHNGAICSHGNLKSSNCVV
ļ				1		DGRFVLKITDYGLESFRDLDPEQGHTVYAKK
ļ				1		LWTAPELLRMASPPVRGSQAGDVYSFGIILQE
1		j		Ì		IALRSGVFHVEGLDLSPKEHERVTRGEQPPFR
1		1	1		ļ	PSLALQSHLEELGLLMQRCWAEDPQERPPFQ
1	İ			j	j	QIRLTLRKFNRENSSNILDNLLSRMEQYANNL
	[	i			į	EELVEERTQAYLEEKRKAEALLYQILPHSVAE
	}		1			QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE
1	<b>!</b>		Ì		•	STPMQVVTLLNDLYTCFDAVIDNFDVYKVET
	ĺ					IGDAYMVVSGLPVRNGRLHACEVARMALAL
	l	1	İ			LDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGV
1	i	1	1	]		VGLKMPRYCLFGDTVNTASRMESNGEAL\KI
1		1	1			HLSS\ETKAVL\EEFGGFELELRGDVEMKGKG
1		1		1	†	KYRTYWLLGERGSSTRG
804	2154	A	6585	12	3837	DAPGRPPVRLPTMELEDGVVYQEEPGGSGAV
804	2134	1 ~	رەدە [	2	3057	MSERVSGLAGSIYREFERLIVRYDEEVVKELIP
1	1		1			LVVAVLENLDSVFAQDQEHQVELELLRDDNE
	İ			}	1	QLITQYEREKALRKHAEEKFIEFEDSQEQEKK
1	ĺ	1	1		İ	DLQTRVESLESQTRQLELKAKNYADQISILEE
		1				REAELKKEYNALHORHTEMIHNYMEHLERT
		i		1		KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP
. [		1		į	1	AGDGLLTPDAQKGGETPGSEQWKFQELSQPR
1	ŀ				1	SHTSLKDELSDVSQGGSKATTPASTANSDVA
		1				TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV
1	1	i	İ		1 .	QVAQETRNVSTGSAENEEKSEVQAIIESTPEL
1	1			!	]	DMDKDLSGYKGSSTPTKGIENKAFDRNTESL
•	1		1		1	FEELSSAGSGLIGDVDEGADLLGMGREVENLI
		1	Į			LENTQLETKNALNIVKNDLIAKVDELTCEK
	1	1	1		1	DVLOGELEAVKQAKLKLEEKNRELEEELRKA
1		1	{			RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE
ì	1	1	1			MARVLMERNQYKERLMELQEAVRWTEMIR
1	1	1		1		
ł	1	i	i	ŀ	İ	ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK
	1	1	1			KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP
	1	1	1			GDKSKAFDFLSEETEASLASRREQKREQYRQ
1		1	1	1	1	VKAHVQKEDGRVQAFGWSLPQKYKQVTNG
1	1	1			l	QGENKMKNLPVPVYLRPLDEKDTSMKLWCA
1	1	1	ì			VGVNLSGGKTRDGGSVVGASVFYKDVAGLD
1	}	1		1	1	TEGSKQRSASQSSLDKLDQELKEQQKELKNQ
1				1	1	EELSSLVWICTSTHSATKVLIIDAVQPGNILDS
1					1	FTVCNSHVLCIASVPGARETDYPAGEDLSESG
		ł	1	1 .	1	QVDKASLCGSMTSNSSAETDSLLGGITVVGC
			1	1		SAEGVTGAATSPSTNGASPVMDKPPEMEAEN
1	1	1			1	SEVDENVPTABE\ATEATEGNAGSAEDTV\DIS
1		1	1	1	1	QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND
1			1		1	SDAYKDQISVLPNEQDLVREEAQKMSSLLPT
1	Ì		1			MWLGAONGCLYVHSSVAQWRKCLHSIKLKD
1	}	1	}	1	1	SILSIVHVKGIVLVALADGTLAIFHRGVDGQW
1	1 .		1		1	DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG
1			1	l	1	YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ
				1		LAWVGDGVWVSIRLDSTLRLYHAHTYQHLQ
	1	1	1	l		DVDIEPYVSKMLGTGKLGFSFVRITALMVSC
L						

	SEQ ID	SEQ ID	1/~	Tero	Dead:	T D	
			Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq-	uence	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
	uence		İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			,		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l	1		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	1	I	peptide	podanaco	/=possible nucleotide deletion, \=possible
				1	sequence		nucleotide insertion
		<del> </del>	-	<del> </del>	sequence		MUCIEOTICE INSCIDENT
ı	Í	İ	İ	İ	į	ĺ	NRLWYGTGNGVIISIPLTETVILHQGRLLGLR
			1 .	i	1		ANKTSGVPGNRPGSVIRVYGDENSDKVTPGT
			l	İ	]		FIPYCSMAHAQLCFHGHRDAVKFFVAVPGQV
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Ì	805	2155	A	6605	469	2602	FGRLLWGTAFKSWKMKAPIPHLILLYATFTQ
			1	1	j		SLKVVTKRGSADGCTDWSIDIKKYQVLVGEP
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							YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA
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	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW NSARGGVGVRGARAMATVQEKAAALNLSAL
	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW NSARGGVGVRGARAMATVQEKAAALNLSAL
	806	2156	A	6614	3	1584	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA LPLLPRETSISSVIW NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLOT
	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
,	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE
, I	806	2156	Α	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKRTFEDSSCSLYRFTTIPNQD
,	806	2156	Α	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED
,	806	2156	Α	6614	3	1584	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWOE
,	806	2156	A	6614	3	1584	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPOPK
,	806	2156	A	6614	3	1584	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHINDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA
,	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEOPDRTDLVKE
,	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV
,	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKRTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF
,	806	2156	A	6614	3	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIFNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV MGKTEIALEATQLLKKLDFQNREEFRRLLYF MAVAANPSEFKLOKESDNRMVVKRIFSKAIV
	806	2156	A	6614	3	1584	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHOKDVFKIPGT
	806	2156	A	6614	3	1584	YCNIPMTILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKILDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LUHKIVSVKLMAIONGRDPNRDAGYIYCORI
	806	2156	A	6614	3	1584	YCNIPMTILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKILDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LUHKIVSVKLMAIONGRDPNRDAGYIYCORI
		•			3	1584	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHOKDVFKIPGT
	806	2156	A	6614	4198	1584	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPPJK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVKVLMAIQNGRDPNRDAGYIYCQRI DQRDYSNTTEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIFGD
		•					YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVVK\LMAIQNGPPNRDAGYIYCQRI DQRDYSNITEKTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR
		•					YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVKVLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHDDIFIEIIFGD FGIVOTFALETDELDSDRDPAIFSLCDFGAMR PQILLLLALLTLGLAAQHODKYPCKMVKMI.
		•					YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LUHKIVSVKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD PGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKMVKMIL CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD
		•					YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIFNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKILDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVFLMDHQKDVFKIPGT LUHKIVSVKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL
		•					YCNIPMTILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKILDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LUHKIVSVKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAFFSLCDFGAMR PQILLLLALLTILGLAAQHQDKVPCKM/VKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHILDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LUHKIVSVKLLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLLALLTLGLAAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS
		•				2094	YCNIPMTILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNI.SAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVS\VK\LMAIQNGRDPNRDAGYIYCQRI DQRDYSNTTEKTTIDELLYLLKTLDEDSKLSA KEKKK\LLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKM/VKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEOLDLHS
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSIVK\LMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKM/VKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLGEAPS LHTLSLAENSLTRLTRHTFDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVK\LMAIQNGDPNRDAGYIYCQRI DQRDYSNITEKTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKM/VKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTASQPQAEFOLT
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTASQPQAEFQLT WLDLRENKLLHPPDLAALPRLIYLNLINNLIR
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTASQPQAEFQLT WLDLRENKLLHPPDLAALPRLIYLNLINNLIR
		•				2094	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIFGD FGIVGTFALETDELDSDRDPAFFSLCDFGAMR PQILLLALLTILGLAAQHQDKVYCKMVKMI CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPTLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTASSQPQAEFQLT WLDLRENKLLHPPDLAALPRLIYLNLSNNLIR LPTGPPQDSKGIHAPSEGWSALPLSVAPSGNAS
		•				2094	YCNIPMILINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKILDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVFLMDHQKDVFKIPGT LUHKIVSVKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLLALLTLGLAAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTASQPQAEFQLT WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR LPTOPPQDSKGHAPSEGWSALPLSVAPSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFI.
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LHKIVSVKKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAPGTASSQPQAEFQLT WLDLRENKLLHFPDLAALPRLIYILNLSNNLIR LPTGPPQDSKGHAPSEGWSALPLSVAPSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPPPK RQSTMVNSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LVHKIVSVKVLMAIQNGRDPNRDAGYIYCQRI DQRDYSNTTEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFTYALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAFQTASNQPQAEFQLT WLDLRENKLLHPPDLAALPRLIYLNLSNNLIR LPTGPPQDSKGHAPSEGWSALPLSVAPSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE TLELGARALGNSLRTLLLQGNALRDLPPYTFA
		•				2094	YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA ILPLLPRETSISSVIW  NSARGGVGVRGARAMATVQEKAAALNLSAL HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFE AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD SQLGKENKLYSPARYADALFKSSDIRSASLED LWENLSLKPANSPHVNISTTLSPQVINEVWQE ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV NGKTEIALEATQLLKLLDFQNREEFRRLLYF MAVAANPSEFKLQKESDNRMVVKRIFSKAIV DNKNLSKGKTDLLVLFLMDHQKDVFKIPGT LHKIVSVKKLMAIQNGRDPNRDAGYIYCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA KEKKKLLGQFYKCHPDIFIEIIFGD FGIVGTFALETDELDSDRDPAIFSLCDFGAMR PQILLLALLTLGLAAQHQDKVPCKMVKML CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD LSGNQLRSILASPLGFYTALRHLDLSTNEISFL QPGAFQALTHLEHLSLAHNRLAMATALSAG GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD FSLQQLRVLDLSCNSIEAPGTASSQPQAEFQLT WLDLRENKLLHFPDLAALPRLIYILNLSNNLIR LPTGPPQDSKGHAPSEGWSALPLSVAPSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE

	T		Lone	<del></del>	<del> </del>	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Atanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ŀ	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	İ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	Į	Į.	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	i i	peptide		/=possible nucleotide deletion, \=possible
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SEQ ID	T SEO ID	Met	SEQ	Predicted	N	
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		j	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		i		residue of	sequence	Y='iyrosine, X=Unknown, *=Stop codon,
1				peptide	1	/=possible nucleotide deletion, \=possible
}	ļ	ļ	ļ	sequence		nucleotide insertion
						FGHSKANGEPTWALLLTAAJAELGILJASLDI.
1	1	1	1	i	1	VAPILSMFFLMCYLFVNLACALQTLLRTPNW
İ		l	1		1	RPRFRYYHWALSFMGMSICLALMFISSWYYA
						IVAMVIAGMIYKYIEYQGAEKEWGDGIRGLS
	į			}		LSAARFALLRLEEGPPHTKNWRPQLLVLLKL
		İ			-	DEDLHVKHPRLLTFASQLKAGKGLTIVGSVIV
ł	i	l	1			GNFLENYGEALAAEQTIKHLMEAEKVKGFCO
						LVVAAKLREGISHLIQSCGLGGMKHNTVVM
		1				GWPNGWRQSEDARAWKTFIGTVRVTTAAHL
}						ALLVAKNISFFPSNVEQFSEGNIDVWWIVHDG
ĺ	ĺ	1	1			GMLMLLPFLLK\QHKVWRKCSIRFF\TVAQLE
1						DNSIQMKKDLATFLYHLRIEAEVEVVEMHDS
	1	ļ	ļ			DISAYTYERTLMMEQRSQMI.RHMRLSKTER
1		]	1			DREAQLVKDRNSMLRLTSIGSDEDEETETYQ
						EKVHMTWTKDKYMASRGQKAKSMEGFQDL
						LNMRPDQSNVRRMHTAVKLNEVIVNKSHEA
	}	}	j .			KLVLLNMPGPPRNPEGDENYMEFLEVLTEGL
-	24.6	<u></u>				ERVLLVRGGGSEVITTYS
812	2162	A	6628	66	640	AVCTMSEMAELSELYEESSDLQMDVMPGEG
						DLPQMEVGSGSRELSLRPSRSGAQQLEEEGP
						MEEEEAQPMAAPEGKRSLANGPNAGEQPGQ
			!			VAGADFESEDEGEEFDDWEDDYDYPEEEQLS
					;	GAGYRVSAALEEADKMFLRTREPALDGGFQ
			ľ		į	MHYEKTPFDQLAFIEELF\SLMVVNRLTEELG
813	21/2		((00			CDEUDRE
613	2163	A	6630	708	1355	AKMGAYKYIQELWRKKQSDVMRFLLRVRC
ľ						WQYRQLSALHRAPRPTRPDKARRLGYKAKQ
						GY/VYIYIGFVFAVIYRIRVRRGGRKRPVPKG
						ATYGKPVHHGVNQLKFARSLQSVAEERAGR
1						HCGALRVLNSYWVGEDSTYKFPEVILIDPFHK
						AIRRNPDTQWITKPVHKHREMRGLTSAGRKS
						RGLGKGHKFHHTIGGSRRAAWRRRNTLQLH
814	2164	A	6635		1505	RYR
דגט	2104	Α.	0033	201	1705	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLR
						DSEDRSDSRAAQPAHDSGHGDDESPSTSSGT
						AGTSSVPELPGFYFDPEKKRYFRLLPGHNNCN
						PLTKESIRQKEMESKRLRLLQEEDRRKKIARM
						GFNASSMLRKSQLGFLNVTNYCHLAHELRLS
1		- 1		J	J	CMERKKVQIRSMDPSALASDRFNLILADTNS
		l		.		DRLFTVNDVTVGGSKYGIINLQSLKTPTLKVF
				l		MHENLYFTNRKV\NSVCWASLNHLDSHILLC
	<b> </b>					LMGLAETPGCATLLPASLFVNSHPAGIDRPG\
		- 1	]	j	J	MLCSFRIPGAWSCAWSLNIQANNCFSTGLSR RVLLTNVVTGHRQSFGTNSDVLAQQFALMA
		- 1	1			
	1			İ	ļ	PLLFNGCRSGEIFAIDLRCGNQGKGWKATRLF HDSAVTSVRILODEOYLMASDMAGKIKLWD
· i	1	ľ	١ ١	ł	1	LRTTKCVRQYEGHVNEYAYLPLHVHEEEGIL
	ļ		l	1		VAVGQDCYTRIWSLHDARLLRTIPSPYPASKA
			- 1			DIPSVAFSSRLGGSRGAPGLLMAVGQDLYCY
			. [			SYS
815	2165	A	6643	659	3282	NKNILEVPSARTTRIMGDHLDLLLGVVLMAG
		***	30.5		3202	PVFGIPSCSFDGRIAFYRFCNLTQVPQVLNTTE
j	j	ļ	ļ	1		RLLLSFNYIRTVTASSFPFLEQLQLLELGSQYT
Ì	[	- 1	ļ	ĺ	ſ	
	j	ŀ	ŀ	J		PLTIDKEAFRNLPNLRILDLGSSKIYFLHPDAF QGLFHLFELRLYFCGLSDAVLKDGYFRNLKA
	ŀ	1	ĺ	ł	l	LTRLDLSKNQIRSLYLHPSFGKLNSLKSIDFSS
	- 1	J	J	,	ļ	NQIFLVCEHELEPLQGKTLSFFSLAANSLYSR
				[	1	VSVDWGKCMNPFRNMVLEILDVSGNGWTV
1	Ţ	- 1	1	ŧ	i	DITGNFSNAISKSQAFSLILAHHIMGAGFGFHN
-				l		IKDPDQNTFAGLARSSVRHLDLSHGFVFSLNS
		1			1	***** ~ VITE TO LARGE V KALDLEARUR V PSLNS

n e s	SEQ ID NO: of nucl- sotide eq- sence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RVFETLKDLKVLNLAYNKINKIADEAFYGLD NLQVLNLSYNLLGELYSNFYGLPKVAYIDL QKNHIAIIQDQTFKFLEKLQTLDRDNALTTIH FIPSIPDIFLSGNKLVTLPKINLTANLIHLSENR
							LENLDILYFLLRVPHLQILILNQNRFSSCSGDQ TPSENPSLEQLFLGENMLQLAWETELCWDVF EGLSHLQVLYLNHNYLNSLPPGVFSHLTALR GLSLNSNRLTVLSHNDLPANLEILDISRNQLL APNPDVFVSLSVLDITHNKFICECELSTFINWL NHTNVTIAGPPADIYCVYPDSLSGVSLFSLSTE GCDEEEVLKSLKFSLFIVCTVTLTLFLMTILTV TKFRGFCFICYKTAQRLVFKDHPQGTEPDMY KYDAYLCFSSKDFTWVQNALLKHLDTQYSD QNRFNLCFEERDFVPGENRPANIQDAIWNSR KIVCLVSRHFLRDGWCLEAFSYAQGRCLSDL NSALIMVVVGSLSQYQLMKHQSIRGFVQKQQ YLRWPEDLQDVGWFLHKLSQQILKKEKEKK KDNNIPLQTVATIS
1	316	2166	A	6646	1	3811	RDRAGVRPAGKQHAAAAFYDVGGDRPWDS GNTQLPPRNPVKANAMFGAGDEDDTDFLSPS
							GGARLASLFGLDQAAAGHGNEFFQYTAPKQP KKGQGTAATGNQATPKTAPATMSTPTILVAT
1							AVHAYRYTNGQYVKQGKFGAAVLGNHTTR
			·	,			EYRILLYISQQQPVI'VARIHVNFELMVRPNNY STFYDDQRQNWSIMFESEKAAVEFNKQVCIA
1	ĺ						KCNSTSSLDAVLSQDLIVADGPAVEVGDSLE
1							VAYTGWLFQNHVLGQVFDSTANKDKLLRLK LGSGKVIKGWEDGMLGMKKGGKRLLIVPPA
1		,					CAVGSEGVIGWTQATDSILVFEVEVRRVKIA
							KDSGSDGHSVSSRDSAAPSPIPGADNLSADPV   VSPPTSIPFKSGEPALRTKSNSLSEQLAINTSPD
							AVKAKLISRMAKMGQPMLPILPPQLDSNDSEI
							EDVNTLQGGGQPVVTPSVQPSLQPAHPALPQ MTSQAPQPSVTGLQAPSAALMQVSSLDSHSA
							VSGNAQSFQPYAGMQAYAYPQASAVTSQLQ
					ļ		PVRPLYPAPLSQPPHFQGSGDMASFLMTEAR OHNTEIRMAVSKVADKMDHLMTKVEELQKH
1					į		SAGNSMLIPSMSVTMETSMIMSNIQRIIQENER
							LKQEILEKSNRIEEQNDKISELIERNQRYVEQS
				1			NLMMEKRNNSLQTATENTQARVLHAEQEKA KVTEELAAATAQVSHLQLKMTAHQKKETEL
				1			QMQLTESLKETDLLRGQLTKVQAKLSELQET SEQAQSKFKSEKQNRKQLELKVTSLEEELTDL
					1		RVEKESLEKNLSERKKKSAQERSQAEEEIDEI
1				}			RKSYQEELDKLRQLLKKTRVSTDQAAAEQLS LVQAELQTQWEAKCEHLLASAKDEHLQQYQ
							EVCAQRDAYQQKLVQLQEKSVCFA\CLALQA
							QITALTKQNEQHIKELEKNKSQMSGVEAAAS DPSEKVKKIMNQVFQSLRREFELEESYNGRTI
Ţ				1	}		LGTIMNTIKMVTLQLLNQQEQEKEESSSEEEE
							EKAEERPRRPSQEQSASASSGQPQAPLNRERP ESPMVPSEQVVEEAVPLPPQALTTSQDGHRR
							KGDSEAEALSEIKDGSLPPELSCIPSHRVLGPP
							TSIPPEPLGPVSMDSECEESLAASPMAAK\PDN
							PSGK\VCVREVAPDGPLQESSTRLSLTS\DPEE GDPLALGPESPGEPQPPQLKKDDVTSSTGPHK
							ELSSTEAGSTVAGAALRPSHHSQRSSLSGDEE
							DELFKGATLKALRPKAQPEEEDEDEVSMKGR PPPTPLFGDDDDDDDDDDDWLG
L	817	2167	A	6649	63	1073	FFRSSSDNGSPIRQYE/HSTPAHQGPVMGLEG

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  KS/ARNSOLRIVLVØKTGAGKSATGNSILGRK VFHSGTAAKSITKKCEKRSSSWKETELVVVD TPGIFDTEVPNAETSKEIIRCILLTSPGPHALLL VVPLGRYTEEHKATEKILKMFGERARSFMIL IFTRKDDLGDTNLHDYLREAPEDIQDLMDIFG DRYCALNNKATGAEQEAQRAQLLGLIQRVV RENKEGCYTNRMYQRAEEEIQKQTQAMQEL HRVELEREKARREEYEEKIRKLEDKVEQEKR KKQMEKKLAEQEAHYAVRQQRARTEVESKD
818	2168	A	6660	357	1890	GILELIMTALQIASFILLRLFAED  APSGSWTRVVLTLDPCSLRSRSPRSLLDPGMP GISARGLSHEGRKQLAVNLTRVLALYRSILDA YIIEFFITDNLWDTLPCSWQEALDGLKPPQLA TMLLGMPGEGEVVRYRSVWPLTLLALKSTA CALAFTRMPGFQTPSEFLENPSQSSRLTAPFR KHVRPKKQHEIRRLGELVKKLSDFT/GLHPGC RRGLRPG/HLSRFMALGLGLMVKSIEGDQRL VERAQRLDQELLQALEKEEKRNPQVVQTSPR HSPHHVVRWVDPTALCEELLLPLENPCQGRA RLLLTGLHACG/DLSVALLRHFSCCPEVVALA SVGCCYMKLSDPGGYPLSQWVAGLPGYELP YRLREGACHALEEYAERLQKAGPGLRTHCY RAALETVIRRARPELRRPGVQGIPRVHELKIEE YVQRGLQRVGLDPQLPNLAALQAHLAQEN RVVAFFSLALLLAPLVETLILLDRLLYLQEQA LSPGFHAELLPIFSPELSPRNLVLVATKMPLG QALSVLETEDS
819	2169	A	6661	65	2686	SGSGHCLAEAASMGPWGWKLRWTVALLLA AAGTAVGDRCERNEFQCQDGKCISYKWVCD GSAECQDGSDESQETCLSVTCKSGDFSCGGR VNRCIPQFWRCDGQVDCDNGSDEQGCPPKTC SQDEFRCHDGKCISRQFVCDSDRDCLDGSDE ASCPVLTCGPASFQCNSSTCIPQLWACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEFH CLSGECIHSSWRCDGGPDCKDKSDBENCAVA TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRD WSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGVSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKKLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQVLCLPAPQINPHSPKFTCACPDGM LLAR\DMRSCLTEG\EAAVATQETSTVRLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAG\GRGN\EKKPSSVRALSIVL PIV\LLVFLCLGVFLLWKNWRLKNINSINFDNP VYQKTTEDEVHICHNQDGYSYPSRQMVSLED
820	2170	A	6666	17		DVA ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI EGYLHILLISKAEDYRSYRFPKLTVITEYLLLF RVAGLESLGDLFPNLTVIRGWKLFYNYALVIF

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, P=possible nucleotide deletion, \=possible nucleotide insertion
				sequence		EMTNIKDIGLYNLRNITRGAIRIEKNADLCYL STVDWSLILDAVSNNYIVGNKPPKECGDLCP GTMEEKPMCEKTTINNEYNYRCWTTNRCQK MCPSTCGKRACTENNECCHPECLGSCSAPDN DTACVACRHYYYAGVCVPACPPNTYRFEGW RCVDRDFCANILSAESSDSEGFVIHDGECMQE CPSGFIRNGSQSMYCIPCEGPCPKVCEEKKT KTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIA SELENFMGLIEVVTGYVKIRHSHALVSLSFLK NLRLILGEEQLEGNYSFYVLDNQNLQQLWD WDHRNLTIKAGKMYFAFNPKLCVSEIYRMEE VTGTKGRQSKGDINTRNNGERASCESDVLHF TSTTTSKNRIIITWHRYRPPDYRDLISFTVYYK EAPFKNVTEYDGQDACGSNSWNMVDVDLPP NKDVEPGILLHGLKPWTQYAVYVKAVTLTM VENDHIRGAKSEILYIRTNASVPSIPLDVLSAS NSSSQLIVKWNPPSLPNGNLSYYIVRWQRQP QDGYLYRHNYCSKDKIPIRKYADGTIDIEEVT ENPKTEVCGGEKGPCCACPKTEAEKQAEKEE AEYRKVFENFLHNSIFVPRPERKRRDVMQVA NTTMSSRSRNTTAADTYNITDPEELETEYPFF ESRVDNKERTVISNLRPFTLYRIDIHSCNHEAE KLGCSASNFVFARTMPAEGADDIPGPVTWEP RPENSIFLK WPEPENPNGLILMYEIKYGSQVE DQRECVSRQEYRKYGGAKLNRLNPGNYTARI QATSLSGNGSWTDPVFFYVQAKRYENFIHLII ALPVAVLLIVGGLVIMLYVFHRKNNSRLGN GVLYASVNPEYFSAADVYVPDEWEVAREKIT MSRELGQGSFGMVYEGVAKGVVKDEPETRV AIKTVNEAASMRERIEFLNEASVMKEFNCHH VVRLLGVVSQGQPTLVIMELMTRGDLKSYLR SLRPEMENNPVLAPPSLSKMIQMAGEIADGM AYLNANKFVHRDLAARNCMVAEDFTVKIGD FGMTRDIYETDYYRKGGKGLLPVRWMSPESL KDGVFTTYSDVWSFGVVLWEIATLAEQPYQ GLSNEQVLRFVNMEGGLLDKPDNCPDMLFEL MRMCWQYNPKMRPSFLEIISSIKEEMEPGFRE VSFYYSEENKLPEPEELDLEPENMESVPLDPS
821	2171		6691	106	825	ASSSSLPLPDRHSGHKAENGPGPGVLVLRASF DERQPYAHMNGGRKNERALPLPQSSTC GRVLFRGCGVGHKGQVLMGTFILAQDWLSE
	51/1	**	·			SNHVFCVSSMLRLQKRLASSVLRCGKKKVW LDPNETNEIANANSRQURKLIKDGLIIRKPVT VHSRARCRKNTLARRKGRHMGIGKRKGTAN ARMPEKVTWMRRMRILRRLLRRYRES/KRYR ESKKIDRHMYHSLYLKVKGNVFKNKRILMEH IHKLKADKARKKLLADQAEARRSKTKEARK RREERLQAKKEEIKTLSKEEETKK
822	2172	A	6715	772	21	DFRPGLLLPRKKKMFGFHKPKMYRSIEGC\CI SGAKSSSS\RFTDSKRYEK\DFQ\SCFGLHETR\ SGDI\CNA\CVLL\LKRWKKLPAGSKK\NWNH VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST QISKLQKEFKR\HNSDAHSTTS\SASP\AQSPLF TVNQFRWTGSDTGVGFPGSNRNHPVFSFLDL\ TYWKRQKICCGI\IYKGRFGEVLIDTHLFKPCC SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM
823	2173	Ą	6727	3	4063	PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS VGGQNPSTGGISADRTQGNIGCGGDTDPGQS

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	,,,,,,,	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	•	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ĺ	l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	İ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i		i		peptide	·	/=possible nucleotide deletion, \=possible
1		l		sequence		nucleotide insertion
ļ				acquatico		SSQPSQDGQESNVPSVGSLADPDYLNTPQMN
Ì	ł	1	1			
						TPVTLNSAAPASNSGAGVLPSPATPRFSVPTP
	1					RTPRTPRTPRGGGTASGQGSVKYDSTDQGSP
[	1	ĺ				ASTPSTTRPLNSVEPATMQPIPEAHSLYVTLIL
1	l					SDSVMNIFKDRNFDSCCICACNMNIKGADVG
	l	}	l i	i		LYIPDSSNEDQYRCTCGFSAIMNRKLGYNSGL
1	l	İ				FLEDELDIFGKNSDIGQAAERRLMMCQSTFL
ł	l	l				PQVEGTKKPQEPPISLLLLLQNQHTQPFASLN
İ	1		1 1			FLDYISSNNRQTLPCVSWSYDRVQADNNDY
	ŀ					I
	ĺ					WTECFNALEQGRQYVDNPTGGKVDEALVRS
		1	1			ATVHSWPHSNVLDISMLSSQDVVRMLLSLQP
		1	1			FLQDAIQKKRTGRTWENIQHVQGPLTWQQFH
1	1	ł	† I			KMAGRGTYGSEESPEPLPIPTLLVGYDKDFLT
	1					ISPFSLPFWERLLLDPYGGHRDVAYTVVCPEN
	1			1		EALLEGAKTFFRDLSAVYEMCRLGQHKPICK
	}		] ]	i .		VLRDGIMRVGKTVAQKLTDELVSEWFNQPW
			1			SGEENDNHSRLKLYAQVCRHHLAPYLATLQL
	•		]			DSSLLIPPKYQTPPAAAQGQATPGNAGPLAPN
	1		1			GSAAPPAGSAFNPTSNSSSTNPAASSSASGSSV
						PPVSSSASAPGISQISTTSSSGFSGSVGGONPST
			1			GGISADRTQGNIGCGGDTDPGQSSSQPSQDG
	1					
	-					QESVTERERIGIPTEPDSADSHAHPPAVVIYM
İ			ł			VDPFTYAAEEDSTSGNFWLLSLMRCYTEMLD
ŀ						NLPEHMRNSFILQIVPCQYMLQTMKDEQVFY
	1		1			IQYLKSMAFSVYCQCRRPLPTQIHIKSLTGFGP
1	·					AASIEMTLKNPERPSPIQLYSPPFILAPIKDKQT
						ELGETFGEASQKYNVLFVGYCLSHDQRWLL
1	· ·					ASCTDLHGELLETCVVNIALPNRSRRSKVSAR
				*		KIGLQKLWEWCIGIVQMTSLPWRVVIGRLGR
į						LGHGELKDWSILLGECSLQTISKKLKDVCRM
						CGISAADSPSILSACLVAMEPQGSFVVMPDAV
						TMGSVFGRSTALNMQSSQLNTPQDASCTHIL
						VFPTSSTIQVAPANYPNEDGFSPNNDDMFVDL
-			ĺ			
						PFPDDMDNDIGILMTGNLHSSPNSSPVPSPGSP
						SGIGVGSHFQHSRSQGERLLSREAPEELKQQP
						LALGYFVSTAKAENLPQWFWSSCPQAQ:\\QC
						PLFLKASLHHHISVAQTDELLPARNSQRVPHP
1 1						LDSKTTSDVLRFVLEQYNALSWLTCNPATQD
					_	RTSCLPVIIFVVLTQLYNAIMNIL
824	2174	Α	6732	2440	365	VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR
						RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG
1						GGGGGTIKRPGITGPTAATSPSGEPGNAASAP
1				1		LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC
						ASLVFGRLOHRGGDRKRGLLGRSSGDAASD
1						
] .				1		QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV
				į		GLAAREGNVKVLRKLLKKGRSVDVADNRG
				:		WMPIHEAAYHNSVECLQMLINADSSENYIKM
				i		KTFEGFCALHLAASQGHWKIVQILLEAGADP
						NATTLEETTPLFLAVENGQIDVLRLLLQHGAN
				ļ		VNGSHSMCGWNSLHQASFQENAEIIKLLLRK
1						GANKECQDDFGITPLFVAAQYG\KLESL\SILIS
						SG\ANVNCQALDKATPLFIAAQEGHTKCVELL
						LSSGADPDLYCNEDSWOLPIHAAAOMGHTKI
						LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE
			l j	j		DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ
					ļ	KDCEFFGIVNILLKYGAQINELHLAYCLKYEK
					İ	PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN TH
						FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA
						KYKEWLPHLLVAGFDPLILLCNSWIDSVSIDT
				ļ		LIFTLEFTNWKTLAPAVERMLSARASNAWIL
L			1			QQHIATVPSLTHLCRLEIRSSLKSERLRSDSYIS

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	- CEO TO	1 3 6 4	Loro	Dog 0.4.1	1 To 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	l		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ.		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
}	ļ	}		peptide	ļ ·	/=possible nucleotide deletion, \=possible
			]	sequence		nucleotide insertion
						QLPLPRSLHNYLLYEDVLRMYEVPELAAIQD
l						G
825	2175	A	6735	277	1252	RIMGLEDRGVQMLLTTVGAFAAFSLMTIAVG
623	21/3	^	0/33	2//	1232	
	1		ĺ	[		TDYWLYSRGVCKTKSVSENETSKKNEEVMT
l	i					HSGLWRTCCLEGNFKGLCKQIDHFPEDADYE
1	ŀ	1	ł		ĺ	ADTAEYFLRAVRASSIFPILSVILLFMGGLCIA
		İ	1	l .		ASEFYKTRHNIILSAGIFFVSAGLSNIIGIIVYIS
	1				}	ANAGDPSKSDSKKNSYSYGWSFYFGALSFIIA
l	ì	ł	1	1		EMVGVLAVHMFIDRHKQLRATARA\TDYLQ
1		1	1	Ì		ASAITRIPSYRYRYQRRSRSSSRSTEPSHSRDA
			ł			SPVGIKGFNTLPSTEISMYTLSRDPLKAATTPT
			1		1	ATYNSDRDNSFLQVHNCIQKENKDSLHSNTA
	1		1	İ		NRRTTPV
826	2176	A	6744	3	5177	SDDLRTGLFQDVQDAESLKLPGVYEVLFYNE
020	21,0	^	0,	'.	51,77	TEDCPGMMLWRYPEPRGLTLVRITPVPFNTT
	İ	I	1	1		EDPDISTADLGDVLODPCSLEYWDELQKVFV
ŀ			1	l	1	AFREFNLSESKVCELOLPDINLVNDOKKLVSS
	<b> </b>		1			
1		l	1			DLWRIVLNSSQNGADDQSSASESGSQSTCDPL
l		1	1			VTPTALAACTRVDSCFTPWFVPSLCVSFQFAH
J		Į	1	1	ļ	LEFHLCHHLDQLGTAAPQYLQPFVSDRNMPS
1	ł	Ι.		1		ELEYMIVSFREPHMYLRQWNNGSVCQEIQFL
			1			AQADCKLLECRNVTMQSVVKPFSIFGQMAVS
1	1	ļ	<b>\</b>			SDVVEKLLDCTVIVDSVFVNLGQHVVHSLNT
		1	j .			AIQAWQQNKCPEVEELVFSHFVICNDTQETL
l		1	ŀ	1	ľ	RFGQVDTDENILLASLHSHQYSWRSHKSPQL
ſ	1	1	1	[	ĺ	LHICIEGWGNWRWSEPFSVDHAGTFIRTIQYR
1	İ	l	1			GRTASLIIKVQQLNGVQKQIIICGRQIICSYLSQ
1	]					SIELKVVQHYIGQDGQAVVREHFDCLTAKQK
1			1			LPSYILENNELTELCVKAKGDEDWSRDVCLE
1	1	i	1		İ	
ł	ł	ł	}	l		SKAPEYSIVIQVPSSNSSIIYVWCTVLTLEPNS
			1			QVQQRMIVFSPLFIMRSHLPDPIIIHLEKRSLGL
1	i	l	Į.	1		SETQIPGKGQEKPLQNIEPDLVHHLTFQAREE
		1			Į.	YDPSDCAVPISTSLIKQIATKVHPGGTVNQILD
ŀ		l				EFYGPEKSLQPIWPYNKKDSDRNEQLSQWDS
1	}	İ	J	1	Ì	PMRVKLSIWKPYVRTLLIELLPWALLINESKW
l	i .	1				DLWLFEGEKIVLQVPAGKIIIPPNFQEAFQIGIY
1		1	1			WANTNTVHKSVAIKLVHNLTSPKWKDGGNG
1		1	1	I	1	EVVTLDEEAFVDTEIRLGAFPGHQKLCQFCIS
				1	!	SMVQQGIQIIQIEDKTTIINNTPYQIFYKPQLSV
1		1	1	}	}	CNPHSGKEYFRVPDSATFSICPGGEQPAMKSS
1	1	1		i	l	SLPCWDLMPDISQSVLDASLLQKQIMLGFSPA
1	1	1	1	1	1	PGADSSQCWSLPAIVRPEFPRQSVAVPLGNFR
1		1		1		ENGFCTRAIVLTYQEHLGVTYLTLSEDPSPRV
	1	1		1		IJHNRCPVKMLIKENIKDIPKFEVYCKKIPSECS
	1	1	1	1		IHHELYHOISSYPDCKTKDLLPSLLLRVEPLDE
		ł	1	!	]	
	1		1	1	1	VTTEWSDAIDINSQGTQVVFLTGFGYVYVDV
	1	I	1	1	1	VHQCGTVFITVAPEGKAGPILTNTNRAPEKIV
		1	1	1	1	TF/KMFITQLSLAVFDDLTHHKASAELLRLTL
1		1	1	1		DNIFLCVAPGAGPLPGEEPVAALFELYCVEIC
		1		ŀ	1	CGDLQLDNQLYNKSNFHFAVLVCQGEKAEPI
		1	1	1		QCSKMQSLLISNKELEEYKEKCFIKLCITLNEG
1			1	l	1	KSILCDINEFSFELKPARLYVEDTFVYYIKTLF
	[	Ì	1	}		DTYLPNSRLAGHSTHLSGGKQVLPMQVTQH
	1	1	ì	l	1	ARALVNPVKLRKLVIQPVNLLVSIHASLKLYI
			1	1		
		1			1	ASDHTPLSFSVFERGPIFTTARQLVHALAMHY
	1	1		1	1	AAGALFRAGWVVGSLDILGSPASLVRSIGNG
		1	i	1		VADFFRLPYEGLTRGPGAFVSGVSRGTTSFVK
		ļ		[	1	HISKGTLTSITNLATSLARNMDRLSLDEEHYN
	1	1		1	1	RQEEWRRQLPESLGEGLRQGLSRLGISLLGAI
	1	1	1	1	[	AGIVDQPMQNFQKTSEAQASAGHKAKGVISG
·		4	<del> </del>	I.,	<del></del>	

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	L Amino cold converse (A. Alistin C. C. and
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	"04	in NO.	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	1	USSN	location		F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence		09/496		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
uence	ucijos	İ	1	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
delice	1	ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l		peptide		/=possible nucleotide deletion, \=possible
	<del> </del>	ļ		sequence	<u> </u>	nucleotide insertion
}	ļ	!	ļ	!	!	VGKGIMGVFTKPIGGAAFLVSQTGYGILHGA
		ŀ		<u> </u>		GLSQLPKQRHQPSD\VHADQAPNSHVKYVW
1	İ	l	1		ł	KMLQSLGRPEVHMALDVVLVRGSGQEHEGC
	Į.		ļ			LLLTSEVLFVVSVSEDTQQQAFPVTEIDCAQD
i	ł					SKQNNLLTVQLKQPRVACDVEVDGVRERLSE
1	į	1	ŀ			QQYNRLVDYITKTSCHLAPSCSSMQIPCPVVA
ł	1		1	1	l	AEPPPSTVKTYHYLVDPHFAQVFLSKFTMVK
					ł	NKALRKGFP
827	2177	A	6748	2	1662	FVGAPRRGNPFGSPGNPGRHQGPCHRPRGTK
1		ĺ				ASGVSPTLWRPQAAATGLEMPSSGRALLDSP
						I Decel Tel Decreceporceni Al oportuni
1						LDSGSLTSLDSSVFCSEGEGEPLALGDCFTVN
1						VGGSRFVLSQQALSCFPHTRLGKLAVVVASY
1			i i			RRPGALAAVPSPLELCDDANPVDNEYFFDRS
			1			SQAFRYVLHYYRTGRLHVMEQLCALSFLQEI
i						QYWGIDELSIDSCCRDRYFRRKELSETLDFKK
			i .		·	DTEDQESQHESEQDFSQGPCPTVRQKLWNIL
1	1		]			EKPGSSTAARIFGVISHFVGVSHNMALMSAEL
1		'				SWLDLQLLEILEYVCISWFTGEFVLRFLCVRD
1	1		·		•	RCRFLRKVPNIIDLLAILPFYITLLVESLSG\SQT
1						TQEL\ENVGAHCPGCLRLLRAL\RMLKAWGR
1				1		HSTGLRSLGMTITQCYEEVGLLLLFLSVGISIF
1						STVEYFAEQSIPDTTFTSVPCAWWWATTSMT
						TVGYGDIRPDTTTGKIVAFMCILSGILVLALPI
1	1		1			AIINDRFSACYFTLKLKEAAVRQREALKKLTK
			1			NIATDSYISVNLRDVYARSIMEMLRLKGRER
						ASTRSSGGDDFWF
828	2178	A	6786	5672	1360	GTHPASSGPVPLPPAAVSAATREELGEPVPFV
				1		TASSGFQSMHSSNPKVRSSPSGNTQSSPKSKQ
	'		· ·			EVMVRPPTVMSPSGNPQLDSKFSNQGKQGGS
				j		ASQSQPSPCDSKSGGHTPKALPGPGGSMGLK
1		- 1	' ł			NGAGNGAKGKGKRERSISADSFDQRDPGTPN
1 1						DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT
				1		APRSSTPPHGQTTATEPTPAQKTPAKVVYVFS
1 1		ĺ		1		TEMANKAAEAVLKGQVETIVSFHIQNISNNK
ļ				ł		TERSTAPLNTQISALRNDPKPLPQQPPAPANQ
			]	ł		DQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRE
		ŀ	}	į		SPGVENKI IDGVGGDA GETDI DDDGTGDAIGMAL
	1		- 1	ĺ	i	SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN
,	i	l		ļ	l	NRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPT
1 1	- 1	J		ļ	1	LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP
			į		1	DEKEPTGAQSGGPQQNPGVLDGPQKKPEGPI
] [	i	-			ŀ	QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR
[			ļ	ľ	ŀ	DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP
]	į		I		ļ	EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ
] [	1	- 1	- 1		i	DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP
	ļ	'				GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ
, ,	į	J	}	1	j	MRLPGFAGMINSEMEGPNVPNPASRPGLSGV
		i		1	1	SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP
		į			İ	NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR
			1	1	ł	PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP
		i		1	į	LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM
	1	- 1		[	ľ	KGDVNLNVNMGSNSQMIPQKMREAGAGPEE
	1	- 1		l		MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE
}	- 1		J			YGMGPRPFLPMSQGPGSNSGLRNLREPIGPDO
	1	}		l		RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG
				Į.		LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ
			1	1		SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA
	1	- 1	ļ	l	l	SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS
	- 1		į	,	ľ	PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG
		İ	1	-		GPPPPTA SODA SYNIDOLGI POGERNAM CONVESC
	J	1	ſ		}	GPPPPTASQPASVNIPG\SLPSSTPYTMPPEPTL
<u>-</u>						SQNPLSIMMSR\MSKFAM\PS\SNPGYNHDAI

SSQ ID NO: of nucleotide peptide control of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of pe				T SHA	<del></del>		Amino acid sequence (A=Alanine C=Cysteine,
in mucleotide location (1946) wence where the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corre	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Ariannie C-Cystenie,
eside sequence      Sequence			hod	1 -			D=Aspartic Acid, E=Glutainic Acid,
1946   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914   914			ł	,			F=Phenylalanme, G=Glycine, n=ristianie,
uence    14	eotide	seq-	1	1			
### ### ### ### ### ### ### ### ### ##	seq-	uence	1	09/496			
reidue of peptide sequence y=Tyrosine, X=Unknown, *=Stop codon, 'possible nucleotide insertion (	uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
peptide		ļ		Į .	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1		pentide	1 - 1	/=possible nucleotide deletion, \=possible
KTYASSDDDSPRARSPILIFSMNNMFGMGINT			1	1	,		
		<u> </u>		<del> </del>	sequence	<del></del>	KTVASSDDDSPPARSPNI PSMNNMPGMGINT
		ĺ			•	}	
			l	}		ł	
INITESGGCASFFGGMGFFGGPLGRPSNLV  SADAALCKPGGFGPDSTIVLGNSMPSVFT  DPDLQEVIRPGATGIPEDILSRIIPSEKPSGTI, PPDLQEVIRPGATGIPEDILSRIIPSEKPSGTI, VPPRGGPTGRKGPQOPGFGFSTRMQGMMGBG AFRAGLALPGMGGPGPVGTPDILGTAPSKW GHNPMRPPAFLQGMMGPHRMMSPAQST MRGQFTLMSNPAAAVGMFGKRGPAGLYT HPGRVGSFGMMMSMQGMMGPNRTS  829 2179 A 6797 433 3 ASFFINSICICKILE VOFFVGHFAHDDVGGRH GPGGRGSSRSRSLQCAPGGGRRSGCPAGSS- ASTCPPSRGGSGADRGSPSPPSERAAPTAG AAASSTSSGASCPPVPASSRWGVRSRTRSGGS GEREPKDRPSERFLV  830 2180 A 6800 3 1911 LPERAFGPRFFRAPRRRRRRLLLSPPFEPPPF BEFARGFMCFFTRAPRRRRRRLLLSPPFEPPPPF BEFARGFMCFTRAPRRRRRRLLLSPPFEPPPPPF BEFARGFMCFTRAPRRRRRRLLLSPPFEPPPPF BEFARGFMCFTRAPRRRRRRLLLSPPFERPPPP BEFARGFMCFTRAPRRRRRRLLLSPPFEPPPP BEFARGFMCFTRAPRRRRRRLLLSPPFEPPPP BEFARGFMCFTRAPRRRRRRLLLSPPFEPPPP BEFARGFMCFTRAPRRRRRRLLLSPPFEPPPP BEFARGFMGFMCFTRAPRRRRRRRLLLSPFERFPPP BEFARGFMGFMCFTRAPRRRRRRLLLSPFERFPPP BEFARGFMGFMCFTRAPRRRRRRRLLLSPFERFPPP BEFARGFMGFMGFMGFMGFMGFMGFMGFMGFMGFMGFMGFMGFMG		Ì	1				
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Sequence   USSN   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocation   Ocatio			nou				D=Aspartic Acid, E=Glutamic Acid,
Sequence	1	1	1				r=Phenylalanine, G=Glycine, H=Histidine,
uenice    914   ne pio first anino acid residue of peptide residue of peptide sequence   Q=Gluzaniae, N=Arginie, N=Typupipan, Y=Typusia, N=Typusia, N=Typupipan, Y=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Typusia, N=Ty	1						1=Isoleticine, K=Lysine, L=Leucine,
amino acid pepide residue of pepide sequence		401.00					M=Methionine, N=Asparagine, P=Proline,
residue of peptide sequence   Y=Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Y=Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Tyrosine, X=Unknown, *=Stop codon, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide sequence   Tyrosine, X=Unknown, peptide s	1	1	İ	714	, .		Colutainine, K=Arginine, S=Serine,
Peptide		1					VarTransing Valleton walryptophan,
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836 2186 A 6862 315 11 PPRSRPSCWRKKVGPGRPWWGGTGPPGQG REEIRLLPLPMTGACGAVAASRTGSSGPG/SSL PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT GPGSGRPPP  837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APPPGLVQRSRLLIVSQVRYPLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNEL WTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGTTQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMGMAE LLVSHGANLNARTSMDEMPIDLCEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GBEAI					1	ļ	CNSARNVPDDILQLLEEERWAFVMVSLFHGE
2186 A 6862 315 II PPRSRPSCWRKKVGPGRPWWWGGTGPPGQG RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT GPGSGRPPP  VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GBEAI					]	ŀ	
837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANVLNARTSMDEMPIDLCEEEFKVL LLELKVHKHDVIMKSQLRHKSSLSRRTSHRQA S/SYGKVVRRTQPVGTGPNLYYRKEYE/GEBAI	924	0106		1,000			GGDYDGAGKYRKKTTCKAPWRTSSRMSS
RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT GPGSGRPPP  837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI	030	2186	A	6862	315	11	PPRSRPSCWRKKVGPGRPWWWGGTGPPGQG
PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT GPGSGRPPP  837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELKHKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNLYYRKEYE/GEBAI				] [			RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL
837 2187 A 6863 2 1615 VLRGQRGPAGGLAEERRGRNEWRIHDVTT APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGAN\LNARTSMDEMPIDLCEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GBEAI			•			1	PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT
APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELKHKHDVIMKSQLRHKSSLSRRTSHRQA S/SYGKVVRRTQPVGTGPNLYYRKEYE/GEEAI	027	0105		<u> </u>	1		
APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC NEDGLTALHQCCIDNFEEIVKLLLSHGANVN AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKNEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGAN\LNARTSMDE.MPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI	637	2187	A	6863	2	1615	
AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGAN\LNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SYGKVVRRTQPVGTGPNL\YRKEYE/GEEAI	l				l	l	APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC
AKDNELWTPLHAAATCGHINLVKILVQYGA DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGAN\LNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SYGKVVRRTQPVGTGPNL\YRKEYE/GEEAI	ļ				l		NEDGLTALHQCCIDNFEEIVKLLLSHGANVN
DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI					Į.	l	AKDNELWTPLHAAATCGHINLVKILVOYGA
QGITQEKINEMRVAPEQQMIADIHCMIAAGQ DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL, LLELKHKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI					į		DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY
DLDWIDAQGATLLHIAGANGYLRAAELLLDH GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI		ļ			ł	ŀ	QGITQEKINEMRVAPEQQMIADIHCMIAAGQ
GVRVDVKDWDGWEPLHAAAFWGQMQMAE LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI					ļ		DLDWIDAQGATLLHIAGANGYLRAAELLLDH
LLVSHGANLNARTSMDEMPIDLCEEEEFKVL LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI					1	l	GVRVDVKDWDGWEPLHAAAFWGOMOMAE
LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI		ľ			ł	ļ	LLVSHGAN\LNARTSMDEMPIDLCEEEEFKVL
S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI		}			Ì	.	LLELK\HKHDVIMKSQLRHKSSLSRRTSHROA
LWQRSA\AEDQRTSTYNGDIRET\RTDOENKD		}					S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI
							LWQRSA\AEDQRTSTYNGDIRET\RTDQENKD

.*						
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		}	i	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		İ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			Ì	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						PNPRLEKIPVLLSEFPTKIPRGELDMPVENGLR
		j	]	1		APVSAYQYALANGDVWKVHEVPDYSMAYG
	· ·					NPGVADATPPWSSYKEQSPQTLLELKRQRAA
	ŀ					AKLLSHPFLSTHLGSSMARTGESSSEGKAPLI
	!		ļ		1	GGRTSPYSSNGTSVYYTVTSGDPPLLKFKAPI
						EEMEEKVHGCCRIS
838	2188	A	6865	6291	739	AGPLEPRVQGAMALQLWALTLLGLLGAGAS
0.50	2100	1 "	0005	0251	1 ""	LRPRKLDFFRSEKELNHLAVDEASGVVYLGA
		1				VNALYQLDAKLQLEQQVATGPVLDNKKCTP
		1	1	1		PIEASOCHEAEMTDNVNQLLLVDPPRKRLVE
İ		i	Į			CGOLLKGI\CALRALSNISLRLFYEDGSGEKSF
1		1			i	VASNDEGVATVGLVSSTGPGGDRVLFVGKG
)	1	1			Į.	NGPHDNGIIVSTRLLDRTDSREAFEAYTDHAT
		]				YKAGYLSTNTQQFVAAFEDGPYVFFVFNQQD
		1	İ	l		KHPARNRTLLARMCREDPNYYSYLEMDLQC
				1		RDPDIHAAAFGTCLAASVAAPGSGRVLYAVF
	į	1	ł			SRDSRSSGGPGAGLCLFPLDEVHAKMEANRN
1	1					ACYTGTREARDIFYKPFHGDIQCGGHAPGSSK
l	ĺ	ĺ				SFPCGSEHLPYPLGSRDGLRGTAVLQRGGLN
	1	1		1	1 .	LTAVTVAAENNHTVAFLGTSDGRILKVYLTP
	Ì	1		1		DGTSSEYDSILVEINKRVKRDLVLSGDLGSLY
	1	1	]		1	AMTODKVFRLPVQECLSYPTCTQCRDSQDPY
ĺ		1	1	1	1	CGWCVVEGRCTRKAECPRAEEASHWLWSRS
		ŀ				KSCVAVTSAQPQNMSRRAQGEVQLTVSPLPA
			1		ļ	LSEEDELLCLFGESPPHPARVEGEAVICNSPSS
						IPVTPPGQDHVAVTIQLLLRRGNIFLTSYQYPF
1		1				YDCRQAMSLEENLPCISCVSNRWTCQWDLR
! '		i	1	ı	1	YHECREASPNPEDGIVRAHMEDSCPQFLGPSP
	Į			1	1	LVIPMNHETDVNFQGKNLDTVKGSSLHVGSD
1		i		1		LLKFMEPVTMQESGTFAFRTPKLSHDANETL
l						PLHLYVKSYGKNIDSKLHVTLYDCSFGRSDC
Ì						SLCRAANPDYRCAWCGGQSRCVYEALCNTT
1		1	1	1		SECPPPVITRIQPETGPLGGGIRITILGSNLGVQ
					Ì	AGDIQRISVAGRNCSFQPERYSVSTRIVCVIEA
		1	l			AETPFTGGVEVDVFGKLGRSPPNVQFTFQQP
1	l	1				KPLSVEPOOGPOAGGTTLTIHGTHLDTGSQED
			1			VRVTLNGVPCKVTKFGAQLQCVTGPQATRG
	1	1	}	1		OMLLEVSYGGSPVPNPGIFFTYRENPVLRAFE
1			1		1	PLRSFASGGRSINVTGQGFSLIQRFAMVVIAEP
1	1		1	1	1	LQSWQPPREAESLQPMTVVGTDYVFHNDTK
1			ĺ		}	VVFLSPAVPEEPEAYNLTVLIEMDGHRALLRT
1	1		1			EAGAFEYVPDPTFENFTGGVKKQVNKLIRAR
1	1	1	1			GTNLNKAMTLOBAEAFVGAERCTMKTLTET
1	1	1	1	1		DLYCEPPEVQPPPKRRQKRDTTINLPEFIVKF
		1	1			GSREWVLGRVEYDTRVSDVPLSLILPLVIVPM
					1	VVVIAVSVYCYWRKSQQAEREYEKIKSQLEG
1				1		LEESVRDRCKKEFTDLMIEMEDQTNDVHEAG
1		1	1	1	1	
				1	1	IPVLDYKTYTDRVFFLPSKDGDKDVMITGKL
1				1		DIPEPRRPVVEQALYQFSNLLNSKSFLINFIHT
1				1		L\ENQPEFSARAKVYFASLLTVALHGKLEYYT
	1			1	1	DIMHTLFLELLEQYVVAKNPKLMLRRSETVV
1			]	}	1	ERMLSNWMSICLYQYLKDSAGEPLYKLFKAI
	1	1		1		KHQVEKGPVDAVQKKAKYTLNDTGLLGDD
1	1	1	1	1	1	VEYAPLTVSVIVQDEGVDAIPVKVLNCDTISQ
1		- 1	1	1	1	VKEKIIDQVYRGQPCSCWPRPDSVVLEWRPG
	· i	1				
						STAQILSDLDLTSQREGRWKRVNTLMHYNVR
						DGATLILSKVGVSQOPEDSQQDLPGERHALL
						DGATLILSKVGVSQQPEDSQQDLPGERHALL EEENRVWHLVRPTDEVDEGKSKRGSVKEKE
				·		DGATLILSKVGVSQOPEDSQQDLPGERHALL

CEPO ID		157	1			
SEQ ID NO: of	SEQ ID NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-		USSN	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence		09/496	correspondi	corresponding to last amino	
uence			914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		Ì		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
-	1	1	1	peptide	1 .	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
1						HIWKTNSLPLRFWVNILKNPHFIPDVHVHEVV
İ	ĺ	Ì	Ì	j	j	DASLSVIAQTFMDACTRTEHKLSRDSPSNKLL
		1	ł	İ		YAKEISTYKKMVEDYYKGIRQMVQVSDODM
			1	İ	1	NTHLAEISRAHTDSLNTLVALHOLYOYTOKY
1					ļ	YDEIINALEEDPAAQKMQLAFRLQQIAAALE
839	2189	A	6872	ļ	1400	NKVTDL
1 657	2107	^	00/2	1	1485	RARRLALQCHVCVCALTPGEQSGRRLPGQT
i	1	İ		İ	1	WLMFSCFCFSLQDNSFSSTTVTECDEDPVSLH
1	i	1	1	l		EDQTDCSSLRDENNKENYPDAGALVEEHAPP
ŀ		ł	1		,	SWEPQQQNVEATVLVDSVLRPSMGNFKSRKP
	į		1		1	KSIFKAESGRSHGESQETEHVVSSQSECQVRA
ļ					]	GTPAHESPQNNAFKCQET\VRL\QPRIDQRTAT
		l			1	SPKDAFETR\QDI.NEEEAAQVHGVKDPAPAS TQSVLA\DGTDSADPSPVHKDGQNEADSAPE
		1				DLHSVGTSRLLL/YHITDGDNPTAVRHGCSL/F
		İ		•		SGQSQRFNLDPESAPSPPSTQQFMMPRSSSRC
	1					SCGDGKEPQTITQLTKHIQSLKRKIRKFEEKFE
1		}				QEKKYRPSHGDKTSNPEVLKWMNDLAKGRK
1		}				QLKELKLKLSEEQGSAPKGPPRNLLCEOPTVP
1						RENGKPEAAGPEPSSSGEETPDAALTCLKERR
	ľ	l				EQLPPQEDSKVTKQDKNLIKPLYDRYRIKOIL
840	2190	<u> </u>	6000			STPSLIPTIVSQDTCMLLLCTDV
040	2190	Α	6873	2	2054	FFRFYFSFIRLFAMSLADLTKTNIDEHFFGVAL
						ENNRRSAACKRSPGTGDFSRNSNASNKSVDY
			1 1			SRSQCSCGSLSSQYDYSEDFLCDCSEKAINRN
			'			YLKQPVVKEKEKKKYNVSKISQSKGQKEISV
			i			EKKHTWNASLFNSQIHMIAQRRDAMAHRILS
	1 1					ARLHKIKGLKNELADMHHKLEAILTENQFLK QLQLRHLKAIGKYENSQNNLPQIMAKHQNEV
						KNLRQLLRKSQEKERTLSRKLRETDSQLLKT
						KDILQALQKLSEDKNLAEREELTHKLSIITTK
						MDANDKKIQSLEKQLRLNCRAFSRQLAIETR
						KTLAAQTATKTLQVEVKHLQQKLKEKDREL
						EIKNIYSHRILKNLHDTEDYPKVSSTKSVQAD
				1		RKILPFTSMRHQGTQKSDVPPL/TTKGKKATG
	1		i	!		NIDHKEKSTEINHEIPHCVNKLPKOEDSKRKY
·			-	i		EDLSGEEKHLEVQILLENTGROKDKKEDOEK
			i	i	ļ	KNIFVKEEQELPPKIIEVIHPERESNOEDVLVR
			į	ĺ		EKFKRSMQRNGVDDT\LGKGTAPYTKGPLRO
		l	ĺ		l	RRHYSFTEATENLHHGLPASGGPANAGNMR
		ĺ	ļ:		i	YSHSTGKHLSNREEMELEHS\DSGYEPSFGKS
		- 1	j			SRIKVKDTTFRDKKSSLMEELFGSGYVLKTD
		ŀ		:		QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSIKPSSPTEGKRKIII
841	2191	A	6874	3	2867	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHG
	I					NAPAPGTPAASGWQPPTYHSGRAFSARYPRP
				ļ	ŀ	SRRGYSSHHGPSWRKKYSLVNRPPGPSDPPA
	J	- 1	1	1		DHAVRPLHGARGGQPPVPQQHVLERQVQLS
	1			1	ļ	QGQNVVIKVKPPSKSGSASASGAORGSLEEFE
	1	- 1	ļ	1	1	DTPWSDQRPREGEGEPPRGOLOPSRPTRARG
	l		- 1	1	į	TCSVEDPLLVCQKEPGKPRMVKSVGSVGDSP
		- 1	- 1	ı	İ	REPRRTVSESVIAVKASFPSSALPPRTGVALG
	1		}	İ		RKLGSHSVASCAPOLLGDRRVDAGHTDOPVP
	-		1			SGSVGGPARPASGPROAREASLVVTCRTNKF
		1	.	ļ	ļ	RKNNYKWVAASSKSPRVARRALSPRVAAEN
	i				1	VCKASAGMANKVEKPOLIADPEPKPRKPATS
1						SKPGSAPSKYKWKASSPSASSSSSFRWOSEAG
			-		j	SKDHASQLSPVLSRSPSGD\RPALAHSGLKPLS
1		- 1				GETPLSAYKVKTRTKIIRRRGSTSLPGDKKSG
						TSPAATAKSHLSLRRRQALRGKSSPVLKKTPN

	070 70	3.6-4	Lero	Deadistad	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methiorine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence	Ļ		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
	ł	ł	1	peptide	1	
	Ì	ŀ	i	sequence		nucleotide insertion
						KGLVQVTKHRLCRLPPSRAHLPTKEASSLHA
	1	i	1	1	1	VRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLS
	l .		1	ļ	İ	LPSWRARRLSLSRSLVLNRLRPVASGGGKAQ
	l	J	}	j	1	PGSPWWRSKGYRCIGGVLYKVSANKLSKTSG
	1		1	1		QPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
	ł	l	1		ļ	RSLAIIRQARQRREKRKEYCMYYNRFGRCNR
	1	1				GERCPYIHDPEKVAVCTRFVRGTCKKTDGTC
	1	1	1			PFSHHVSKEKMPVCSYFLKGICSNSNCPYSHV
	l			Į	1	YVSRKAEVCSDFLKGYCPLGAKCKKKHTLLC
	ł	ł	1	1	ľ	YVSRKAEVCSDFLKGTCFLUARCKRITTLLC
			1	İ	ł	PDFARRGACPRGAQCQLLHRTQKRHSRRAAT
	1	1			1	SPAPGPSDATARSRVSASHGPRKPSASQRPTR
	}	1	1	j		QTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
· ·		i		1		SSSSSSSPPASLDHE\APSLQEAALAAACSNR
i		1	1	j		LCKLPSFISLQSSPSPGAQPRVRAPRAPLTKDS
ĺ			Î	1 .		GKPLHIKPRL
0.40	10100	A	6898	506	2071	WPDLVHTWSSEEAMGSCCSCPDKDTVPDNH
842	2192	A	0690	300	2071	RNKFKVINVDDDGNELGSGIMELTDTELILYT
· ·	Į					RKRDSVKWHYLCLRRYGYDSNLFSFESGRRC
	ł	i	i	1		QTGQGIFAFKCARAEELFNMLQEIMQNNSIN
	ł	٠.	1			QIGQGIFAFKCAKAEELFNWLQDIWQAADIA
1	}	]	1	ļ	1	VVEEPVVERNNHQTELEVPRTPRTPTTPGFAA
	1	i	1		1	QNLPNGYPRYPSFGDASSHPSSRHPSVGSARL
1	1		1			PSVGEESTHPLLVAEEQVHTYVNTTGVQEER
1	1				į	KNRTSVHVPLEARVSNAESSTPKEEPSSIEDR
l		1	ļ	ì		DPQILLEPEGVKFVLGPTPVQKQLMEKEKLE
1	1	1	1		1	OLGRDOVSGSGANNTEWDTGYDSDERRDAP
l	1	1	ł	1	İ	SVNKLVYENINGLSIPSASGVRRGRLTSTSTSD
1	1		1	-		TQNINNSAQRRTALLNYENLPSLPPVWEARK
1		į		1	ì	LSRDEDDNLGPKTPSLNGYHNNLDPMHNYV
l	İ	j		ļ	1	NTENVTVPASAHKIEYSRRRDCTPTVFNFDIR
İ	ļ	1				RPSLEHRQLNYIQVDLEGGSDSDNPQTPKTPT
j	1	j .	1	1	1	TPLPQTPTRRTELYAVIDIERTAAMSNLQKAL
	1		1			
						PRDDGTSR\KTRHNST\DLPL
843	2193	Α	6919	2	663	AGRPGTTHASGKMAYQSLRLEYLQIPPVSRA
1	ì	1		1		YTTACVLTTAAVQLELITPFQLYFNPELIFKHF
1		1	ł		i	QIWRLITNFLFFGPVGFNFLFNMIFLYRYCRM
Í	1	1	[		1	LEEGSFRGRTADFVFMFLFGGFLMTLFGLFVS
			1			L/VFLGPGLYNN/GSSMCGAE\EPLCPHELLRP
l .	1		ļ			SQLPGPLSALGAHGIFLVVGELNHCGPFGYCS
1		1		1	1	WTHIFFLGRCISQSTWWNKNSENTIYFESYF
044	12104	+	6928	902	366	HRLCMPIQGACGERME/FSLLLPGLECNGVIL
844	2194	A	0928	302	200	AHCNLRLPGSSNSPASASQVAGITGVCHHAR
1	ļ		l	1	ł	LIFVFSVETGFLHAGQAGLELLTSGDPPASAS
ĺ	1	1	1			QSAGITGKSQHTRPGYEFIIPYSAAQEDALKA
Ī						
1		1		1		LM
845	2195	A	6939	1660	317	LYPENLGESLFPILLLPPPWPDGGRPCCVEMS
1	1	1		1	1	TRAKKLRRIWRILEEKESVAGAVQTLLLRSQE
1	Į	1	1	1	1	GGVTSAAASTLSEPPRRTOESRTRTRALGLPT
1		1		1	1	LPMEKLAASTEPOGPRPVLGRESVQVPDDQD
	İ			i	1	FRSFRSECEAEVOWNLTYSRAGVSVWVQAV
1				1	1	EMDRTLHKIKCRMECCDVPAETLYDVLHDIE
1		1		ı	ĺ	YRKKWDSNVIETFDIARLTVNADVGYYSWR
1		1		1	1	I KVV M DOMATE L DINKET AND A OF LOAN
1	1	1	1		i	CPKPLKNRDVITLRSWLPMGADYIIMNYSVK
1	1	1		1	1	HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT
1		1		1	1	YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK
1	1	1			1	MYKACLKYPEWKQKHL\PHFKPWL\HPEQSP
1	İ	1	1			LPSLALS\ELSVOHADS\LENIDESAV\AESREE
J		1	1	l	1	RIMGGAGGEGISDDDTSLYAEAPHRFRETETG
1	1			1	1	PGAGRALGAAAAPALSPLHPPGTWWHRARP
						PGAGRALGAAAAPALSPLHPPGTWWHRARP RRVLQPGWTEPQ

	SEQ ID	SEQ ID	Met	SEQ	Predicted	( Day 1/2)	
	NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
	nucl-	peptide	1.00	in	nucleotide	location	D-Aspartic Acid, E-Glutamic Acid,
	eotide	seq-		USSN	location		F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	uence		09/496	correspondi	to last amino	
	uence		1	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline,
				1	amino acid	of peptide	Q=Glutamine, R=Arginine, S=Serine,
		1	1	1	residue of	sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
					peptide	bodamico	/=possible nucleotide deletion, \=possible
		1	1	1	sequence	1	nucleotide insertion
	846	2196	A	6944	42	2672	RRKMAGCRGSLCCCCRWCCCCGERETRTPE
į		İ	ĺ	i i	į .	1	ELTILGETQEEEDEILPRKDYESLDYDRCINDP
1			1		l	1	YLEVLETMDNKKGRRYEAVKWMVVFAIGV
ı		1	ł	}	ł		CTGLVGLFVDFFVRLFTQLKFGVVQTSVEECS
		<b>!</b>	i i		İ		QKGCLALSLLELLGFNLTFVFLESLLGLIEPVE
-		l	1		}		AGSGITEGKCYLYAROVPGLVRLPTLLWKAI
1			1	1			GVLLTVAAMLLI\GLGSPMIHSGSVVGAGLPO
		ł	}		ļ	1	FQSISLRKIQFNFPYFRSDRYGK\DKRDFVSAG
- 1		ļ		1			AAAGVAAAFGAPIGGTLFSLEEGSSFWNOGI
- 1			1			1	TWKVLFCSMSATFTLNFFRSGIOFGSWGSFOL
ı				]		1	PGLLNFGEFKCSDSDKKCHLWTAMDLGFFV
Į			1	1		i	VMGVIGGLLGATFNCLNKRLAKYRMRNVHP
							KPKLVRVLESLLVSLVITVVVFVASMVLGEC
-		1		1			RQMSSSSQIGNDSFQLQVTEDVNSSIKTFFCP
-			1				NDTYNDMATLFFNPQESAILQLFHQDGTFSPV
-		· ·					TLALFFVLYFLLACWTYGISVPSGLFVPSLLC
-1							GAAFGRLVANVLKSYIGLGHIYSGTFALIGAA AFLGGVVRMTISLTVILIEST\NEITYGLPIMVT
-		ļ		l i		1	LMVGKWTGDFFNKGI\YDIHVGLRGVPLLEW
				.		1	ETEVEMDKLRASDIMEPNLTYVYPHTRIQSLV
-				1 1			SILRTTVHHAFPVVTENRGNEKEFMKGNQLIS
-						ĺ	NNIKFKKSSILTRAGEQRKRSQSMKSYPSSEL
						1	RNMCDEHIASEEPAEKEDLLQQMLERRYTPY
				1			PNLYPDQSPSEDWTMEERFRPLTFHGLILRSQ
ı	ĺ			!			LVTLLVRGVCYSESQSSASOPRLSYAEMAED
1		ľ		1		ĺ	YPRYPDIHDLDLTLLNPRMIVDVTPYMNPSPF
1	.			ŀ			TVSPNTHVSQVFNLFRTMGLRHLPVVNAVGE
H	847	2197	A	6951	3	1004	IVGIITRHNLTYEFLQARLRQHYQTI
ı	١	217/		10901	3	1994	NTNSSSVTNSAAGVEDLNIVQVTVPDNEKER
1	- 1	ł					LSSIEKIKQLREQVNDLFSRKFGEAIGVDFPVK
ı				-			VPYRKITFNPGCVVIDGMPPGVVFKAPGYLEI
ı			1				SSMRRILEAAEFIKFTVIRPLPGLELSNGEYST
ı	I			. [			VGKRKIDQEGRVFQEKWERAYFFVEVQNIST
1	1	1	1	1			CLICKRSMSVSKEYNLRRHYQTNHSKHYDQY MERMRDEKLHELKKGLRKYLLGLSDTECPE
	}	·	ł	1			QKQVFANPSPTQKSPVQPVEDLAGNLWEKLR
1	1			Į.	j		EKIRSFVAYSIAIDEITDINNTTQLAIFIRGVDE
1			I	1			NFDVSEELLDTVPMTGTKSGNEIFSRVEKSLK
1				-			NFCINWSKLVSVASTGTPPMVDANNGLVTKL
							KSRVATFCKGAELKSICCIIHPESLCAQ\KLKM
	-	1	ļ	J	]	ļ	DHVMDVVVKSVNWICSRGLNHSEFTTLLYEL
1						1	DSQYGSLLYYTEIKWLSRGLVLKRFFESLEEI
	ļ				j	ļ	DSFMSSRGKPLPQLSSIDWIRDLAFLVDMTM
		1		1		l	HLNALNISLOGHSOIVTOMYDLIRAFLAKI.CI
1	1	ſ		- 1	1	· 1	WETHLTRNNLAHFPTLKLVSRNESDGLNVIP
	[			- 1		]	KIAELKTEFQKRLSDFKLYESELTLFSSPFSTKI
1	- 1	- 1	- 1	- 1	İ	l	DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE
	ſ	ľ	I	1		1	FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ
8	48	2198	Ā	6985	3	289	LFSIMKLSKTKYCSQLKDSQWDSVLHIAT
l					-		SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK
L			- 1	- 1	ļ	1	ASAPVQCLLLMAATFSPQGLAKPHSGTIPIT\C CFNAINTKIPIQRLESYTRITNIQCPKEAVM
8	49	2199	A	6999	963	5	LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM
	1	1		1		-	LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP
	İ	- 1				Ī	MYFFLSHLAVVDIAYACNTVPRMLVNLLHP
	1	1		1			AKPISFAGRMMQTFLFSTFAVTECLLLVVMS
		İ	1	- 1		ŀ	YDLYV\AICHPLRYLAIMTWRVCITLAVTSWT
l	1	- 1		-	1	1	TGVLLSLIHLVLLLPLPFCRPQKIYHFFCEILA
ĺ	1		- 1				VLKLACADTHINENMVLAGAISGLVGPLSTIV
<u></u>	L						VSYMCILCAILQIQSREVQRKAFCTCFSHLCVI

ano ID	Gro in	Mot	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	1.00	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
*				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ			peptide		nucleotide insertion
	<del>                                     </del>	,		sequence		GLFYGTAUMYVGPRYGNPKEQKKYLLLFHS
	ŀ					LFNPMLNPLICSLRNSEVKNTLKRVLGVERAL
850	2200	A	7001	1	1011	MGNDSVSYEYGDYSDLSDRPVDCLDGACLAI
050				-	1.	DPLRVAPLPLYAAIFLVGVPGNAMVAWVAG
						KVARRRVGATWLLHLAVADLLCCLSLPILAV
	1	1		1	Ì	PIARGGHWPYGAVGCRALPSIILLTMYASVLL
		İ	†		<u> </u>	LAALSADLCFLALGPAW\CLRFS/GACGVQVA
			1		l	CGAAWTLALLLTVPSAIYRRLHQEHFPARLQ
			1			CVVDYGGSSSTENAVTAIRFLFGFLGPLVAVA SCHSALLCWAARRCRPLGTAIVVGFFVCWAP
	1	1	ļ			YHLLGLVLTVAAPNSALLARALRAEPLIVGL
		1	}			ALAHSCLNPMLFLYFGRAQLRRSLPAACHW
						ALRESQUESVDSKKSTSHDLVSEMEV
851	2201	A	7011	1	2310	AAASPLRMSRKGPRAEVCADCSAPDPGWASI
021	2201	1	/011	1	23.0	SRGVLVCDECCSVHRSLGRHISIVKHLRHSA
}	,	1	i	] .	1	WPPTLLQMVHTLASNGANSIWEHSLLDPAQV
		1		1 .		QSGPALKQTPKDKV\HPIKSEFIRAKYQMLAF
			1.	1	į	VHKLPCRDDDGVTAKDLSKQLHSSVRTGNLE
	İ					TCLRLLSLGAQANFFHPEKGTTPLHVAAKAG
			1			QTLQAELLVVYGADPGSPDVNGRTPIDYARQ
	1			1		AGHĤELAERLVECQYELTDRLAFYLCGRKPD HKNGHYIIPQMADSLDLSELAKAAKKKLQAL
{				1		SNRLFEELAMDVYDEVDRRENDAVWLATQN
1		1	1	1	l	HSTLVTERSAVPFLPVNPEYSATRNQGRQKL
1						ARFNAREFATLIIDILSEAKRRQQGKSLSSPTD
1	1			i	1	NLELSLRSQSDLDDQHDYDSVASDEDTDQEP
			ł			LRSTGATRSNRARSMDSSDLSDGAVTLQEYL
ì			1	1		ELKKALATSEAKVQQLMKVNSSLSDELRRLQ
1				ļ		REIHKLQAENLQLRQPPGPVPTPPLPSERAEH
1	1	1	ł	ł	İ	TPMAPGGSTHRRDRQAFSMYEPGSALKPFGG
		1	1	1		PPGDELTTRLQPFHSTELEDDAIYSVHVPAGL
		1 .	1			YRIRKGVSASAVPFTPSSPLLSCSQEGSRHTSK LSRHGSGADSDYENTQSGDPLLGLEGKRFLE
1		1		ł	1	LGKEEDFHPELESLDGDLDPGLPSTEDVILKT
	İ	1			1	EOVTKNIQELLRAAQEFKHDSFVPCSEKIHLA
i		1		ł	· L	VTEMASLFPKRPALEPVRSSLRLLNASAYRLQ
		ŀ				SECRKTVPPEPGAPVDFQLLTQQVIQCAYDIA
ł	1	1		1	1	KAAKQLVTITTREKKQ
8.52	2202	A	7016	484	1777	RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLL
			1	1	1	TVKGLLKPSFSPRNYKALSEVQGWKQRMAA
			1			KELARONMOLGFKLLKKLAFYNPGRNIFLSP
1	1	1		1		LSISTAFSMLCLGAQDSTLDEIKQGFNFRKMP
1	1		1			EKDLHEGFHYIIHELTQKTQDLKLSIGNTLFID ORLOPORKFLEDAKNFYSAETILTNFQNLEM
	1				İ	AOKOINDFIÆSKTHGKINNLIENIDPGTVMLL
1		1		1	ľ	ANYIFFRARWKHEFDPNVTKEEDFFLEKNSS
				1	1	VKVPMMFRSGIYQVGYDDKLSCTILEIPYQK
1				1	]	NITAIFILPDEGKLKHLEKGLQVDTFSRWKTL
1	1	1		1	1	LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVS
1		]			1	KIFEEHGDLTKIAPHRSLKVGEAVNKAELKM
		1			1	DERGTEGAAGTGAQTLPMETPLVVKIDKPYL
1						LLIYSEKIPSVLFLGKIVNPIGK
853	2203	A	7017	1	3293	MTHACNPSTLGGQGRRITRSHGRRRSSRGPV
1				1	1	ARHVAAGAGHENKHGGSRRFPAGVAPRRAM
1	1	1				ANVSKKVSWSGRDRDDEEAAPLLRRTARPG
1					1	GGTPLLNGAGPGAARQSPRSALFRVGHMSSV ELDDELLEPDMDPPHPFPKEIPHNEKLLSLKY
		1				ESLDYDNSENQLFLEEERRINHTAFRTVEIKR
				l l		WVICALIGILTGLVACFIDIVVENLAGLKYRVI
	- [	}		1		KGSILPNIDKFTEKGGLSFSLLLWATLNAAFV
L	i .	1	1	_L		

## PCT/US01/03800

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	,,,oa	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
1		$\vdash$		Jugana	<del> </del>	LVGSVIVAFIEPVAAGSGIPQIKCFLNGVKIPH
İ		l			1	VVRLKTLVIKVSGVILSVVGGLAVGKEGPMI
1	1	l			1	HSGSVIAAGISQGRSTSLKRDFKIFEYFRRDTE
ŀ			1			KRDFVSAGAAAGVSAAFGAPVGGVLFSLEEG
	1		,			ASFWNQFLTWRIFFASMISTFTLNFVLSIYHG
1	1					NMWDLSSPGLINFGRFDSEKMAYTIHEIPVFI AMGVVGGVLGAVFNALNYWLTMFRIRYIHR
	1					PCLQVIEAVLVAAVTATVAFVLIYSSRDCQPL
					1	QGGSMSYPLQLFCADGEYNSMAAAFFNTPEK
	]				l	SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWT
					1	YGLTVSAGVFIPSLLIGAAWGRLFGISLSYLTG
1						AAIWADPGKYALMGAAAQLGGIVRMTLSLT VIMMEATSNVTYGFPIMI.VLMTAKIVGDVFIE
						GLYDMHIQLQSVPFLHWEAPVTSHSLTAREV
						MSTPVTCLRRREKVGVIVDVLSDTASNHNGF
						PVVEHADDTQPARLQGLILRSQLIVLLKHKVF
1	1 .				ŀ	VERSNLGLVQRRLRLKDFRDAYPRFPPIQSIH
	:					VSQDERECTMDLSEFMNPSPYTVPQEASLPR VFKLFRALGLRHLVVVDNRNQVVGLVTRKD
}						LARYRLGKRGLEELSLAQTGPKAQATAEGRV
}						AGAAQQPCQLRAVTLEDLGLLLAGGLASPEP
ļ						LSLEELSERYESSHPTSTASVPEQDTAKHWNO
1			1	•		LEQWVVELQAEVACLREHKQRCERATRSLL
			- 1			RELLQVRARVQLQGSELRQLQQEARPAAQAP EKEAPEFSGLQNQMQALDKRLVEVRE.ALTRL
	•					RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ
			1			QEEQGREVACGALQKNQEDSSRRVDLEVAR
854	2204		7007			M
634	2204	A	7037	139	2604	-AGTWEPRPYDQAKETGAPGSQPPVPPMELRP
1			1			WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY
1						HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL
		ļ				EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG
		1				VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI
	,	l				EKNHPDLAGNYDPGASFDVNDQDPDPQPRY
					ļ	TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN
		1				HIHIYSASWGPEDDGKTVDGPARLAEEAFFR
1					Ì	GVSQGRGGLGSIFVWASGNGGREHDSCNCD
		ł	ì			GYTNSIYTLSISSATQFGNVPWYSEACSSTLA
						TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS
		- 1				APLAAGIIALTLEANKNLTWRDMQHLVVQTS
		- 1	- 1	1		KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWITVAPQRKCIIDILTEPKDI
			- 1	]		GKRLEVRKTVTACLGEPNHITRLEHAOARLT
		]	1	j		LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY
	Ì		l			SADGFNDWAFMTTHSWDEDPSGEWVLEIEN
<u> </u>		İ	ŀ	1	1	TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS
				}		GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS
		1	1	ł		CATCQGPALTDCLSCPSHASLDPVEQTCSRQS
		1		ľ		QSSRESPPQQQPPRLPPEVEAGORLRAGLLPS
, 1	- 1	- 1	- 1		ļ	HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS
1	1				•	FRGVKVYTMDRGLISYKGLPPEAWQEECPSD
			l		ř	
855	2205	A	7058	3	1441	SEEDEGRGERTAFIKDQSAL
855	2205	A	7058	3	1441	SEEDFGRGERTAFIKDQSAL  QRPASQLLAPFAAEALPGAPRAAMAQHFSLA
855	2205	A	7058	3		SEEDFGRGERTAFIKDQSAL  QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL
855	2205	A	7058	3		SEEDFGRGERTAFIKDQSAL  QRPASQLLAPFAAEALPGAPRAAMAQHFSLA

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible mucleotide deletion, \=possible nucleotide insertion YFDLPGALLCARVVDYLTKLNNGQKTFDFW KDIVAAIQHNYKMSAFKENCGIYFPEIKRDPG RYLHSRPESVKKWLRQLKNAGKILLLITSSHS DYCRLLCAIYILGNDFTDLFDIVITNALKPGFF SHLPSQRPFRTLENDEEQEALPSLDKPGWYSQ GNAVHLYELLKKMTGKPEPKVVYFGDSMHS DIFPARHYSNWETVLILEELRGDEGTRSQRPE ESEPLEKKGKYEGPKAKPLNTSSKK WGSFFI DSVLGLENTEDSLVYTWSCKRISTYSTIAIPSI EAIAELPLDYKFTRFSSSNSKTAGYYPNPPLV LSSDETLISK
856	2206	A	7082	396	1635	SSPSVFEFEHAVQPVFTMEFLKTCVLRRNACT AVCFWRSKVVQKPSVRRISTTSPRSTVMPAW VIDKYGKNEVLRFTQNMMMPIIHYPNEVIVK VHAASVNPIDVNMRSGYGATALNMKRDPLH VKIKGEEFPLTLGRDVSGVVMECGLDVKYFK PGDEVWAAVPPWKQGTLSEFVVVSGNEVSH KPKSLTHTQAASLPYVALTAWSAINKVGGLN DKNCTGKRVLILGASGGVGTFAIQVMKAWD AHVTAVCSQDASELVRKLGADDVIDYKSGSV EEQLKSLKPFDFILDNVGGSTETWAPDFLKK WSGATYVTLVTPFLLNMDRLGIADGMLQTG VTVGSKALKHFWKGVHYRWAFFMASGPCL DDIAELVDAGKIRPVNEQTFPFSKVPEAFLKV ERGHARGKTVINVV
857	2207	A	7088	320	2417	LRRRKMTPQSLLQTTLFLLSLLFLVQGAHGR GHREDFRFCSQRNQTHRSSLHYKPTPDLRISIE NSEEALTVHAPFPAAHPASRSFPDPRGLYHFC LYWNRHAGRLHLLYGKRDFLLSDKASSLLCI- QHQEESLAQGPPLLATSVTSWWSPQNISLPSA ASFTFSFHSPPHTGAHNASVDMCELKRDLQL LSQFLKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMGSFEEDRINATVWKLQPTAGLQ DLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKG RSGEAEKRLLLVDFSSQALFQDKNSSQVLGE KVLGIVVQNTKVANLTEPVVLTFQHQLQPKN VTLQCVFWVEDPTLSSPGHWSSAGCETVRRE TQTSCFCNHLTYFAVLMVSSVEVDAVHKHY LSLLSYVGCVVSALACLVTIAAYLCSRVPLPC RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPV ALTGSEAGCRASAIFLHFSLLTCLSWMGLEG YNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPIILAVHRTPEGVIYPS MCWIRDSLVSYITNLGLFSLVTLFNMAMLAT MVVQILRLRPHTQKWSHVLTLLCLSLVLGLP WALIFFSFASGTFQLVVLYLFSITTSFQGFLIFI WYWSMRLQARGGPSPLKSNSDSARLPISSGS TSSSRI
858	2208	A	7091	185	415	DAGAVKSSDTNIWFRGMCDDKKGHRCPS*G QPQHFHVAFHTEAEGAMFYFRLHVIHRVMQS OOOLFPSTLFSWLLE
859	2209	A	7136	3	302	FFFWRQSLALLPRLECSGATGAHCNLHFPGSS DCPTSAS*IAGITGACYHAWLLFVFLAETGFH HVGQGGLELLTSSDPSGSASQSAGITGVSHCT WPI
860	2210	A	7156	23	591	ALSTETRTPDMRRLLLVTSLVVVLLWEAGAV PAPKVPIKMQVKHWPSEQDPEKAWGARVVE PPEKDDQLVVLFPVQKPKLLTTEEKPRGQGR GPILPGTKAWMETEDTLGRVLSPEPDHDSLY

SOUTH   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involved   DNO: 1   Involve	SEQ ID	SEQ ID	Met	GEO	T 20 17 17 1	1 5 0 1 7	
Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Deat			Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Section			1100	]			
	1						r=Phenylalanine, G=Glycine, H=Histidine,
United   1914   a to first amino scid residue of peptide residue of peptide sequence   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917   1917	1			1	1	to lest amine	I I Isoleucine, K Lysine, L Leucine,
mainto scid   residue of   peptide   residue of   peptide   residue of   peptide   sequence   sequence   residue of   peptide   sequence   residue of   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   pe		dence					M=Methionine, N=Asparagine, P=Proline,
Preiduc of peptide   Sequence   Prilyrosine, X=Usknown, *=Siop codon,   Proposible insuelotide deletion, \( \text{ \phi} \) peptide   Proposible insuelotide deletion, \( \text{ \phi} \) Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insuelotide insertion   Proposible insertion   Proposible insertion   Proposible insuelotide insertion   Proposible insuelotide   Proposible insertion   Proposible insuelotide   Proposible insertion   Proposible insuelotide   Proposible insertion   Proposible insuelotide   Proposible insertion   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible insuelotide   Proposible	uonee	İ	1	714			T-There in V-Velia W. T-unt land
				ļ			V-Typeoine, V-Valine, w=1ryptopnan,
		1	{	1		sequence	= 1-1yrosine, x=0inchown, -= 5top codon,
		İ	l			1	
B61   2211   A   7161   1220   1003   NYVCTIAFPEKKMGFYLSLCVLLEVLFLDCT LTTTTRIMFLCTYLFASVCLSLINTLSPNCL KSAMILQ   S62   2212   A   7211   665   847   LKYYHITMGIYKTGKVILFASVCLSLINTLSPNCL KSAMILQ   LKYYHITMGIYKTGKVILFASVCLSLINTLSPNCL KSAMILQ   LKYYHITMGIYKTGKVILFASVCLSLINTLSPNCL KSAMILQ   LKYYHITMGIYKTGKVILFASVCLSLINTLSPNCL KSAMILQ   LKYYHITMGIYKTGKVILFASSMSNFSVIF   KNINGKLSSNYYYHGNVYFSSDWSYDF   KNINGKLSSNYYYHGNVYFSSDWSYDF   KNINGKLSSNYYHGNVYFSSDWSYDF   KNINGKLSSNYYHGNVYFSSDWSYDF   LYVNDSPSCLATOFIT*GLVLVLGGPGCYMAKKKKKTDQ   CIKPNYQSPFKECDYVILLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKYTVINLANSVA   KROHEHKARRAF*GCKHYTINLANSVA   HKARRAF*GCHYTINLANSVA   KROHEHKARRAF*GCHYTINLANSVA   KROHEHKARRAF*GCHYTINLANSVA   KROHEHKARRAF*GCHYTINLANSVA   KROHEHKARRAF*GCHYTINLANSVA   KROHEHKARRAF*GCHYTINLANSVA   KROHEHKARRAF*GCHYTINLANSVA   KROHEHKARRAF*GCHYTINLANSVA   KROHE		<b></b>	<del>                                     </del>	<del> </del>	Sequence		
861   2211   A   7161   1220   1003   NYUCTIAPPEKKMGF¹LSLSCLVLLFVLFLDCI LTTTTRIMFHCTYLFASVCLSLNTLLSPNCL KSAMILQ     862   2212   A   7211   665   847   LKYYHTMGIYKTGKVIL*KSSMSNRFSVIF YKNIQKLSFSNYVYKQNYVFSSDWSYDF     863   2213   A   7212   924   1273   HGSSCALGDLAPG²LPSGPYLSSPAVRLFAKP     LVWDSPSCLPATGP†*GLVLVLGGPCCT*WA     RGQHEHKRMAP*SCXTVMLAKKKKTDQ     CKPNYQSPFKECDYNILANSVA     864   2214   A   7214   845   1619   SDKGGKKADRKNFLRFAFFLLPBKYRELH     PDKYVPUADHVQGDPGRAAHDHGEDYTE     KVSKDPLAPDEVQDTDEGHDRHGHREVGQF     FISHAVPPKPDOSLQKKLK VPREPRYQCSDP     PAPSDKSVKIEEREGITVYSMQFGGYAKEAD     YVAQATRLRAALBGTATYRGDIYTCTGYDPP     MEPYGRNEWILKIT     REGAVAHAYTSSTLGGRGGWIT*GQELQTS     LANMAKRLY     S66   2216   A   7257   641   1310     CTYTKYLMGWIRGRSRHISWEMSEFHYNNL     LANMAKRLY     CTYTKYLMGWIRGRSRHISWEMSEFHYNNL     LANMAKRLY     CTYTKYLMGWIRGRSRHISWEMSEFHYNNL     KSYHWMGLYHIPTINGSWQWEDGSLSFNLLT     IEMMCROCALYASSFKQUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS     RGGAVAHAYTSSTLWGRGGVUENCSTPHTYTUS	İ	Ì	Ì	ĺ		ĺ	DHIVHPO*GSRGHHCPRPVPRPPI I GLGPSI P
861   2211	1	1	1			1	
B62   2212   A   7211   665   847	861	2211	A	7161	1220	1003	
SAMILQ	·l		1				
862   2212   A   7211   665   847	İ		ŀ				
Section	862	2212	A	7211	665	847	
B63			ļ			1	YKNIOKI SESNYVVHONVVESSDWSVDE
LVWDSPSCLPATGFT*GLVLVLGGPDCT*WA ROQHEHRCMRAP*SCRYTVNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYQSPFRECDYNLAKKKKTDQ CKPNYDSPKYDVDD4UXQDOPGRAAHDHGUTE KVSKDPLAPDEVGDTDEGIDRHGHREWGOR HCHDQEBVAYEERACEGGKRATVEVTDKPY DEALREAMFEVAKYAGGTDNEGIGMGMTY PISFAVFFRDGSLQKKLKWFRIPNGPQSDP APSDESVKIEREGGTYYSMQFGGYAKEAD YVAQATRLRAALEGTATYRGDIYPCTGYDPP MKPYGRRNEWLLKT	863	2213	A	7212	924	1273	HGSSCALGDI APG*I PSGPVI SSPAVDI *PVD
RGOHEHKRMRAP*SCRYTVINAKKKKTDQ	ì					12.13	I.VWDSPSCI.PATGPT*GI.VI.VI.GGPDCT*WA
	ł		}			ļ	RGOHEHKRMRAP*SCRVTVNI AKKKKKTDO
\$64	1						CIKPNYOSPPKECDYNILANSVA
DPKYPVADHYQGQDPGRAAHDIIGEDVTE	864	2214	Λ	7214	845	1610	SDKCCKK VDKNITI BRACKI I BUBARCHI II
KVSKDPLAPDEVGDTDEGHDRHGHREVGOR   HGHDQEBVAYEERACEGGKFATVEVTDKPV   DEALREAMFKVAKYAGGTDKGIGMGMTV   PISPAVFPNEDGSLQKKLKVWFRIPNCFQSDP   PAPSDKSVKLEREGITYVSROGYAKEAD   A PYSADKSVKLEREGITYVSROGYAKEAD   YVAQATRLRAALEGTATYRGDIYFCTGYDPP   MKPYGRNEIWLLKT     865   2216   A 7246   559   682   RRIGAVAHAYTSSTLGGRGGWTI*GQELQTS   LAMMAKPRLY     866   2216   A 7257   641   1310   TCTYKYLIMGWIRGRSRHSWEMSEFHNYNL   DLKKSDPSTRWQKQRCPVYKSKCRENASPFF   FCCFLAVAMGIRFIIMVAIWSAVFLINSLFNQEV   QIPLTESYCOPCPKNWICYKNNCYGFDESKN   WYESQASCMSQNASLLKYSKEDDDLLKLV   KSYHWMGLVHIPINOSWQWEDGSILSPNLT   IEEMQKGDCALYASSFKGYIENCSTPNTYICM   QRTV     867   2217   A 7288   151   396   SIKIIEAFGSNGPDFWFFRYWSP*LFRQQVVFI   MPFFQTLWLMANNRCSSITITNVANNCWW   TPYHCWLSVVVCRCESHGI     868   2218   A 7298   3   272   PDTVIGGRGSGGKEFGRWVLW*VFF*RLGTP   KGSCPAGGSRMVSESP*EGRGC*ASYPCAC*   AGS*WR*GSRRAGRGTPFRSI.SHARPP   FROAEDRESCLNPAFPIGILLPRNSVNSMAR   FLITLCTWLLLLGFGLLAVKAECSQDCATCS   YRLVRPADINFLACVMECGGKLPSLKIWETC   KELLQLSSPELPDGGTSTLRSKPEESHLLA   KRYGGFMKRYGGFMKKDAEEDDSLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNLANSSDLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHHQDGSDNANSVLL   KELLETIGNNERFSHINGNAVYSTT   TEEDPGPARGPRSGLAAYFFNGRLPLRRVL   KGCQLLISILLAFICEEVVSCTCGCL   FPFFYTTIGT   KEALTIFLNA   KGCQCRGREDASGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	İ		]	''	0.5	10.5	
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TEEDPGPARGPRSGLAAYFFMGRLPLLRRVL KGLQLLLSLLAFICEEVVSQCTLCGGLYFFEF VSCSAFLLSLLILIVYCTPFYERVDTTKVKSSD FYITLGTGCVFLASIIFVSTHDRTSAEJAAIVF GFIASFMFLLDFITMLYEKRQESQLRKPENTT RAEALTEPLNA 871 2221 A 7403 3 393 SCAMCSGLL*LLLPIWLSWTLGTRGSEPRSVN DPGNMSFVKETVDKLLTGFRCFREREAAPRR				1			
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ALRGAALPGESEAGDPESLRSSVNADWIQYS	1	- 1	l	i	ľ		DPGNMSFVKETVDKLLTGFRCFREREAAPRR
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SEQ ID	SEQ ID	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of peptide	noa .	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-			USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	İ	ļ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		Ì	ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ĺ	ĺ	i	peptide	acquaire	/=possible nucleotide deletion, \=possible
	1	1		sequence		nucleotide insertion
			<u> </u>	Soquence		DLWEAEVSTPRCEAGFCQECFRTPGNQEKDG
		J	j	j	}	PFIC
872	2222	A	7413	1061	359	FVDIVSVVEFPHCPEARFPAQHGQDSKRLTLC
0/2	2222	١^	7413	1001	333	PGGS*POATLHLDRMRVSASPTKEIQVKKYK
		1		1	Į.	CGLIKPCPANYFAFKICSGAANVVGPTMCFED
		ł	1		1	RMIMSPVKNNVGRGLNIALVNGTTGAVLGQ
		l				KAFDMYSGDVMHLVKFLKEIPGGALVLVAS
		Į .			1	YDDPGTKMNDESRKLFSDLGSSYAKQLGFRD
	1	į .			1	SWVFIGAKDLRGKSPFEQFLKEQPQTQNKYE
	İ	ĺ			[	GWPELLEMEGCMPPKPF
873	2223	A	7429	2242	2394	ILKCAGHGGSCL*SQHFGRLRWEDRLRLGVQ
0.5		1	1			DHPGOHCETPSLLKIERKLF
874	2224	A	7468	146	894	PCTSCVLWATLHLPASTRKAPQAECGMISITE
· ·			1 ' '	1		WOKIGVGITGFGIFFILFGTLLYFDSVLLAFGN
	1	1	1	ļ		LLFLTGLSLIIGLRKTFWFFFQRHKLKGTSFLL
		1	1		ł	GGVVIVLLRWPLLGMFLETYGFFSLFKGFFPV
		1	1	l		AFGFLGNVCNIPFLGALFRRLQGTSSMV*KTE
		1	1			MSSLNLDHWLKGAKREEWEPPPQSPALTHSP
	1	1	1 .			TYPGPPQVQKERNGAEQLTSNPQVDSRGCQE
		1				AEMQTPRRLGWGWYHTLTLYLWEEK
875	2225	A	7498	91	251	GEKPVPTWLQDEAGQWLLGFVAQPWGWPG
		1	ì	1		SERHEP*HGGVLFRLGPSAPPGKL
876	2226	A	7544	403	587	YSCLCFLFKHITSFKNSVHIWLGTVVHAYNPN
		1				ILGGQGGWIA*GQEFKTSLGNTVRPCLYK
877	2227	A	7566	2	940	GCAPDTRFFVPEPGGRGAAPWVALVARGGC
		j	.]	i	ļ	TFKDKVLVAARRNASAVVLYNEERYGNITLP
				1		MSHAGTGNIVVIMISYPKGREILELVQKGIPV
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1	1	1	1	1	1	GQLLLHTVKHGEKGIDVDAENCAVCIENFKV
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1		1	1			DVIKALGYWGEPGDVQEMPAPESPPGRDPAA
	·1	1			1	NLSLALPDDDGSDESSPPSASPAESEPQCDPSF
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878	2228	A	7586	315	1232	ERSLLCKVDVRWIYVSEGTKTQRRHRQGSLR RGRMQAACWYVLFLLQPTVYLVTCANLTNG
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		1		ŀ		GKSELLKSGSSKSTLKHIWTESSKDLSISRLLS OTFRGKENDTDLDLRYDTPEPYSEQDLWDW
				1		LRNSTDLQEPRPRAKRRPIVKTGKFKKMFGW
		1	1	1		GDFHSNIKTVKLNLLITGKIVDHGNGTFSVYF
	1		}		ļ	RHNSTGQGNVSVSLVPPTKIVEFDLAQQTVID
Ì			}	l		AKDSKSFNCRIEYEKVDKATKNTLCNYDPSK
		j	1	ì	1.	TCYQEQTQSHVSWLCSKPFKVICIYISFYSTD
		1				YKLVOKVCPDYNYHSDTPYFPSG
970	2220	+	7605	479	391	TESWKLKWWSPTCLDQLNGSAPGNVFIHG
879	2229	A	7612	93	659	DAAVAMTAQGGLVANRGRRFKWAIELSGPG
880	2230	Α	/012	1 23	0.59	GGSRGRSDRGSGOGDSLYPVGYLDKQVPDTS
	1	1	1			VQETDRILVEKRCWDIALGPLKQIPMNLFIMY
1	,			l .	1	MAGNTISIFPTMMVCMMAWRPIQALMAISAT
	1		1	1	I .	
	,				ļ	FKMLESSSOKFLOGLVYLIGNLMGLALAVYK
						FKMLESSSQKFLQGLVYLIGNLMGLALAVYK
						FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPTHASDWLAFIEPPERMEFSGGGL
001	2221		7615	291	1452	FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPTHASDWLAFIEPPERMEFSGGGL LL
881	2231	A	7615	291	1452	FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPTHASDWLAFIEPPERMEFSGGGL LL SPQKTMRSHTITMTTTSVSSWPYSSHRMRFIT
881	2231	A	7615	291	1452	FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPTHASDWLAFIEPPERMEFSGGGL LL SPQKTMRSHTITMTTTSVSSWPYSSHRMRFIT NHSDQPPQNFSATPNVITCPMDEKLLSTVLTT
881	2231	A	7615	291	1452	FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPTHASDWLAFIEPPERMEFSGGGL LL SPQKTMRSHTITMTTTSVSSWPYSSHRMRFIT NHSDQPPQNFSATPNVITCPMDEKLLSTVLTT SYSVIFIVGLVGNIIALYVFLGIHRKRNSIQIYL
881	2231	A	7615	291	1452	FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPTHASDWLAFIEPPERMEFSGGGL LL SPQKTMRSHTITMTTTSVSSWPYSSHRMRFIT NHSDQPPQNFSATPNVTTCPMDEKLLSTVLTT SYSVIFIVGLVGNIIALYVFLGHRKRNSIQIYL LNVAIADLLLIFCLPFRIMYHNQNKWTLGVIL
881	2231	A	7615	291	1452	FKMLESSSQKFLQGLVYLIGNLMGLALAVYK CQSMGLLPTHASDWLAFIEPPERMEFSGGGL LL SPQKTMRSHTITMTTTSVSSWPYSSHRMRFIT NHSDQPPQNFSATPNVITCPMDEKLLSTVLTT SYSVIFIVGLVGNIIALYVFLGIHRKRNSIQIYL

munce ordice seq	SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO:	Predicted beginning nucleotide	Predicted end nucleotide location	D=Aspartic Acid, E=Glutamic Acid.
1949   14   18   1949   1944   18   18   18   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   1941   194	cotide	seq-	1	USSN			l=Isoleucine, K=Lysine, I=I encine
September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   September   Sept		uence		09/496	correspondi	to last amino	
minito acid peside squence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence   cesidence	uence		1	914			Q=Glutamine, R=Arginine, S=Serine
Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   Pepide   P		ł					T=Threonine, V=Valine, W=Tryptophan.
Poptide   Sequence		1				sequence	Y=Tyrosine, X=Unknown, *=Ston codon.
	1		1	1		1	/=possible nucleotide deletion, /=possible
SIGKYATTARNSFYLLIPTICFVPYHAFRFYTISS   QLNVSSCYMEINHKINSMILMLLSSINSMILMLLSSINSMILMLSSINSMILMLSSINSMILMLSSINSMILMLSSINSMILMLSSINSMISSSSST   SEKROFQ SHIDTINVAVIOSSSSST   SEKROFQ SHIDTINVAVIOSSSSST   SEKROFQ SHIDTINVAVIOSSSSST   ROMALLKANKOLISAGTKEFSVILNQQVFND   PLVSEEDMYTVVEDWMNFYINTYRQQVTGE   PQREVARLQELRQELINLANFILAKYRDFLK   SHELPSHPPOS   SHELPSHPPOS   SHELPSHPPOS   SHELPSHPPOS   SHELPSHPPOS   SHELPSHPPOS   AVATVOPISVAVQASHVFQFYKKGKHLSS   SHELPSHPPOS   AVATVOPISVAVQASHVFQFYKKGKHLSS   AVATVOPISVAVQASHVFQFYKKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVATVOPISVAVQASHVFQFYKGKHLSS   AVASLPMGFQFVKTSTXTTRDIVKELLISL   VASLPMGFQVLFLILLWYGIYV   ALGENFASHVFLTVALVILFQLKVQHFQFYKGLTSLISL   VASLPMGFQVLFLILLWYGIYV   APATVAFYASHVFLILLFTLCLLISEMASGQ   AFRIPPISVAVQHTAVATVASHVBLAVQHFYV   AVATVAPISVAVQHTAVATVASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHVBQASHV		<del> </del>	<del> </del>	<b>-</b>	sequence	ļ	nucleotide insertion
	1	}	ł	ł	ł	}	VVMFWLIFLLIILSVIKIGKNI I RISKRRSKEPN
WAYFLMSSNIRKIMCQLLFRRPGGEPSRSEST   SEFEPGYSHIDTSVAVKIGSSSKST   SEFEPGYSHIDTSVAVKIGSSSKST   SEFEPGYSHIDTSVAVKIGSSKST   SEFEPGYSHIDTSVAVKIGSSKST   PLYSEEDMITVVEDWINPYINVYRQVYTGE   PQERDKALQELRQELNITANPFLAKYRDFLK   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SHELPSHIPPSS   SH		1	1	1	ł	ļ	SGKYATTAKNSFIVLIIFTICFVPYHAFRFIYISS
882   2232   A 7617   67   379   ROMALIZANDOLISAGIZEFSVILINQQVPND   PLVSEEDMITYVEDWMNFYINYYROQVTGE   POEBDKALQELRQELNTLANFFLAKYRDFLK   SHELPSHPPSS   PSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHELPSHPSS   SHEL			1				QUIVASCA MKRIAHKINRIMTATSELDB
883			1				SEEKPGVSI HDTSV AVKIOSSSKST
R83	882	2232	A	7617	67	379	ROMALI KANKDI ISA GI VERGITI I MONTAND
PQERDKALQELRQELNITLANPFLAKYRDFLK		1					PLVSEEDMVTVVEDWAMEVNIVVEOOXTOR
SHELPSHPPPSS	1	1				Į.	POBRDKALOEL ROEL NIT ANDEL AKVEDELK
883   2233   A   7622   400   215   KVKTCRYNPKYSAANDTGEVDIPSREKDLAK AVATVGPISVAVQASHVFROFYKKOKHLISS						1	SHELPSHPPPSS
884   2234   A   7638   2640   2861   APULLOWKISTYLTPOJESHOGOTIKELO OHVKSVTCPCEYLRKVSECROMOPGALEOFP OLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG   GLSCHTSHISG	883	2233	A	7622	400	215	
2234   A   7638   2640   2861							AVATVGPISVAVGASHVFFOFYKKGKHLSS
See	884	2234	A	7638	2640	2861	APVLILOMVKLSIVLTPOFLSHDOGOLTKELO
885   2235   A   7642   201   455   PSRGKMELEAMSRYTSPVNPAVPPHLTVVLL AIGMFFTAWFFVYEVTSKYTRDIYKELLISL VASLFMGFGVLFLLLWYGIYV     886   2236   A   7692   61   569   APENPFSRQIPNESTKYKLSLKTGTWLGNIA   HLGEHFSTHHELGLSGKVVGFLVKNILEVIRN GGMETRHPGKVSSWFHRWDSRAEQHNHAE   HHEDVPQGDEDSKVSRQQEFPDVVTCAGLP     61   64   APENPFSRQIPNE   GLIPKALRVLLFQLKVQHRPGHQQRPEQQD   VSDHRYGRSVRQNRK     887   2237   A   7693   85   315   NPGCCLPVAMRTSYLLLFTLCLLISEMASGG   NPLTGLGHRSDHYNCVSSGQQCLYSACPIFTK   IQGTCYRGKAKCK   APSHRRYLSPSRSAGQLGNMALERLCSVLK   VLLITVLVVEGIAVAQKTQDGQNIGIKHBAT   QGGWVRTSNGGHFASPNYPDSYPPNKECTYI   LEAAPRQRIELTFDEHYYIEPSFCRFDHLEVR   DCPFGSPLDRYGGVSSPTLAGFMWIKF   SSDEELEGLGFRAKYSFIPDPDFTYLGGLINPP   DCQFELSGADGIVRSSQVEQEEKTKRGQAVD   CIWIKATFKAKIVLRFLDYQMEHSNECKNYG   GVIRMWADEGSRLNRFRMLFTSFGGAVD   CIWIKATFKAKIVLRFLDYQMEHSNECKNYG   GVIRMWADEGSRLNRFRMLFTSFGGAVD   CIWIKATFKAKIVLRFLDYQMEHSNECKNYG   GVIRMWADEGSRLNRFRMLFTSFGGAPQA   ALSFCHSNMCINNSLVCNGVQNCAYPWDEN   HC   CHYIMNPSTHHPASAGGSLGLFDFFGLGLGE   MTMDALLARLKLNPDDLREEIVKAGLKCCP   ITSTTRFPEKKLAQALLEQGGRLSSFYHHEA   GVIALSQDPORILRPAGRAFTDOAGFSEDRDF   GYSVGLNPPEEAVTSXTCSVPPSDTDTYRAG   ATASKEPPLYYGVCPVYEDVP ARNEBIVYYE   NKKEAQAAVMIKGSRFAAFSTREDAEKFAR   GICDYPPSPSKTSLPLSPVKTAPLFSNDRLKDG   LCSSSTYNKERANSVKNPTQDLTAKLRK   AVEKGEEDTFSDLIWSNPRYLIGSGDNPTIVQ   EGCRYNVMHVAAKENQASICQLTLDVLENP   DFMKLMYPDDDEAMLQKRIFYQELWSPDTA   ESSHVSRYGGSPRPPVLTLRAPAGGLSCQLTLDVLENP   DFMKLMYPDDDEAMLQKRIFYGELWSPDTA   ESSHVSRYGGSPRPPVLTLRAPAGGLSCRPLKKERIR   EYLKGGTYPVLERSKNKSVELKERIR   EYLKGGTYPVLERSKNKSVELKERIR   EYLKGGTYPVLERSKNKSVELKERIR   EYLKGGTYPVLERSKNKSVELKERIR   EYLKGGTYPVLERAEGFBPR   GREAHFLICGFFOLSSCG   GLQRLEFLTQQEIGKKAQQETGREASSCRD   KATTGSSNISISVAFLIDEDDWAGELWRNOON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHARLON   CARCHAR		ľ	1	1 1		,	QHVKSVTCPCEYLRKVSECROMGPGALEOFP
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	P-Phenylalanine, G-Glycine, H-Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
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l	ł					YGLRVKLLEPVPVSVTRCSFRVNENTHNLQIH
1	l	1	i	1	į.	AGDILKFLKKKKPEDAFCVVGITMIDLYPRDS
i	j	1			ŀ	WNFVFGQASLTDGVGIFSFARYGSDFYSMHY
	1	1			Į .	KGKVKKLKKTSSSDYSIFDNYYIPEITSVLLLR
}		Į	1			SCKTLTHEIGHIFGLRHCQWLACLMQGSNHL
		i	1	İ		EEADRRPLNLCPICLHKLQCAVGFSIVERYKA
	ł	1		İ	1	LVRWIDDESSDTPGATPEHSHEDNGNLPKPV
]	1	}		Į	1	EAFKEWKEWIIKCLAVLQK
l	1-2-2	٠.	6502	<u> </u>	1660	SAPTAPARPCRAERGSGGGMLALLAASVALA
892	2242	A	7723	2	1650	VAAGAQDSPAPGSRFVCTALPPEAVHAGCPL
1		1	1	1		PAMPMQGGAQSPEELRAAVLQLRETVVQQ
1	1.	1	j.	}		KETLASARAIRELTGKLARCEGLAGGKARGA
1		ļ	1	1		KEILASARAIRELIGKLARCEGLAGGAARGA
1			i			GATGKDTMGDLPRDPGHVVEQLSRSLQTLK
1	1	1	ı	1	1	DRLESLEPLPAMPMQGGAQSPEEELRAAVLQ
1	ļ	1 .	1			LRETVVQQKETLASARAIRELTGKLARCEGL
1			1			AGGKARGAGATGKDTMGDLPRDPGHVVEQ
1	1	1	ļ	İ	1	LSRSLQTLKDRLESLEHQLRANVSNAGLPGD
	<b>\</b>	1				FREVLQQRLGELERQLLRKGAELEDEKSLLH
1	1	1	1	1		NETSAHROKTESTLNALLQRVTELERGNSAF
ļ	j			1	ļ	KSPNAFKVSLPLRTNYLYGKIKKTLPELYAFT
	1	1		1	1	ICLWLRSSASPGMGTPFSYAVPGQANEIVLIE
			l		1	WGNNPIELLINDKVAQLPLFVSDGKWHHICV
1	1	1	j	1		TWTTRDGMWEAFQDGKKLGTGENLAPWHPI
1	1	1		1		KPGGVLILGQEQDTVGGRFDATQAFVGELSQ
	]	1	}	1		FNIWDRVLRAQEIVNIANCSTNMPGNIIPWVD
	1	1			1	NNVDVFGGASKWPVETCEERLLDL
		<del></del>	1	+	0410	LTAGTAMNYPLTLEMDLENLEDLFWELDRL
893	2243	A	7729	3554	2419	PRODUCT AND LEGISTATION AND AND AND AND AND AND AND AND AND AN
1	1	1	1		1	DNYNDTSLVENHLCPATEGPLMASFKAVFVP
	1	1	1		1	VAYSLIFLLGVIGNVLVLVILERHRQTRSSTET
	ļ	1	1	Į.	1	FLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
1		1	1		1	LCKTVIALHKVNFYCSSLLLACIAVDRYLAIV
	1		1			HAVHAYRHRRLLSIHITCGTIWLVGFLLALPEI
1	1	1	1			LFAKVSQGHHNNSLPRCTFSQENQAETHAWF
1		1		1		TSRFLYHVAGFLLPMLVMGWCYVGVVHRLR
1		1		1		QAQRRPQRQKAVRVAILVTSIFFLCWSPYHIV
1	1			1		IFLDTLARLKAVDNTCKLNGSLPVAITMCEFL
1			1	1		GLAHCCLNPMLYTFAGVKFRSDLSRLLTKLG
1	ŀ		1	1	1	CTGPASLCQLFPSWRRSSLSESENATSLTTF
1004	10044	+	7720	+ 670	287	FVTRAGRWGAGARVRGGAGGMASGAARWL
894	2244	Α	7738	670	201	VLAPVRSGALRSGPSLRKDGDVSAAWSGSGR
1	1		1	1	1	
1		1			1	SLVPSRSVIVTRSGAILPKPVKMSFGLLRVFSI
		-		1	i	VIPFLYVGTLISKNFAALLEEIIDIFVPEDDDDD
	1			1		D
895	2245	A	7753	119	278	APYAHSQVHCLDKVCGLLPFLNPEVPDQFYR
			1	1 .	1_	LWLSLFLHAGKEAPHCPRTRPL
896	2246	A	7754	1	372	SPAWWNSQQRVVSPFLALLTLEPTFHHLLPIM
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Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Deptide   Dept							
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Seq							F-Prienylalanine, G-Glycine, H-Mistidme,
Beach			Ì				1 - Isbicucine, K-Lysine, L-Leucine,
amino acid peptide squence y-frame, w-frame, w-frame, w-frame, peptide squence y-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-frame, w-fra		ucito	ļ				
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Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate   Populate			l				1=1 hreonine, V=Valine, W=1 ryptophan,
	ł		1	ļ		sequence	
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S97   2247   A   7761   1725   445   RPRRETHIPSCVLOSERYSAMFPRVSTIFLE,   RPS.RS.HPLSGSPFTSAAAMILLTVRHOTVRY   RSSALLARTKNNIQRYFGTISVLOKKDIKQSV   RESTRIPSESQDSEKENTKKDLLGIIKGMK   VELSTYNVRTTKFPKRPLKSLBATLGRLRRA   TEYAFKKREPLSPELVAAASAVADSLIPFOR   TIKSELLSQLQQHEESRAQRDAKRKISFSNI   ISDMKVASKATARVSRSPELRIQFDSEQTVAAASAVADSLIPFOR   GGEKTDDLKKRKNITGKRINIFDMMAVTKE   APETDTSS-WDVLPFAKQLATINGQLQRAD   RELIQWTKEGKL WEPPINNEAGFDDIGSEPH   BHFIEKHLESPFKQDFRHFWELVTGGLSKNJP   RELIQWTKEGKL WEPPINNEAGFDDIGSEPH   BHFIEKHLESFFKQDFRHFWELVTGGLSKNJP   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRWKLFRNN   KLRW	!	ļ	ļ	ļ	!	!	QVSTAALAVLLCTMALCNQVLSAPLAADTPT
S97   2247   A   7761   1725   445   RPRREGTHIFSCV/GGSFRVSAMMERVSTFLPL   RPLSRIPS-SGSPETSAAMMLLTVRIGTORY   RSSALLARTKNNIQRYFGTNSVICSKLDKG9K   RTEFTSKETSESQDSEKENTKKDLLGIKGMK   VELSTYMVRITKFPKRPLKSLBATLGRLRRA   TEYAPKKRIEPLSPELVAAASAVADSLPFDKG   TIKSELLSQLQQHEESEAQRDAKRKFISFSNI   ISDMKVARSATARVRSRPERIQFDEGYDNYP   GQEKTDLJKKRKNITGRKLNIFDMAVTKE   APETDTSPS, WDVEPAKQLATVNNEQPLQNGF   EHIFLEKHLESFPKQGPRHFMELVTCGLSKNP   YLSVKQKVEHBWERNYFNEKKDLKKESNIQP   KLRPWKFLERNN   CSPGAVCKEPQEEVYPGGGRSKRDPDLYQLL   QREKSHISSELGLLKALSQASTDFKESTSPEK   RDMHDFVGLMGKSVQPDSPTDVNQENVP   SPGILKYPPRAE   SQCITQPPAGSCSTGTMRIMLIFTAILAFSLA   QSFGAVCKEPQEEVYPGGGRSKRDPDLYQLL   QREKSHISSELGLLKALSQASTDFKESTSPEK   RDMHDFVGLMGKSVQPDSPTDVNQENVP   SPGILKYPPRAE   SPHLGASSNTFRLQVQTQESKAQKEVKMGFI   FSKSMMESMKNQKEPMLMNARQLERQLIM   QSEMRERQMAMQLAWSREFLKYFGTFGLA   ALSLTAGAIKKKPAFLVPPVPSTTVQYDL   GYGTLLERMKGBAEDILETEKSKLQL PRGMTT   FSISKAKREQSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTI	i			ļ	l		ACCFSYTSRQIPQNFIADYFETSSQCSKPSVIFL
S97   2247   A   7761   1725   445   RPRREGTHIFSCV/GGSFRVSAMMERVSTFLPL   RPLSRIPS-SGSPETSAAMMLLTVRIGTORY   RSSALLARTKNNIQRYFGTNSVICSKLDKG9K   RTEFTSKETSESQDSEKENTKKDLLGIKGMK   VELSTYMVRITKFPKRPLKSLBATLGRLRRA   TEYAPKKRIEPLSPELVAAASAVADSLPFDKG   TIKSELLSQLQQHEESEAQRDAKRKFISFSNI   ISDMKVARSATARVRSRPERIQFDEGYDNYP   GQEKTDLJKKRKNITGRKLNIFDMAVTKE   APETDTSPS, WDVEPAKQLATVNNEQPLQNGF   EHIFLEKHLESFPKQGPRHFMELVTCGLSKNP   YLSVKQKVEHBWERNYFNEKKDLKKESNIQP   KLRPWKFLERNN   CSPGAVCKEPQEEVYPGGGRSKRDPDLYQLL   QREKSHISSELGLLKALSQASTDFKESTSPEK   RDMHDFVGLMGKSVQPDSPTDVNQENVP   SPGILKYPPRAE   SQCITQPPAGSCSTGTMRIMLIFTAILAFSLA   QSFGAVCKEPQEEVYPGGGRSKRDPDLYQLL   QREKSHISSELGLLKALSQASTDFKESTSPEK   RDMHDFVGLMGKSVQPDSPTDVNQENVP   SPGILKYPPRAE   SPHLGASSNTFRLQVQTQESKAQKEVKMGFI   FSKSMMESMKNQKEPMLMNARQLERQLIM   QSEMRERQMAMQLAWSREFLKYFGTFGLA   ALSLTAGAIKKKPAFLVPPVPSTTVQYDL   GYGTLLERMKGBAEDILETEKSKLQL PRGMTT   FSISKAKREQSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFPIDK   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTIT   PSISKAKPGSRFTI	L					ĺ	TKRGRQVCADPSEEWVQKYVSDLELSA
RPLSRIPH.SSOSPETSAAAMMLITVRIGITVRY RSSALLARTKNNIQRYKGTINSVICKSKOKQSV RIESTSKETSSQDSEKENTKKDLLGIIKGIMK VELSTVAVRITTEPREKPELSSLAATI.GRLRRA TEYAPKKRIEPLSPELVAAASAVADSLPFDKQ TITKSELLSQLQQHEEESSRAQRDAKRKISFSNI ISDMKVARSATARVRSSPERLQFDEOYDNYP GQEKTDDLKKRINIFIGKBLNIPDMMAVTKE APETDISPS.WDVEHSRQLAITVNEQFLQNGF EELIQWITKEGKLWEFPINNEAGFDDDGSEPH EHIPLEKHLESPPKQOPIRPIMELVTGLSKNP VISVKQKVEHIEWRRNYFNEKKDILKESNIQF KLRPWKFLRRNN SCQITTQPFAQSCSTGTMRIMLIFTAILAFSLA QSFGAVCKEPQEEVVPGGGRSKRDPDLYQLI QRIKSHSLEGILKAJQASTDYKESTSPEK RDMHDFFVGLMGKRSVQPDSPTDVNQENVP SFGILKYPFAE  899 2249 A 7785 179 703 PFHLGASSNITELQVGTQSKKOPEDLYQLI QRIKSHSLEGILKAJQASTDYKESTSPEK RDMHDFFVGLMGKRSVQPDSPTDVNQENVP SFGILKYPFAE FRISMMENSKKNCKEFMIMARAQLERQLIM QSEMRERQMAMQIAWSREILKYFGTFFGLA AISLTAGAIKKKKPAFLVPIVPLSFETTYQYDL QYGTILLERMKGEAEDILETEKSKLQLPRGMIT FRISMAFSKKNOKGFFIDK VQTIVKSSKGGTGSAVSPYTFINSSDVAALH KAIMVKGVDEATIDILTKRNNAQRQQIKAAY LQETGKPLDETLKKALTGHEEVVLALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AQFDADELRAAMKGLGTDEDTLIEILASRTIN KERDINEVYTEELEKTHOHAEDVALALIKTT AGFDASSRTERQKGTARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAARROKGTAAA	897	2247	Α	7761	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPL
RTESTSKETSSSQÖSEKENTKKDLLGIIKGÖMK VELSTVAVETTEPREKPELKSIENAT GELRAA TEYAPKKRIEPLSPEL VAAASAVADSLPFDKQ TITKSELLSQLQQHEEESIKAQRDAKRYKISFSNI ISDMKVARSATARVRSKPERLQFDEGYDNYP GQEKTDDLKKRINIFTGKBLINIPDMMAVTKE APETDISPSILMVDYBAKQLAIVNROPLONGF EELLQWTKEGKI WEFPINNEAGFDDDGSEPH EIHLE KEHLESPPKQGPPHFMPELIVTCGLSKNP YLSVKQKVEHIEWFRNYFNEKKDILKESNIQF KIRPWKRLERNN  898 2248 A 7775 85 496 SQCTTOPPAGSCSTGMRMILLFTAILAFSLA QSFGAVCKEPQEEVVPGGGRSKRDPDLYQLL QRLKSHSSLEGILKASQASTDPKESTSPEK RDMHDFFVGLMGKRSVQPDSPTDVNQENVP SGULKYPRAE 899 2249 A 7785 179 703 PFHLGASSNITFRLQVQTQESKAQKEVKMGFI FSKSMMESMKNQKEFMLMNARLQLERQLIM QSEARREQMAMQLAWSRELKYFGTFGLA AISLTAGAIKKKPAFLVPIVPLSFILTYQYDL GYGTLLERMKGGREDULETEKSKLQLPRGMIT FESIEKAARKOSRFFIDK  900 2250 A 7789 1465 300 VWEPLKSYKIRSPSLHCQCEIFREFELFSSLQE GRIDKOTTSKMANVSEFLKQAWFIENEGGPY VQTVKSSKGGRGSAVSPYFIFNSSDVAALH KAIMVKQVDEATIDLITKRNNARQRGKAAY LQETGKPLDETLKKALTOHLEEVVLALLKTF AQFDADELRAAMKGJGTDETLEILASRTN KERDDNFVYREELKRDLASDITSDTSGDFRN ALLSLAKGDRSEDFGVNEDLADSDARALLYA- GERRKGTDVNVFNTILTTRSYPQLRRVFQKY TKYSKHDMNVXLDLELKGDIEKCLTAIVKCA GERRKGTDVNVFNTILTTRSYPQLRRVFQKY TKYSKHDMNVXLDLELKGDIEKCLTAIVKCA GERRKGTDVNVFNTILTTRSYPQLRRVFQKY TKYSKHDMNVXLDLELKGDIEKCLTAIVKCA GERRKGTDVNVFNTILTTRSYPQLRRVFQKY TKYSKHDMNVXLDLELKGDIEKCLTAIVKCA GERRKGTDVNVFNTILTTRSYPQLRRVFQKY TKYSKHDMNVXLDLELKGDIEKCLTAIVKCA GAPFSEETLRGLJGRCFLGULVKTREGH GERRKGTDVNVFNTILTTRSYPQLRRVFQKY TKYSKHDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYGKNYGTSKLAKIRIMVS RSEIDMNDIKAFYQKNYGTSKLAKIRIMVS RSEIDMNDIKAFYYGKYTSKARHOKOTAARRX RCKGTARRQKGTAARRRQKGTAARRR RCKGTAARRQKGTAARRRQ			i	1			
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Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence			1,000				F=Phenylalanine, G=Glycine, H=Histidine,
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uence  914 ang to first amino acid residue of peptide requence peptide sequence 903 2253 A 7807 1 584 PWLPWSDGRARSSRCPRSRFPVQVGK 904 2254 A 7813 40 821 GAGRAICHLETGAGDVAAALPARKFPRS AGARLATERILLYBENGRAMENCILLSLETAKERILOH EKQLNLYDRLINEPSNDWDIYYWATEAK EIFENEVMALLRDFAKNKNKEQRLARDILINGSROWPOKERTDESIGN AGARLATERILATERILYBENGRMENCILLSLETAKERILOH EKQLNLYDRLINEPSNDWDIYYWATEAK EIFENEVMALLRDFAKNKNKEQRLARDILINGSROWPOKERTDESIGN AGARLATERILOH EKQLNLYDRLINEPSNDWDIYYWATEAK EIFENEVMALLRDFAKNKNKEQRLARDILINGSROWPOKERTDESIGN AGARLATERILOH EKQLNLYDRLINGPSNDWDIYYWATEAK EIFENEVMALLRDFAKNKNKEQRLARDILINGSROWPOKERTDESIGN AGARLATERILIPSNRTAMENVORIGENEVAL EIFENEVMALLRDFAKNKNKEQRLARDILINGSROWPOKERTDESIGN AGARLATERILIPSNRTAMENVORIGENEVAL EIFENEVMALLRDFAKNKNKEQRLARDILINGSROWPOKERTDESIGN AGARLATERILIPSNRTAMENVORIGENEVAL EIFENEVMALLRDFAKNKNKEQRLARDILINGSROWPOKERTDESIGN AGARLATERILIPSNRTAMENVORIGENEVAL EIFENEVMALLARDILINGSROWPOKERTDESIGN AGARLATERILIPSNRTAMENVORIGENEVAL EIFENEVMALLARDILINGSROWPOKERTDESIGN AGARLATERILIPSNRTAMENVORIGENEVAL EIFENEVMALARDILIPSNRTAMENVORIGENEVAL EIFENEVMALARDILIPSNRTAMENVORIGENEVAL EIGENVALLERILIPSNRTAMENVORIGENEVAL EIGENVALLERILIPSNRTAMENVORIGENEVAL EIGENVALLERILIPSNRTAMENVORIGENEVAL EIGENVALLERILIPSNRTAMENVORIGENEVAL EIGENVALLERILIPSNRTAMENVORIGENEVAL EIGENVALLERILIPSNRTAMENVORIGENEVAL EIGENVALLERILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAMENVALLEDILIPSNRTAME			1				M=Methionine, N=Asparagine, P=Proline,
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Peside of peptide sequence	ucilioo		1			of peptide	T=Threonine, V=Valine, W=Tryptophan,
			İ			sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
903   2253   A   7807   1   584   PWLPWSDGRAARSSRKCPRSRFPVQVGK			ļ		peptide	,	/=possible nucleotide deletion, \=possible
VSTVFSTSIMLALSRISLLSPLSVTSFR				1	sequence	l	nucleotide insertion
RGDSPTDSQKDMEPLP,PWQERTDESIET	903	2253	Α	7807	1	584	PWLPWSDGRAARSSRKCPRSRFPVQVGKMA
ARLLYSSKERGM.ENCILLSI.PAREHLOR							
BEKQLNLYDRLINEPSIDWDIYYWATEAK   EIFENEVMALLRDFAKNKNEQRLRAPDI   LPEKPR			ľ	]		1	RGDSPTDSQKDMIEIPLPPWQERTDESIETKR
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				1	İ		EKQLNLYDRLINEPSNDWDIYYWATEAKPAP
904   2254   A   7813   40   821   GAGRALGHLETGAGDVAAALPARKFPES   AGARLTGWTMNVFRILGDLSHLLAMILLI   IWRSKCKGISGKSQILFALVFTTRYLDLF   ISIYNIVMKVVFLLCAYVTVYMYGKFRK   DSENDIFRLEFILLVPVIGLSFLENYSFILLI   WTFSIYLESVALIPQLFMISK TGEAETIL'IH   FFLGLYRALYLANWIRRYQTENYSFILLI   WTFSIYLESVALIPQLFMISK TGEAETIL'IH   FFLGLYRALYLANWIRRYQTENYSPILLI   WTFSIYLESVALIPQLFMISK TGEAETIL'IH   FFLGLYRALYLANWIRRYQTENYSPILLI   WTFSIYLESVALIPQLFMISK TGEAETIL'IH   FFLGLYRALYLANWIRRYQTENYSPILLI   WTFSIYLESVALIPQLFMISK TGEAETIL'IH   FFLGLYRALYLANWIRRYQTENYSPILLI   WTFSIYLESVALIPQLFMISK TGEAETIL'IH   FFLGLYRALYLANWIRRYQTENYSPILLI   WTFSIYLSVALIPQLFMISK TGEAETIL'IH   FFLGLYRALYLANWIRRYQTENYSPILLI   WTFSIYLSVALIPQLFMISK TGEAETIL'IH   TSPIYLI   WTFSIYLSVALIPQLFMISK TGEAETIL'IH   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSPIYLI   TSP						l	
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IWRSKCKGISGKSQILFALVFTTRYLDLF   ISIYNTVMKVVFLLCAYVTVYMIYGKFRK   DSENDITFILEFILLVPVIGLISTLENYSFILL]   WITFSIYLESVAILPQLFMISKTGEAETITIH   FFLGLYRALYLANWIRRYQTENFYDQIAA   GVVQITFYCDFFYLTVVTKGRSWDDSNAD   RSYSSI   LSNKDVLSPQLKDENSKLRRKLNEVQSFS   QTEMVRTLERKLEAKMIKEESDYHDLES'   QVQNIEMTKRAVKAENHVVKLKQEIS   QAQVSNFQREALRCGQGASLTVVKQV   VALQNLRVVMNSAQASIEQLVSGAETLN   EILKSIDRISEVKDEEEDS	904	2254	A	7813	40	821	GAGRALGHLETGAGDVAAALPARKFPRSLLC
SIYNTYMKVYFLLCAYVTVYMYGKFRK   DSENDITRIEFLLVPVIGLSFLENYSFILL    WITSIYLESVALI-PQLFMISKTGEAETII II-FFLGLYRAL YLANWIRRYQTENFYDQIAN   GVVQTIFYCDFFYLYVTKGRSWDDSNAD   RSYSSI			İ	1		ŀ	AGARLTGWTMNVFRILGDLSHLLAMILLLGK
DSENDITRLEFLLVPVIGLSFLENYSFILLI   WITSIYLESVALIPQLFMISKTGEAETII'II   WITSIYLESVALIPQLFMISKTGEAETII'II   FFICILYRALYLANWIRRYQTENFYDQIAY   GVVQTIFYCDFFYLYVTKGRSWDDSNAD   RSYSSI   LSNKDVLSPQLKDENSKLRRKLNEVQSFS   QTEMVRTLERKLEAKMIKEESDYHDLES'   QVEQNLELMTKRAVKAENHVVKLKQEIS   QAQVSNFQRENEALRCGQASLTVVKQV   VALQNLRVVMNSAQASIEQLVSGAETLN   EILKSIDRISEVKDEEEDS   DSPRNRFEILGPTRTPTRFOPRPAMEDLI   LSDLETTISHMPRSGAPKERPAEPLTPPPS   HOPOTGSGESSGASGDKDHLYSTVCKPR   PAAPAAPPFSSSSGVLGTGLCELDRLLQEI   TOPNITDEMSQFPSSKVASGEQKEDQSEI   RPSLPSSPSPGLPKASATSATLELDRLMAS   FRVQNHLPASGPTQPPVVSSTNEGSPSPP   KGSLDTML.GLLQSDLSRRGVPTQAKGLC   NKPIAGQVVTALGRA WHPEHFVCGGCST   GRSSTFEKDGAPFCPECYFERFSPRCGFC   RHKMYTALGTHWHPEHFCCVSCGEPFGI   FHEREGRPYCRRDFLQLFAPRCQGCQGPI   YISALSALWHPDCFVCRCCFAPPSGGSFF   GRRLCENHFHARRGSLCATCGLPVTGRC   LGRRFHPDHFTCTFCLRPLTKGSFQERAG   CQPCFLKLFG   GRRLCENHFHARRGSLCATCGLPVTGRC   LGRRFHPDHFTCTFCLRPLTKGSFQERAG   CQPCFLKLFG   FIVVNQSFAPSPDQEVGTLYECFGSDGKL   YCKSQAWG   SLQPPSGLKQSSHLSLSSSWDFRHAPTH   YTCPKMIEMEQAEAQLABLDLLASMFFG   LIVNDQLAVAELKDCIEKKTMEGRSSKV   NMNLDVSDEKMAMFSLACILPFKYPAVI   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKICH   TYRSYYLLSRSOOTOLNTDLTAFLOKKIC			1	1.		i	
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PFLGLYRALYLANWIRRYQTENFYDQIAW				1			DSENDTFRLEFLLVPVIGLSFLENYSFTLLEIL
905   2255   A   7817   1399   881   LSNKDVLSPQLKDENSKLRKLNEVQSFS   QEMYRTLERKLEAKMIKEESDYHDLES   QEQNLELMTKRAVKAENHVVKLKQEIS   QAQVSNFQRENEALRCGQGASLTVVKQN   VALQNLRVVMNSAQASIEQLVSGAETLN   EILKSIDRISEVKDEEEDS   DSFRNFFEILGRPTRTPTRFGRPAMEDIL   LSDLETTISHMPRSGAPKERPAEPLTPPPS   HQPQTGSGESSGASGDKDHLYSTVCKPR   PAAPAAPPFSSSSGVLGTGLCELDRLLQE   TQFNITDEIMSQFPSSKVASGEQKEDQSEI   RPSLPSSPSGPLFKASATSATLELDRLMAS   FRVQNHLPASGPTQPPVVSSTNEGSPSPP   KGSLDTMLGLLQSDLSRRGVPTQAKGLC   NKPIAGQVVTALGRA WIPPEHFVCGGCST   GGSSFFEKDGAPFCPECYFERFSPRCGFC   RHKMVTALGTHWHPEHFCCVSCGEPFGI   FHEREGRPYCRRDFLQLFAPRCQGCQGP   YISALSALWHPDCFVCRECFAPPSGGSFF   GRPLCENHFHARRGSLCATCGLPVTGRC   LGRRFHPDHFTCTFCLRFLTKGSFQERAG   CQPCFLKLFG   GPLCENHFHARRGSLCATCGLPVTGRC   LGRRFHPDHFTCTFCLRFLTKGSFQERAG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKLFG   CQPCFLKT   CQPCFL   CQPCFL   CQPCFLKT   CQPCFL   CQPCFL   CQPCFL   CQ	•			j	1		WTFSIYLESVAILPQLFMISKTGEAETII'IHYL
905   2255   A   7817   1399   881			Į.	1	1		
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nucleotide sequence    Sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence   Destide sequence
cotide sequence  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496 914  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN 09/496  USSN
sequence    Sequence   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914
uence  914  ng to first amino acid residue of peptide sequence  914  ng to first amino acid residue of peptide sequence  925
amino acid residue of peptide sequence peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s
residue of peptide sequence Peptide sequence Peptide sequence Peptide sequence Peptide sequence Proceedings of the sequence Processible nucleotide deletion, possible nucleotide insertion TNGQCHCKEFHYRERGSDSCLPCDCYPV.  SRSCAPHSQCPCRPGALGRQCNSCDSPF TASGCRVLYDACPKSLRSGVWWPQTKFG ATVPCPRGALGLRGAGAAVRLCDEAQGY PDLFNCTSPAFREISLLLDGLELNKTALD AKKLAQRLREVTGHTDHYPSQDVRVTAR AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDLWAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEPGISIILLVYRTLGGLLPAG AERRGARLPQNPVMNSPVVSVAVHGRA GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEILIFLLGIHRTHNQLVCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
peptide sequence /=possible nucleotide deletion, \=possible nucleotide insertion  TNGQCHCKEFHYRERGSDSCLPCDCYPV.  SRSCAPHSQCPCRPGALGRQCNSCDSPF TASGCRVLYDACPKSLRSGVWWPQTKFG ATVPCPRGALGLRGAGAAVRLCDEAQGY PDLFNCTSPAFRELSLLLDGLELNKTALD AKKLAQRLREVTGHTDHYFSQDVRVTAF AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDLWAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEPGISIILLVYRTLGGLLPAG AERRGARLPQNPVMNSPVVSVAVHGRM GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV. VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEILIFLLGHRTHNQLVCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGMI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
sequence  TNGQCHCKEFHYRPRGSDSCLPCDCYPV  SRSCAPHSGQCPCRPGALGRQCNSCDSPF TASGCRVLYDACPKSLRSGVWWPQTKPC ATVPCPRGALGLRGAGAAVRLCDEAQGY PDLFNCTSPAFRELSLLLDGLELNKTALD AKKLAQRLREVTGHTDHYPSQDVRVTAR AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDLWAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQPRPSPSEVLPTSSSIENST VVPPPAPPEPEPGISIIILLVYRTLGGLLPAC AERGGARLPQNPVMNSPVVSVAVFHGRA GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEILIFLLGHRTHNQLVCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
TNGQCHCKEFHYRERGSDSCLPCDCYPV SRSCAPHSQCPCRPGALGRQCNSCDSPF TASGCRVLYDACPKSLRSGVWWPQTKFC ATVPCPRGALGRAGAAVALCDEAQGV PDLFNCTSPAFELSLLLDGLELNKTALD AKKLAQRLREVTGHTDHYFSQDVRVTAF AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDLWAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPGISIILLVYRTLGGLLPAC AERGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEI.LFLLGIHRTHNQL.VCTAVVILLH LSTFAWLFVQGLHLYRNQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
SRSCAPHSQCPCRPGALGRQCNSCDSPF TASGCRVLYDACPKSLRSGVWWPQTKFC ATVPCPRGALGLRGAGAAVRLCDEAQQG PDLFNCTSPAFRELSLLLDGLELNKTALD' AKKLAQRLREVTGHTDHYFSQDVRVTAF AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDLWAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLFTSSSIENST VVPPPAPPEPEPGISIIILLVYRTLGGLLPAC AERGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVVV VAALVLTAAILLSLRSLKSNVRGHHANVA LGVAEI.LFLLGHRTHNQI.VCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVVLVIVMNGTMFL
TASGCRVLYDACPKSLRSGVWWPQTKFC ATVPCPRGALGLRGAGAAVRLCDEAQGY PDLFNCTSPAFRELSLLDGLELNKTALD' AKKLAQRLREVTGHTDHYFSQDVRVTAF AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDLWAALGQRAPGGSPOSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEGISIILLVYRTLGGLLPAC AERRGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEI.LFLLGHRTHNQLVCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
ATVPCPRGALGLRGAGAAVRLCDEAQGY PDLFNCTSPAFRELSLLLDGLELNKTALD' AKKLAQRLREVTGHTDHYFSQDVRVTAF AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETODL WAALGQRAPGGSPOSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEGISIILLVYRTLGGLLPAG AERGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEI.LFLLGIHRTHNGLVCTAVVIILH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
PDLFNCTSPAFRELSLLLDGLELNKTALD' AKKLAQRLREVTGHTDHYFSQDVRVTAK AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDLWAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEPGISIIILLVYRTLGGLLPAG AERGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRELEGDLELLAVFTHVVV. VAALVLTAALLSLRSLKSNVRGHANVA LGVAEILFLLGIHRTHNQLVCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
AKKLAQRLREVTGHTDHYFSQDVRVTAH AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDL WAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEPGISIIILLVYRTLGGLLPAC AERRGARLPQNPVMNSPVVSVAVHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV, VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEI.LFLLGIHRTHNQLVCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
AHLLAFESHQQGFGLTATQDAHFNENLL GSALLAPETGDL WAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEPGISIIILLVYRTLGGLLPAC AERRGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVV. VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEI.LFLLGHRTHNQL.VCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
GSALLAPETGDLWAALGQRAPGGSPGSA RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSSEVLPTSSSIENST VVPPPAPPEPEPGISIIILLVYRTLGGLLPAG AERRGALPQNPVMNSPVVSVAVHGRM GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVVV VAALVLTAAILLSLRSLKSNVRGHANVA LGVAEI.LFLLGHRTHNQI.VCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
RHLEEYAATLARNMELTYLNPMGLVTPN SIDRMEHPSSPRGARRYPRYHSNLFRGOD DPHTHVLLPSOSPRPSPSEVLPTSSSIENST VVPPPAPPEPEPGISIIILLVYRTLGGLLPAG AERAGARLPQNPVMNSPVVSVAVHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSRT FGVLMDASPRERLEGDLELLAVFTHVVVV VAALVLTAAILLSLRSLKSNVRGHHANVA LGVAEI.LFLLGHRTHNGI.VCTAVVILLH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
SIDRMEHPSSPRGARRYPRYHSNLFRGQD DPHTHVLLPSQSPRPSPSEVLPTSSSIENST VVPPPAPPEPEGISIIILLVYRTLGGLLPAG AERGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSR: FGVLMDASPRERLEGDLELLAVFTHVVVV VAALVLTAAILLSLRSLKSNVRGIHANVA LGVAEI.LFLLGIHRTHNGLVCTAVVIILH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
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AERRGARLPQNPVMNSPVVSVAVFHGRN GILESPISLEFRLLQTANRSKAICVQWDPP EQHGVWTARDCELVHRNGSHARCRCSR: FGVLMDASPRERLEGDLELLAVFTHVVV. VAALVLTAAILLSLRSLKSNVRGHANVA LGVAFI.IFLLGIHRTHNQL.VCTAVVIILH LSTFAWLFVQGLHLYRMQVEPRNVDRGA FYHALGWGVPAVLLGLAVGLDPEGYGNI CWISVHEPLIWSFAGPVVLVIVMNGTMFL
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911 2261 A 7890 21 806 EFGTSRSSRSMAEDLGLSFGETASVEMLPE
SCRPKARSSSARWALTCCLVLLPFLAGLTT
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VITKVTDSYPEPTQLLMGTKSVCEVGSNW
PIYLGAMFSLQEGDKLMVNVSDISLVDYTI
912 2262 A 7891 1263 111 ACGIRHEGAL PGI. TATPEAMI. RFI. PDI. AFS
ACOINTIDAL TOLIN TELEPOLARS
LILALGQAVQFQEYVFLQFLGLDKAPSPQK
PVPYILKKIFODREAAATTGVSRDLCYVKE
VRGNVLRFLPDQGFFLYPKKISQASSCLQK
YFNLSAIKEREQLTLAQLGLDLGPNSYYNI
ELELALFLVQEPHVWGQTTPKPGKMFVLR

SEQ ID NO: of nucl- eotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence		09/496 914	correspondi ng to first amino acid residue of peptide sequence	to last amino acid residue of peptide sequence	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PWPQGAVHFNLLDVAKDWNDNPRKNFGLFL EILVKEDRDSGVNFQPEDTCARLRCSLHASLL VVTLNPDQCHPSRKRKAAIPVPKLSCKNLCH RHQLFINFRDLGWHKWIIAPKGFMANYCHGE CPFSLTISLNSSNYAFMQALMHAVDPEIPQAV CIPTKLSPISMLYQDNNDNVILRHYEDMVVD ECGCG
913	2263	A	7892	15	849	ASRLPRGPGCGADMRPLLGLLLVFAGCTFAL YLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAE LRELSEVLREYRKEHQAYVFLLFCGAYLYKQ GFAIPGSSFLNVLAGALFGPWLGLLLCCVLTS VGATCCYLLSSIFGKQLVVSYFPDKVALLQR KVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPI LNIPIVQFFFSVLIGLIPYNFICVQTGSILSTLTS LDALFSWDTVFKLLAIAMVALIPGTLIKKFSQ KHLQLNETSTANHIHSRKDT
914	2264	A	7893	815	959	KSGWVWWLTPLIPALWEAQTEGSLRPEVKN RLSNITRPFFSKKKKKILV
915	2265	A	7909	3	641	HASGPGGLLRRRRGSGANMPVARSWVCRKT YVTPRRPFEKSRLDQELKLIGEYGLRNKREV WRVKFTLAKIRKAARELLTLDEKDPRRLFEG NALLRRLVRIGVLDEGKMKLDYILGLKIEDFL ERRLQTQVFKLGLAKSIHHAHVLIQQCHIRVR EQVVNILFFTVRLDSQKHIDFSLCFPIGVANPS HVKRKNASKGQGGAGARDDEEEE
916	2266	A	7914	3	967	VAHTQWHTCQRLSQLTHRSILKYLLIDTHAC QVLILKHTHASLSLPSCQECFPSSIPSASHMVS HPHPPPSPRWGQTPEGLPÄASPCGPGPRSCFS SILPTGDSWGMLACLCTVLWHLPAVPALNRT GDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLN YLGPPFNEPDFNPPRLGAETLPRATVDLEVW RSLNDKLRLTQNYEAYSHLLCYLRGLNRQAA TAELRRSLAHFCTSLQGLLGSIAGVMAALGY PLPQPLPGTEPTWTPGPAHSDFLQKMDDFWL LKELQTWLWRSAKDFNRLKKKMQPPAAAVT LHLGAHGF
917	2267	A	7921	2	1166	RPRRGQGLVQEVQTENVIVAEGGVAEITCRL HQYDGSIVVIQNPARQTLFFNGTRALKDERFQ LEEFSPRRVRIRLSDARLEDEGGYFCQLYTED THHQIATLTVLVAPENPVVEVREQAVEGGEV ELSCLVPRSRPAATLRWYRDRKELKGVSSSQ ENGKVWSVASTVRFRVDRKDDGGIICEAQN QALPSGHSKQTQYVLDVQYSPTARIHASQAV VREGDTLVLTCAVTGNPRPNQIRWNRGNESL PERAEAVGETLTLPGLVSADNGTYTCEASNK HGHARALYVLVVYGESRLRPTEGGGAPDP GAVVEAQTSVPYAIVGGILALLVFLIICVLVG MVWCSVRQKGSYLTHEASGLDEQGEAREAF LNGSDGHKRKEEFFI
918	2268	A	7938	3	2653	RRRLPPASPPSSSVSSSLSPSAVVMACRWSTK ESPRWRSALLLLFLAGVYGNGALAEHSENVH ISGVSTACGETPEQIRAPSGIITSPGWPSEYPAK INCSWFIRANPGEIITISFQDFDIQGSRRCNLD WLTIETYKNIESYRACGSTIPPPYISSQDHIWIR FHSDDNISRKGPRLAYFSGKSEEPNCACDQFR CGNGKCIPEAWKCNNMDECGDRSDEELCAKE ANPPTAAAFQPCAYNQFQCLSRFTKVYTCLP ESLKCDGNIDCLDLGDEIDCDVPTCGQWLKY FYGTFNSPNYPDFYPPGSNCTWLIDTGDHRK

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mucle ceidde cyllogologologologologologologologologolo	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
enice  1 USSN oly496 1 Uence  ptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Ve-Valine, Re-Typtophan, Yeptoche, Thereonine, Yellon, Thereonine, Yellon, Ther			noa				D=Aspartic Acid, E=Glutamic Acid,
Sopuence   09/496   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914	1			1			F=Phenylalanine, G=Glycine, H=Histidine,
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peptide sequence			1				T=Threonine, V=Valine, W=Tryptophan,
	l					sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
VILERTIDEKLOGTGYGDVWKIYDGEENPEK   LLRVITAPDSHAPLTVVDGECLPWEIPCGGNWGCY   TEQRCDGYWHCPNGRDEINCTMCQKEEPP   CSRRGVCYPRSDGRNYQHCPNGSDENGCY   TEQRCDGYWHCPNGSDEDINGTMCQKEEPP   CSRRGVCYPRSDRCNYQHCPNGSDENGCY   CQPGNPHCKNNRCVFESWCDSQDDCDGS   DEENCPVYPYTRVITAAVDICSICGILLVIAG   CTCKLYSLRMFERRSFETQLSRVEABLLREAN   PSYGGLIAGGLIPYCSPNGASVCDS   CGLEVARIA   RLAWRSQLGFTSYRLPMAGRSSNIWNRIPNFA   RSRRISGSLAUSADDDEVPCSPNGASVCDS   RESPONSIVE PROSPROMENT   THRS. FSVESDDTITENERRDMAGASGGVAA   PLPCKVPPTTAVEATVGACASSSTGTRGGH   ADNGRDVTSVEPPSVSRAHQUTSALSRMT   THRS. FSVESDDTITENERRDMAGASGGVAA   PLPCKVPPTTAVEATVGACASSSTGTRGGH   ADNGRDVTSVEPPSVSRAHQUTSALSRMT   GLRWVRFTLGRSSSLSQNQSPLRQLDNGVSG   REDDDDVEMLIPSIDGSSDFVNDCSRFLJDL   ASDQGGGRQPYNATPGGYRSNRDGPCERC   GVHTAGPTCLEVTLKHETSDDEALIL   ASDQGGGRQPYNATPGGYRSNRDGPCERC   GVHTAGPTCLEVTLKHETSDDEALIL   ASDQGGGRQPYNATPGGYRSNRDGPCERC   GVHTAGPTCLEVTLKHETSDDEALIL   ASDQGGGRQPYNATRYGGYRSNLDFFNCWS   GGWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKKNM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMYPRCFDKACHTM   GWWNDVACHTMACHTMACHTMACHTMACHTMACHTMACHTMACHTM	1	1	1	1			/=possible nucleotide deletion, \=possible
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NAARGPNATYQVOGFCLPWEIPCGGRWGCY  TEQQRCDWHCPNORDETNICTMCQREEPP CSRNGVCYPRSDRCNYQNHCPNGSDEKNCE CQPCNTECKNRCVCPSSWCTOSQDDGCDGS DEENCPUVPTRVITAAVIGSLICGLLLVIALG CTCKLYSLRMFERRSFETQLSVSCDEVTSCALLREA PPSYGQLAGGLIPVUPTGSTNAGSVERALLREA PPSYGQLAGGLIPVUPTGSTNAGSVERALLREA RPSYGQLAGGLIPVUPTGSTNAGSVERALLREA RSHRISGSLAUVSADDEVTSQSTSREEPRAM THRSLFSVESDDTDTENERRDMAGASGGVAM ALPQKVPTTAVEATVGACSSSTGVAGH ADNORDVTSVEPPSVSPARHQLTSALSRMTQ GLRVVRFTLGRSSSLSQNGSPLROLDMOSPLROLDMOSP REDDDDVEALIPISDGSSDFDWDCSRPLLDL ASDQGQLRQPYNATHPGVRFSNRDGPCERC GTWTTAQIPTCLSVTLAWFSDEATLAC GRASVPEGALEFRREGHTDRQGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEERC GTWTTAQIPTCLSVTLAWFSDEATLAC GRASVPEGALEFRREGHTDRQGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GLRCUPHLPAICARRMSPRFRGGTEDVLAA GRARATAMARARPPPPRPPPFFGLULICHLL LLPLLLPAGCRALEETLAMDTKWVTSELAWT SHPSGGWEUSGVDEAMMPRRTYCYCNVRES GNNWLRIGTHWRDVQGACKSLSWAPPYKK ASHPSGGWEUSGVDEAMMPRRTYCYCNVRES GNNWLRIGTHWRDVQGACKSLSWAPPYKK ASHTGSGGRGCTEOPGGSTYALAGGGGGTEDVLAA GRARATAMARARPPPRFRGGVILDVEMXYFEKSEG LASTVERDVYVALEKTURA VAGYGGYBRAFETTSLERGGAQQLQEOLD LLYNVICKKCHOAGEGGEVCGGTEN VAGYGRAFEVTARTVYRDEAARMVTDEAARCHAR VAGYGGYBRAFETTSL		1		[	1	1	LLRVLTAFDSHAPLTVVSSSGQIRVHFCADKV
TEQQRCDSYWHCPNGREINCITMCQKEERCP		-	ļ.	ŀ		1	NAARGFNATYQVDGFCLPWEIPCGGNWGCY
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LLYNVICKKCHGAGGASACSRCDDNVEFVPR QLGLSEPRVHTSHLLAHTRYTFEVQAVNGVS GKSPLPPRYAAVNITTINQAAPSEVPTLRLHSS SGSSLTLSWAPPERPNGVILDYEMKYFEKSEG IASTVTSQMNSVQLDGLRPDARYVVQVRART VAGYGQYSRPAEFETTSERGSGAQQLQEQLP LIVGSATAGLVFVVAVVVIAIVCLRKQRHGS DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL KQPGRREVFVAIKTLKVGYTERQRRDFLSEA SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI	ľ	l	- 1	- 1	i	1	VPODDE CARACTET TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
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IASTVTSQMNSVQLDGLRPDARYVVQVRART VAGYGQYSRPAEFETTSERGSGAQQLQEQLP LIVGSATAGLVFVVAVVVIAIVCLRKQRHGS DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL KQPGRREVFVAIKTLKVGYTERQRRDFLSEA SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI			1	ŀ	ļ	j	GROPLEPKY AAVNITINQAAPSEVPTLRLHSS
VAGYGQYSRPAEFETTSERGSGAQQLQEQLP LIVGSATAGLVFVVAVVVIAIVCLRKQRHGS DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL KQPGRREVFVAIKTLKVGYTERQRRDFLSEA SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI			1			ĺ	SGSSLILSWAPPERPNGVILDYEMKYFEKSEG
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DSBYTEKLQQYIAPGMKVYIDPFTYEDPNEA VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL KQPGRREVFVAIKTLKVGYTERQRRDFLSEA SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI		l		ŀ		İ	LIVGSATAGLVFVVAVVVIAIVCLRKQRHGS
VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL KQPGRREVFVAIKTLKVGYTERQRRDFLSEA SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI		ļ		1		· i	DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA
KQPGRREVFVAIKTLKVGYTERQRRDFLSEA SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI	ľ	1	- 1	ł		· 1	VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRI.
SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI	- 1	i	1	ł			KQPGRREVFVAIKTLKVGYTERORRDFLSEA
NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI		ŀ	1	1		1	SIMGQFDHPNIRLEGVVTKSRPVMILTEFME
KYLSEMNYVHRDLAARNILVNSNLVCKVSDF GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI			ļ	1	ļ		NCALDSFLRLNDGOFTVIOLVGMI RGIA AGM
GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPBAI	1	1	į		1	1	KYLSEMNYVHRDLAARNILVNSNI.VCKVSDF
AYRKFTSASDVWSYGIVMWRVAACYGEDDV		1	ļ	- 1		1	GLSRFLEDDPSDPTYTSSLGGKIPIR WTAPRAT
			- 1			1	AYRKFTSASDVWSYGIVMWRVMSVGEDDV

						( ) ( ) ( ) ( )
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	İ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	ł	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	<b>)</b>		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \=possible
	İ			sequence		nucleotide insertion
<del></del>			<del> </del>	sequence		WDMSNQDVINAVEQDYRLPPPMDCPTALHQ
1		į	1 .	{		LMLDCWVRDRNLRPKFSQIVNTLDKLIRNAA
	ĺ		1			SLKVIASAQSGMSQPLLDRTVPDYTTFTTVGD
				Ĭ		WLDAIKMGRYKESFVSAGFASFDLVAQMTA
1	}					EDLLRIGVTLAGHQKKILSSIQDMRLQMNQT
	i	1	1	ł	•	LPVQV
924	2274	A	7985	ī	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNF
		1		1		QLMRELDQRTEDKKABIDILAAEYISTVKTLS
	Ì	1				PDQRVERLQKIQNAYSKCKEYSDDKVQLAM
	ł	}		ŀ	ļ	QTYEMVDKHIRRLDADLARFEADLKDKMEG
1					<b>.</b>	SDFESSGGRGLKKGRGQKEKRGSRGRGRRTS
	1			1	l	EEDTPKKKKHKGG
925	2275	A	7994	447	589	LPCSFCAQCMSSFERVWLQQSHFHNPRWNSR
}	j	1				SPIRCYCQHWPHCVHC
926	2276	A	7996	925	582	GPCKVCCITLAIMLQCHSFYRKDVQVEHPKS
ļ	1	1	1	1		LNPKYSQIENFLSADMALKRKCLLSISDLDFW
İ		1			i	IWDAQPVGIMQTLQNLKKIPNPGCFWSQAFQI
		<u> </u>				RDTQPILPLGGRYYITIRQ
927	2277	Α	7998	2	353	RIQRPLNSRSPNHSLFVKAELTAKQATMKLSV
						CLLLVTLALCCYQANAEFCPALVSELLDFFFI
		1		Į.	•	SEPLFKLSLAKFDAPPEAVAAKLGVKRCTDQ
	<u> </u>	<u> </u>	-			MSLQKRSLIAEVLVKILKKCSV
928	2278	A	8004	130	588	LAPLECOPGTETOPESHPAANDPSAAMSAAG
						ARGLRATYHRLLDKVELMLPEKLRPLYNHPA
			1			GPRTVFFWAPIMKWGLVCAGLADMARPAEK LSTAQSAVLMATGFIWSRYSLVIIPKNWSLFA
	1		Ì			VNFFVGAAGASQLFRIWRYNQELKAKAHK
929	2279	A	8007	2	1016	EFARRVFIAAREMSLLRSLRVFLVARTGSYP
929	122/9	^	8007	2	1010	AGSLLRQSPQPRHTFYAGPRLSASASSKELLM
1						KLRRKTGYSFVNCKKALETCGGDLKQAEIWL
			1			HKEAOKEGWSKAAKLOGRKTKEGLIGLLQE
	1	1		ŀ		GNTTVLVEVNCETDFVSRNLKFQLLVQQVAL
		'				GTMMHCQTLKDQPSAYSKGFLNSSELSGLPA
						GPDREGSLKDQLALAIGKLGENMILKRAAWV
				1		KVPSGFYVGSYVHGAMQSPSLHKLVLGKYG
ļ	1	j	]	ļ		ALVICETSEQKTNLEDVGRRLGQHVVGMAPL
{					Ì	SVGSLDDEPGGEAETKMLSQPYLLDPSITLGQ
1	1		1	1	1	YVQPQGVSVVDFVRFECGEGEEAAETE
930	2280	A	8008	3	1679	NSRVWGPWTEPSAGSLRPMARKQNRNSKEL
	1					GLVPLTDDTSHAGPPGPGRALLECDHLRSGV
	1	1		i		PGGRRKDWSCSLLVASLAGAFGSSFLYGYN
		1			· ·	LSVVNAPTPYIKAFYNESWERRHGRPIDPDTL
		1		]	1	TLLWSVTVSIFAIGGLVGTLIVKMIGKVLGRK
1	1	1	1	1	1	HTLLANNGFAISAALLMACSLQAGAFEMLIV
1	1	1	1	1	1	GRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
		1		1		QVTAIFICIGVFTGQLLGLPELLGKESTWPYLF
1			1	1		GVIVVPAVVQLLSLPFLPDSPRYLLLEKHNEA
1					]	RAVKAFQTFLGKADVSQEVEEVLAESRVQRS
1		1	1	1	1	IRLVSVLELLRAPYVRWQVVTVIVTMACYQL
	I	1		1		CGLNAIWFYTNSIFGKAGIPPAKIPYVTLSTGG
1	1	1	1	1	1	IETLAAVFSGLVIEHLGRRPLLIGGFGLMGLFF
	1	1				GTLTITLTLQDHAPWVPYLSIVGILAIIASFCSG
	1	1	1	1	J	PGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSN
[	1 .					FAVGLLFPFIQKSLDTYCFLVFATICITGAIYL,
		1	1	1		YFVLPETKNRTYAEISQAFSKRNKAYPPEEKI
021	+	<del>      _   _   _   _   _   _   _</del>	9000	961	300	DSAVTDGKINGRP AAGAVVSAMPKAKGKTRRQKFGYSVNRKRL
931	2281	A	8009	861	300	NRNARRKAAPRIECSHIRHAWDHAKSVRQNL
1	1	1	1	1	1	AEMGLAVDPNRAVPLRKRKVKAMEVDIEER
L	L		1	1	1	THE ADDITION AT PUVICE AND AD IDEK

932	2282	A	.8011	412	1	SNLCLGNSWRWRWAKSRHHCIPTVTLSKRSG
132	2202	1	.0011	412	1	SNLCLGNSWRWRWAKSRHHCIPTVTLSKRSG DIRGSHFSSPQRQRSQRVPGKETARVLRAGK
		1	1		İ	QGRGQIPIPCPWPPPPPPPPPPGSPGPGCROFHO
		1	İ	!		SLEAKARHPASVREMRGKVKMRRALRRAPA STRASSROPNPK
933	2283	A	8012	147	1077	PPVPPASRSDMAQNLKDLAGRLPAGPRGMGT
		ľ				ALKLLLGAGAVAYGVRESVFTVEGGHRATFF
						NRIGGVQQDTILAEGLHFRIPWFQYPIIYDIRA RPRKISSPTGSKDLQMVNISLRVLSRPNAQEL
						PSMYQRLGLDYEERVLPSIVNEVLKSVVAKF
				İ		NASQLITORAOVSLLIRRELTERAKDESLILDD
	1					VAITELSFSREYTAAVEAKQVAQQEAQRAQF
			1.		1	LVEKAKQEQRQKIVQAEGEAEAAKMLGEAL SKNPGYIKLRKIRAAQNISKTIATSQNRIYLTA
934	0004	<u> </u>				DNLVLNLQDESFTRGSDSLIKGKK
934	2284	A	8023	255	982	SQFSLSQVLVDSAEEGSLAAAAELAAOKREO
	1		1	İ	1	RLRKFRELHLMRNEARKLNHQEVVEEDKRL KLPANWEAKKARLEWELKEEEKKKECAARG
		ĺ			ļ	EDYEKVKLLEISAEDAERWERKKKRKNPDLG
						FSDYAAAQLRQYHRLTKQKPDMETYERLRE
						KHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLE KQIEKRDKYSRRRPYNDDADIDYINERNAKF
-						NKKAERFYGKYTAEIKQNLERGTAV
935	2285	Α	8027	59	310	LVSSTVNLLTEKAPWNSLAWTVTSYVFLKFL
						QGGGTGSTGMRDSALTLLGIGPSHRHSLSIRL SQHSSPAPMYSQTFHILVLG
936	2286	Α	8032	1	639	SGRECNMAKTYDYLFKLLLIGDSGVGKTCVI.
	1					FRESEDAFNSTFISTIGIDEKIRTIELDGKRIKLO
			1.			IWDTAGQERFRTITTAYYRGAMGIMLVYDIT NEKSFDNIRNWIRNIEEHASADVEKMILGNKC
						DVNDKRQVSKERGEKLALDYGIKFMETSAK
						ANINVENAFFTLARDIKAKMDKKLEGNSPOG
937	2287	A	8039	393	311	SNQGVKITPDQQKRSSFFRCVLL
938	2288	A	8052	675	-1334	EETIHSENSYILEKYIPISANLTLTIA LHPAATSTAWLHVPPGLSMALSWVLTVLSLL
				1		PLLEAQIPLCANLVPVPITNATLDRITGKWFYI
						ASAFRNEEYNKSVQEIQATFFYFTPNKTEDTIF
						LREYQTRQDQCIYNTTYLNVQRENGTISRYV GGQEHFAHLLILRDTKTYMLAFDVNDEKNW
				j		GLSVYADKPETTKEQLGEFYEALDCLRIPKSD
939	2289	Α	9065	10	1000	VVYTDWKKDKCEPLEKQHEKERKOEEGES
,,,	4209	A	8055	12	1039	SSVAEFPERVQLSQPQNWNFSGAGGAWSLDF
	1 1			1		AEQLKWSAELARLGESIMDGKQGGMDGSKP AGPRDFPGIRLLSNPLMGDAVSDWSPMHEAA
						IHGHQLSLRNLISOGWAVNIITADHVSPI.HEA
				ľ		CLGGHLSCVKILLKHGAOVNGVTADWHTPI
				}		FNACVSGSWDCVNLLLQHGASVOPESDLASP
	1 1		1			IHEAARRGHVECVNSLIAYGGNIDHKISHLGT PLYLACENQQRACVKKLLESGADVNQGKGQ
					l	DSPLHAVARTASEELACLLMDFGADTOAKN
						DSPLHAVARTASEELACLLMDFGADTQAKN AEGKRPVELVPPESPLAOLFLEREGPPSI MOI
						DSPLHAVARTASEELACLLMDFGADTQAKN AEGKRPVELVPPESPLAQLFLEREGPPSLMQL CRLRIRKCFGIQQHHKITKLVLPEDLKQFLLH
940	2290	A	8058	2	1203	DSPLHAVARTASEELACLLMDFGADTQAKN AEGKRPVELVPPESPLAOLFLEREGPPSI MOI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	i	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ſ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ł	<b>{</b>	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	<u> </u>	l	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
	}			residue of	sequence	/=possible nucleotide deletion, \=possible
	ł		1	peptide		
			<u> </u>	sequence		nucleotide insertion VVDTVMCPNMPNKSVLLYTLSFIYIFIFVIGMI
	1	1	1	'		ANSVVVWVNIQAKTTGYDTHCYILNLAIADL
		ľ		1		WVVLTIPVWVVSLVQHNQWPMGELTCKVTH
		l	1			LIFSINLFGSIFFLTCMSVDRYLSITYFTNTPSS
		1				RKKMVRRVVCILVWLLAFCVSLPDTYYLKT
		ļ		j	}	VTSASNNETYCRSFYPEHSIKEWLIGMELVSV
	i	l				VLGFAVPFSIIAVFYFLLARAISASSDQEKHSS
	ł			ļ		RKIIFSYVVVFLVCWLPYHVAVLLDIFSILHYI
			1	ļ		PFTCRLEHALFTALHVTQCLSLVHCCVNPVL
	1.	l		1	ł	YSFINRNYRYELMKAFIFKYSAKTGLTKLIDA
		l		ł		SRVSETEYSALEQSTK
041	2201	A	8059	73	432	DMAGLMTIVTSLLFLGVCAHHIIPTGSVVLPS
941	2291	I A	8039	/3	432	PCCMFFVSKRIPENRVVSYQLSSRSTCLKAGV
	Ì	ľ		ĺ	1.	IFTTKKGQQFCGDPKQEWVQRYMKNLDAKQ
						KKASPRARAVAVKGPVQRYPGNQTTC
040	2292	A	8067	278	1262	GGIGEIKQRPSCLGRCLDPSLSVLMNISLGLGS
942	2292	A	0007	270	1202	VFSAVISOKPSRDICORGTSLTIQCQVDSQVT
	1					MMFWYROOPGOSLTLIATANQGSEATYESGF
	١.	1	ĺ			VIDKFPISRPNLTFSTLTVSNMSPEDSSIYLCSA
	Ì	l	[			GROGTYEOYFGPGTRLTVTEDLKNVFPPEVA
		ļ.	1		i	VFEPSEAEISHTQKATLVCLATGFYPDHVELS
	Ì	1	1			WWVNGKEVHSGVSTDPQPLKEQPALNDSRY
	<b>J</b>	1	}			CLSSRLRVSATFWQNPRNHFRCQVQFYGLSE
		ĺ	İ	Ì		NDEWTQDRAKPVTQIVSAEAWGRADCGFTS
	ł	1				ESYQQGVLSATILYEILLGKATLYAVLVSALV
		i	l			LMAMVKRKDSRG
943	2293	A	8070	1	879	MVKVVPATRGNLPRSQLTGTHQHCQPREPKI
				ļ <sup>-</sup>		TASERLRRRPRATARLRAHAAPPEPPLAVFAP
		İ				PSDRKELLALPVACDPVIASVMSWVQAASLI
						QGPGDKGDVFDEEADESLLAQREWQSNMQR
		i	1		1	RVKEGYRDGIDAGKAVTLQQGFNQGYKKGA
		ļ				EVILNYGRLRGTLSALLSWCHLHNNNSTLINK
		ì			1	INNLLDAVGQCEEYVLKHLKSITPPSHVVDLL
	j	}		ļ	1	DSIEDMDLCHVVPAEKKIDEAKDERLCENNA
				i		EFNKNCSKSHSGIDCSYVECCRTQEHAHSGK
	1					PKPHMDFGTDSQF
944	2294	A	8073	1	797	ESARWSRQLRRTLIRLSFPISCGRSHAFGGCK
		}	1	1	1	MAATSGTDEPVSGELVSVAHALSLPAESYGN
		1	1	1		DPDIEMAWAMRAMQHAEVYYKLISSVDPQF
	1	1		*		LKLTKVDDQIYSEFRKNFETLRIDVLDPEELK
		Ł	-	i		SESAKEKWRPFCLKFNGIVEDFNYGTLLRLD
		(	ĺ			CSQGYTEENTIFAPRIQFFAIEIARNREGYNKA
		1	-		1	VYISVQDKEGEKGVNNGGEKRADSGEEENT
		ł		İ		KNGGEKGADSGEEKEEGINREDKTDKGGEK
		1				GKEADKEINKSGEKAM
945	2295	Α	8074	2	505	GAATLLRSASSAARKAAEAEQVWLHLHRYL
1			1			SADRRVLGLREWGRPASERECSLCQRLKREL
	1	1	1	ļ.		NMGDVEKGKKIFIMKCSQCHTVEKGGKHKT
	1.	1	1.	1		GPNLHGLFGRKTGQAPGYSYTAANKNKGIIW
Ī		1	1	1		GEDTLMEYLENPKKYIPGTKMIFVGIKKKEER
		1				ADLIAYLKKATNE
946	2296	A	8081	42	590	EGRRGKFGGKLCNFLFYFHSNSAESRMDVLF
Ì					1	VAIFAVPLILGQEYEDEERLGEDEYYQVVYY
		1		-		YTVTPSYDDFSADFTIDYSIFESEDRLNRLDK
l				f		DITEAIETTISLETARADHPKPVTVKPVTTEPQ
			1			SPRSEAMPCPVLRSPIPLPPVRVPLFRWGCISC
[			1	1		KKVGRRLLMTLWMGVWQEEIGR
947	2297	A	8084	322	549	GGGSSPRELAGAAGLTVTSQAVAARRQQPSF
1 / 7 /					1	SRARAPAHSLRAALSLASSARSWGAVSRDRG

SEQ ID   Not of not   In Not   Seq   Predicted and   Despinating   Predicted and   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Despination   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Descitor   Desci	SEQ II	SEQID	Met	SEQ	Predicted	I be divided	
nucleo de oetide sequence vience unice of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the contrapondia of the							
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Sequence   99496   99496   99496   9949   2299   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9   2374   A   8095   9	eotide	seq-	1	USSN			
go first amino saci of peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide	seq-	uence	1	09/496	correspondi		
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Peptide	ľ		1	ł		of peptide	T=Threonine, V=Valine, W=Tryptophan.
	ļ	l l		1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
948 2298 B 8093 3905 846 MEPGEVERDILENIS VEKTLOSYPAACEDET PARNIDEVULQRILCHILDHALI VOLQDLSSG YAWLVUHTETREAKUGEVULQHIA THILGRE AWLYLALINENIS ESYLRLPQENLGLIKIYV RALVASHIDHILTITUVSGLEFILBFILDDA PARNIDEVULQRILTHITUVSGLEFILBFILDDA PYLDLAPTIMPDYYKRQYLLDFERRILFSSYHG SUSISIA NEFNSYTSTINLEWDDSALAPSEDVY ROLVPAPSVENTOWEDODILDTVSGRYST ASDLTSSKASTIRSTYGRQNPPNEEPASTYSSS DITPWITTISGREEGAQLAPPOASTELPUR YRKKIGKKKSRISERSEPLIPACOGKKCA KQGGDGSROSSFILMPAKOTIVEKER GOPSSTTESSERSBEGLLEPMKDTSAKBERLGQPI SKNUDLINGQLDFSTWCSARAPPOQSFTOSS GDAPESPILLDFSGRAPPOQSFTOSS GDAPESPILLDFSGRAPPOQSFTOSS GDAPESPILLDFSGRAPPOQSFTOSS GDAPESPILLDTVSSSPA GOGGGGGTFRR-LDTTREAQELEAQLSI VRR GPYSEPEGTGEVLQUK KARDOPSRCISSAS GVEGGGGGGGTFRR-LDTTREAQELEAQLSI VRR GPYSEPEGTGEVLQUK KARDOPSRCISSAS GVEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		Ì	ĺ	1	,	1	/=possible nucleotide deletion, \=possible
948 2298 B 8093 3905 846 MEPGEYEDÜLLENIS JVEKULOSYFAACEDET PARMENDEN/LORICEHLOHALI/VIG DLISSG YWVLVVHFTRREAIKQEVLQHVAITM.GRSR AWLTIALINENSLESYTALI/QENIGLIKY YV KNALVCSHIDHTLEFILVSGLEFIKFELDUA PYLDLAPYMPDYYKRQYLLDFEDRIFSSYHG SDSLSLINSKYSTINLEWDDSAIA/PSSEDYD FGDWFPAYPSVPSTDWEDGOLTDTVSGPRST ASDLTSSKASTRSTTQRGWPFNEFFASTYSSS DTTFVHTTSQEKERAQALDPPDACTELEVIRV TKKKKIGKKRSINSDERASPLIPACSQKACA KQGGGOSRNGSPSIGRUSDTMARSPQEEG GPSSTTESSBRSPGLLEPMSGNAKKKRSINSDERASPLIPACSQKACA KQGGGOSRNGSPSIGRUSDTMARSPQEEG GPSSTTESSBRSPGLUFPHSDAIAPSCEDY SWIDDLANGQLDPSTWCSRAEPPOJSFTGSP GDAPERPHCDYSGGI ARAMPYRFYTVSSTS VTSGGHHDPAGI GQPLHVTSSPEAAQQEEG GGGGGGGTFRELDTTREAQLEAQLSI VRF GPVSFEPEGTGPULCQLKRDQPSFCLSSAEDS GVDEGQGSPSTWISSRRSPGLLDPOSPSTLSSAEDS GVDEGQGSPSTWISSRRSPGLUFPUNDALLLUT TICKYVLLRKGATEKPYLVEEAVSYNELDY VSYGLDQYTVSLCYTRKKGPLLDTADVAL ABSFLASILKSAMIKGCREPYPSILTDATMEK LALAKEVAGSKCEASAVTRYPCULVHED PTDESLGPTCHCSPEGTTIKEGMLHYKAGT SYLGKBHWKTGFVULSNGHUQYDPBATDYDLLLSTSWINGGGQGGGGRANTTDRPHAFQVILSD DPFCLELSALGSAENAMGHLCQAVSKGVILDY PQGVAFSCCPCLUTDDRIFTCHEDCOTSF FRSLGTAKGDISAVTREYGLUTHUD LLSVMGGGQGGGGRANTTDRPHAFQVILSD DPFCLELSALGSAENAMGHLCQAVSKGVILYQYDDTDYDLLSSSWINGGGLGGGRANDFWCP ARAMPYTTLSSFSWINGGAMDCYYQGHUD LLSVMGGGQGGGGRANTTDRPHAFQVILSD DPFCLELSALGSAENASGWKTTY QVDLPFTIAGASNKKKFRGEVCVLESTODD QQLLPWVITLSCTSELDRLLSALNSGWKTTY QVDLPFTIAGASNKKKFRGEVCVLEFSDOD QQLLPWVITLSCTSELDRLLSANNGWKTTY QVDLPFTIAGASNKKKFRGEVCVLEFSDOD QQLLPWVITLSCTSELDRLLSANNGWKTTY QVDLPFTIAGASNKKKFRGEVCVLEFSDOD QQLLPWVITLSCTSELDRLLSANNGWKTTY QVDLPFTIAGASNKKKFRGEVCVLEFSDOD QQLLPWVITLSTSSMIGQULPWSILLSANNGWKTY QVDLPFTIAGASNKKFRGENGDCYYQGHUD LLSWMGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		+	├	<del> </del>	sequence		
PARNEDSUNQRICENTIQUES  PARNEDSUNQRICENTIQUES  WWW.TWIFTREARICQIEV.QHWATNI.GRSR  AWW.TALINENSIESYRICEPORGICLIRYV  KNALVCSIDHI.TLF.TLVSGLEFIRFEI.DLDA  PYILDLAPYMPYYKRYVILDEBERI.PSSDV  FORDVFPA.PSVPSTYMEVBODSALAPSSEDYD  FORDVFPA.PSVPSTYMEVBODSALAPSSEDYD  FORDVFPA.PSVPSTYMEVBODSALAPSSEDYD  FORDVFPA.PSVPSTYMEVBODDI.TDTVSGREY  ASDLTSSKASTISSTYGROMPFNEEPAETVSSS  DITP.WITTGGKERAQALD.PPAACTELEVSS  DITP.WITTGGKERAQALD.PPAACTELEVSS  GOSSTTESSERSBEGLI.PPAGCOKKCA  KOGGOEDSRIGSELGROSPDTMLASPQEEGE  GOSSTTESSERSBFOLLI.PBMCDTSMESA.GOREE  GOGGEGGTFRE.DTTEAGALEVSSEN  GOGGEGGTFRE.DTTEAGLE.O.GSL.NA  GOGGEGGTFRE.DTTEAGLE.O.GSL.NA  GOGGEGGTFRE.DTTEAGLE.O.GSL.NA  FORSTSEPS VYTSGGHIDPAGCI.CO.CARDOPSRCI.SSAEDS  GOVDEGGGSSEMMYSSEFWONNILLILLIN  VFRENEGULFKMIRNSTGHMEGNI.QLLYVIL.  TDCYVVLLIKGKATEKFVI.VEAVSYNEDLY  VSVGLDOOTVSLLVCTNRKOFLLDTADVAL  ASFFLASIKSAMIGGGEREYPSILTDATAWAL  ASFFLASIKSAMIGGGEREYPSILTDATAWAL  ASFFLASIKSAMIGGGEREYPSILTDATAWAL  ASFFLASIKSAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREYPSILTDATAWAL  ASFFLASIKAMIGGGEREKYCLEFSODS  QULIPWVYTISCTSELDRILSAMISGWRTY  QVDLPTHAJGASNKKKFEKSYCVLEYGODONYTEPLSPI  LLSVMGGEGGCGCRANTTDRIPHACYLLIN  PARAPOTULISSSMIGGGLAVYQHILM  EKNYDASISTICGLGRYFSODONYTEPLSPI  ROGGHALFKYMTDGGAWYLKKWNILLIN  PARAPOTULISSSMIGGGORYYQHILM  EKNYDASISTICGLGRYFSOODONYTEPLSPI  ROGGHALFKYMTDGGAWYLKKWNILLIN  PARAPOTULISSSMIGGGORYYQHILM  BENDORGHALFKYMTDGGAWYLKKWNILLIN  PARAPOTULISSSMIGHONYDHICHONOCOC  GTSEGCTNICODARTCKKATTOCALGECCE  CORKAGRAPPOVANGTKCO  DRIVCTNABCOPPOLDSSVVHTSITVO  VERMAVEYVVANVIRINGSSEKOKKOOP  VERMAVEYVVANVIRINGSSEKOKKOOP  LETTAVORYVVANVIRINGSSEKOKKOOP  VERMAVEYVVANVIRINGSSERGKKOOP  VERMAVIVANVANVIRINGSSERGKKOOP  VERMAVEYVANVIRINGSSERGKKOOP  VERMAVEYV	948	2298	B	8003	3005	946	
YWVLVVHTRREAIKQIEVLQHVAITIGRES AWLYLAINENSLESYRLEQENGLICHKYYV KNALVCSHOPHLTLFLTLVSGLEFERFELDLDA PYLDLA-PYMPDYKFULPGENGLLHKYYV KNALVCSHOPHLTLFLTLVSGLEFERFELDLDA PYLDLA-PYMPDYKFULPGENGLLHKYYV KNALVCSHOPHLTLFLTLVSGLEFERFELDLDA PYLDLA-PYMPDYKFULPGNULLHKYYV KNALVCSHOPHLTLFLTLVSGLEFERFELDLDA PYLDLA-PYMPDYKFULPGNULLHKYYV KNALVCSHOPHLTLTLVSGREST ASDLTSSKASTRST/GRONPTENERATVSSS DITFVHTTSGEKEEAQALDPPDACTELEVIRV TKKKIGKKKKSRSGEASPERTVSSS DITFVHTTSGEKEEAQALDPPDACTELEVIRV TKKKIGKKKKSRSGEASPEARTVSSGKCA KQGDGDSRNOSPSIGRDSPDTMLASPQEEGE GPSSTTESSERSEPOLIPPENGTSKARDOPKTTVSPST VTSGGHHDPAGLQQPLHVPSSPFAACGEEE GGGEGGTPRPLEDTTREAQELEAQLSI-VRF GVBEPPRJCDFSEGLGA-PUDFYRTTVSPST VTSGGHHDPAGLQQPLHVPSSPFAACGEEE GGGEGGTPRPLEDTTREAQELEAQLSI-VRF GVBEPPRJCDFSEGLGA-PUDFYRTTVSS-SADDS GVDBQ-GSPSEMVHSSEFR-VDNNHILLLLIMH VFRENEGQLFKMIRMSTGHMEGNI-LULYUL TDCYVYLLEKGATEKPYL-VERAVSYNELDY VSVGLDQOTVKL-VCTNRKOFLLDTA-DVAL AAFFLASLKSAMIKGCREPPYSEILTDA-TMEK LALAKFVAGESKCSAAVTVRFVGL-VHWED PTDESI-GPTF-HCSPPEGTTT-KEGMLHYKAGT SYLGKEHWKTCPVVLSNGHL-VFRWD-LYWED PTDESI-GPTF-HCSPPEGTTT-KEGMLHYKAGT SYLGKEHWKTCPVVLSNGHL-VFRWD-LYWED PTDESI-GPTF-HCSPPEGTTT-KEGMLHYKAGT SYLGKEHWKTCPVVLSNGHL-VFRWD-LYWED PTDESI-GPTF-HCSPPEGTT-KEGML-HYKAGT SYLGKEHWKTCPVVLSNGHL-CYPFDENDVIS- PTDESI-GPTF-HCSPPEGTT-KEGML-HYKAGT SYLGKEHWKTCPVVLSNGHL-VFRWD-LYWED PTDESI-GPTF-HCSPPEGTT-KEGML-HYKAGT SYLGKEHWKTCPVVLSNGHL-CYPFD-LYSNGH-TV-TV-TV-TV-TV-TV-TV-TV-TV-TV-TV-TV-TV-			~	د دې	3,03	540	PAIRNIHDRALOPI CEHLONALI VCI ODI COC
AWLYLAINENSESYRLIFORM.CILLHKYYV KNALVCSIDHILTELT.VSGLEFIFEDLDA PYLDLAPYMPDYKRQYLLDEDRLEPSVHG SDSLSLMSENSYTSTINEWDDSALAPSSEDYD FODVPRAYESYPSTDWEDODLTDTVSGPRST ASDLTSSKASTRSPTQRONFPNEBPABTYSSS DTTPVHTTSQREEGAQLIPPDACTILEVIRV TKKKIGKKKKSRSDEASPLHPACSQKCA KQGDGDSRNOSPSIGRDSDTMLASPQEGG GPSSTTESSERSEPGLLIPENKDTSMERLGOPL SKYDDQLNGQLDSTVCSRAPPDQSFRTOSP GDAPERPFLCDTSEGLSAPMDFYRFTVESPST VTSGGGHDPAGLOQLHVPSSEPAAGQEE GGGGGGTPRPLEDTTREAQELEAQLSI VRR GPVSEPPPTOFULOLERDOPSPCT-SSAEDS GVDEQGGSPSEMVHSSEFR VDNNHLLLLMH VFRENEGLFRMIRMSTGHMEGNLQLLVVIL TDCV VYLLARGATEKPTLVESAGDEE GGGGGGTPRYLOTTREAQGEE GGGGGGTPRYLOTTREAQGEE GGGGGGTPRYLOTTREAQGEE GVDEQGGSSBMVHSSEFR VDNNHLLLLMH VFRENEGLFRMIRMSTGHMEGNLQLLVVIL TDCV VYLLARGATEKPTLVESAGDEE GVDEQGGSSBMVHSSEFR VDNNHLLLLMH VFRENEGLFRMIRMSTGHMEGNLQLLVVIL TDCV VYLLARGATEKPTLVESAGDEE GVDEQGGSSBMVHSSEFR VDNNHLLLLMH VFRENEGLFRMIRMSTGHMEGNLQLLVVIL TDCV VYLLARGATEKPTLVESAGDEE GVDEGGGTPRHEDTTREAQELEAQLSI VRR GVDEQGGSSBMVHSSEFR VDNNHLLLMH VFRENEGLFRMIRMSTGHMEGNLQLLVVIL TDCV VYLLARGATEKPTLVESAGDEE GVDEGGTBMVHSSEFR VDNNHLLLLMH VFRENEGLFRMIRMSTGHMEGNLQLLVVIL TDCV VYLLARGATEKPTLVESAGDEE GVDEGGTBMVHSSEFR VDNNHLLLLMH VFRENEGLFRMITMCGREPPYSELIDATMEK LALAKFVAQESKCBASAVTVERYGLLVHWED PTDESLGFTRCHCSPEPTITEGMUTTYKAGT SYLCKBHWKTCFVVLSRGILVQYPDRTDVIP LLSVNMGGGCGGGGRANTTDEPHAFCVULS DPFCLELSADSEAEMAEMMOHLCQAVSKGVIT QOVLPFHAJQEASNKKKFEDALSLHSAWQR SYLCKBHWKTCFVVVJPRLHPLHKREAKEPEQQ QULPPWVYLSCTSELDRLLSALNSGWKTIY QVDLPFTAIQEASNKKKFEDALSLHSAWQR SDSLCRGRASRDWC GVDLFFLKYMTNOKGKHTYSPQIMDDCYYQGHILM KKVDADASSTCGGRGRYFGGQDQXTPGBLSY HENDQGEHALFKYNDFDCRNDATCCMDOVL WAHDLQQONALPARKLVLKLKDRXVQGHEKY EYYLVLINGEFRKYNENGOEKRYFDLSCGPS TICVMDKALSFYTPDFSSCSRLSYDKFFEDRL NCLFWAGTMAHEMGHNGMHDDYSCCPS TICVMDKALSFYTPDFSSCSRLSYDKFFEDRL NCLFWAGTMAHEMGHNGMHDDYSCCPS TICVMDKALSFYTPDFSSCSRLSYDKFFEDRL SNCLFWARLTTDISTFTCGNQLVEMEGDCC GTSECTNICCDAKTCKKATFQCALGGCCK CQKKKAGMVCPRABCBCLPEMCKNGKSNC PDDRFQVNGFECHIGKGHLAMGTCCT GDRKCCTRICKGFTCANDTMCGKLFCQAGSDNLPW KGRNYFLTCKTTPDEDTSQEIMWANGTKCG DNKVCRNECCEGREFFUNDALSSNEEKCKKGHAV CDBELQCCCEGWTPPCDDSSVYHEISIVVG VLFPM							YWVI.VVHFTRREAIKOIFVI OHVATNI ODED
KNALVCSHOPILTLETLTVSGLEFFELDLA   PYLDLAPYMPDYKPYNLDERDLESSYHG   SDSLSLINGENSYTSTINLEWDDSALAPSSEDYD   FODVPAYPSYSTEDYDEDOLITDTVSGPRST   ASDLTSSKASTRSPTQRONPPNEBASTYSS   DTTPVHTTSQEKEEAQALDPPDACTELEVIRV   TKKKIGKKKKSRSBEASPLEARCSQKCA   KOGDODSRNOSPSLGROSPDTMLASPQEEGE   GPSTITESSERSEPOLLPPHKDYTSMERLGOPL   SKYIDQLNOQLDPSTVCSRABPPDQSTRTOSP   GAPERPPLCDFSEGLSAPMDYNRTYPSFST   VTSGGGHHDPAGLQQLHVPSSPAAAQQEEE   GGGGGGTPPRLEDTTREAQELEAQLS; VRR-   GPVSEPPGTQEVLCQLRRQOPSPCLSSAEDS   GUDBGQGSPSEMVHSSERVVDNNHLLLLMH-   VFRENEGLFKMIRMSTGHMEGNLQLYVLL   TDCVYYLLRKGATEKPYLVEEAVSYNELDY   VSVGLDQOTVKLVCTNRKOFLLDTADVAL   AEFFLASLKSAMIKGCREPYYSILTDATMEK   LALAKFVAGSKCEASAVTVEFYGLVHWED-   PTDESLGPTPCHCSPPGGTTKEGMLHYKAGT   SYLKEBWKTCSVVLSGILVQVPDRTDVIP-   LLSVNMGGEQCGCRRANTTDRPHAQVILS-   PQGVAPSCPGCVLVIDDRFTCHEBCQTSF-   FRSLGTAKLGDISAVSTERGKEYCVLEFSQDS-   QQLLPPWVTLSCTSELDRLSALNSGWKTY   QVQLPSTAGLGSANSKWTY-   QVQLPSTAGLGSANSKWTY-   QVQLPSTAGLGSANSKWTY-   QVQLPSTAGLGSANSKWTY-   QVQLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKREDAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKWTY-   QVGLPSTAGLGSANSKAGLGGGCGK-   QLEPAGLGCGCCK-   QUGPTGLHGGGGCGANLPW-   KGRVTFLCKTFIPEDSIGIGMVANGTCCG-   GTERCTNICCDAKTCKIKATFQCALGGCCK-   QLERLQCGCGGWIPPCDDSVYRIEGSNEK-   QCCLECKGWIPPCDDSVYRIEGSNEK-   QCCLECKGWIPPCDSSVYRIEGSSNEK-   QCCLECKGWIPPCDSSVYRIEGSSNEK-   QCCLECKGWIPPCDSSVYRIEGSSNEK-   QCCLECKGWIPPCDSSVYRIEGSSNEK-   QCCLECKG	1	ļ	1		}	İ	AWLYLALNENSLESYLRLFOFNI.GLI.HKVVV
PYLDLAPYMPDYKRQVLLDFEDRLESSYHG SDSLSLMSRNSYTSTILEWDDSALAPSSEDYD FGDVPRAYPSVPSTDWEDODLIDTVSGPRST ASDLTSSKASTRSTYGRONPPNEEPAETVSSS DTTPVHTTSQKEEAQALDPPDACTELEVIRV TKKKKIGKKKKSRSDEASPLHPACSQKCA KQGDGDSRNGSPSIGRSPSDTMLASPGEGG GPSSTTESSERSEPGLLIPEMKDTSMERLGOPL SKVIDQLNGQLDSTVCSRAPPPOSPRTGSP GDAPERPLCDFSEGLSAPMDFYRFTVSSPST VTSGGGHDPPAGLGQPLHVPSSPBAAQGEEE GGGGGGGTPRPLEDTTREAQELAQCIS. VRR GPVSEPPGTTQEVLQLERDQPSPCLSSAEDS GJAPERPLCDFSEGLSAPMDFYRFTVSSPST VTSGGGHDPPAGLGQPLHVPSSPBAAQGEEE GGGGGGGSTSEMVISSERTVDNNHLLLMIH VPRRNEEQLFKMIRMSTGHMEGNLQLLYVILL TDCYVYLLRKGATEKPTVLVEANYSVELDY VSVGLDQGTVKLVCTNRRKQFLLDTADVAL AFFLASIKSAMIKGCRPYPSLTDATMEK LALAKFVAGSSKCEASAVTVRFYGLVHWED PTDESLGPTPCHSSPEGTITKEGMLHYKAGT SYLGKBHWKTCFVVLSGILVYPYDATMEK LALAKFVAGSSKCEASAVTVRFYGLVHWED PTDESLGPTPCHSSPEGTITKEGMLHYKAGT SYLGKBHWKTCFVVLSGILVYPYDATMEK LALAKFVAGSSKCEASAVTVRFYGLVHWED PTDESLGPTPCHSSPEGTITKEGMLHYKAGT SYLGKBHWKTCFVVLSGILVYPYGLVHWED PTDESLGPTPCHSSPEGTITKEGMLHYKAGT SYLGKBHWKTCFVVLSGILVYPYGLVHWED PTDESLGPTPCHSSPCESCGRANTTDRPHARQVILS DPFCLLSABSEAEMAEMQHLCQAVSKGVI PQGVAPSPCIPCCLVLTDDRLTTCHEDCCTSF FRSLGTAKLGDISAVSTEPGKEYCVLEFSQDS QQLLPPWVTLSCTSELDRLLSALNSGWKTTY QVDLPHTAQEASMKKKFEDALSLHHSAWQR SDSLCRGRASDPWC*  ARRADITVLLESFSMLQGLLPVSLLISVAVSAI KELMGVKXYEVVYPRLHPLHKREAKEPEQQ EQFETELKYKNTDKGALVLYKKNKNLLAP GYBETYYNSTGKEITTSPQMDDCYYGGHLD EKVSDASISTCGLRGYFSQGDQRYFPED-SP HRDGGEHALFYXNDFENNDSTCMDGVKKTT PNASFTLENPSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTNCSYSVCVYQGHBD NLRAVAGTMAHEMGHNFGMHDDYSCKCPS TICVMMKALSFYPTDTSSCRLSTANKFSPOKC PDDRFQVNGFPCHHKKGRICLMGTCPTLQEQ CTELWGPGTEHAKKNSCYSVCVYQDISD NLLRVAGTMAHEMGHNFGMHDDYSCKCPS TICVMMKALSFYPTDTSSCRLSTANKSFYNCY RVDDTLIPCKANDTMCGRLFCQGGSDNLPW KGNTYT-LTCKTFPDEDSSCRLSTANKSFYNCY RVDDTLIPCKANDTMCGRLFCQGGSDNLPW KGNTYT-LTCKTFPDETSQEIGMAVANGTKGG DNKYCNABCVÜREXYRNEGGSKYGYCR RVDDTLIPCKANDTMCGRLFCQGGSDNLPW KGNTYT-LTCKTFPDETSQEIGMAVANGTKGG DNKYCNABCVÜREXYRNEGGSKEKKKDROFK PDDRFQVNGFPCHHKKRRPQMYKAVQPGBMSQMK PHYDLPFCKSPPTANGTNGTNGTGD DNKYCNABCVÜREXYRNEGGSKEKKKDROFK PHYDLPFCKSPPTANGTNGTNGTGD DNKYCNABCVÜREXPRENGTNALPTYFKD		į		İ	1	1	KNALVCSHDHLTLFLTLVSGLEFIRFELDLDA
SSSLSLNSENSYTSTNLEWDDSALAPSSED YD FGDVPPAPSPSTBUDGDLTDTVSGPRST ASDLTSSKASTRSPTQRQNPPNEEPABTYSSS DTTPVPHTTSQREEBAGALDPPDACTELEVIRV TKKKKIGKKKSRSDEASPLHFACSQKKCA RQGOGDSRNGSPSLGRDSPDTMLASPQEGG GPSSTIESSERSERGLIPPMACTIFLEVIRV TKKKKIGKKKSRSDEASPLHFACSQKKCA RQGOGDSRNGSPSLGRDSPDTMLASPQEGG GPSSTESSERSERGLIPPMACTIFLSSET UTSGGGHDPAGLQQPLHVPSSPEAAGQEE GGGGGGTPPLEDTTRAQELBAGLSI.VRR GPVSEPPATQEVLCQLKRDQPSPCLSSAEDS GUDEGQGSSPSMVISSERPVDNHILLLLMIH VFRENEBQLFKMIRMSTGHMEGNLQLIVLL TDCVYJLLRKGATSKPYLVEEAVSYNELDY VSVGLOQOTSVLVCTNRRRQFLLDTADVAL AEFFLASLKSAMKGCRPPYPSILTDATMEK LALAKFYAQESKCRASAVTVSPTGULYVHWED PTDESLGFIFCHCSPPEGTITIKEGMLHYKAGT SYLOKBHWKTCFVLVSGILVQYPDRATDVPL LLSVNMGGBCCGGCRANTTDRPHAFQVILS DPPCLELSASSEABARAWQHLCQAVGKVI PQGVAPSPCIPCCLVLTDDRLFTCHEDCQTSF FRSLGTAKLGDBAVSTEPGKSYCVLEFSQDS QQLLPPWVTJSCTSELDKLLSANSKWITY QVDLPFTAIGRASNKKKFEDALSLHISAWQR DSDLCRGRASRDPWC SDSLCRGRASRDPWC QVETYNSTCKSELDLLSALANSKWITY QVDLPFTAIGRASNKKKFEDALSLHISAWQR SDSLCRGRASRDPWC GYETYLYNSTCKEHTSPQMDDCYYQGHILN EKVSDASISTCRGLRGVFSQGOQRYFIELSPI HROQGHALFKYNPDEKNYDSTCGMDOVL WANDLQQNIALPARKLYLKDRKVQCHEKY EYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVMMLYKLNTHVALVKJKDRKVQCHEKY EYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVMMLYKLNTHVALVKJKDRKVQDHEKY EYYLVLDNGEFKRYNENGDEIRKRVFEMAN YVMLYKKLNTHVALVKJKDRKVQDHEKY ETYLVLDNGEFKRYNENGORKSPC PDDRFQVNGFPCHHGKGHCLMGTCPTLOEQ CTELWGPGTEVANSKCSVKYNRNGGSKYGYCR RVDDTLIPCKANDTMCGRLFCQAGGCCK CQKKKAGMVCRPAKBGCLPFEMCRISGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLOEQ CTELWGPGTEVANSKCYNRNGGGSKYGYCR RVDDTLIPCKANDTMCGRLFCQAGSDNLPW KGNTYTFLCKTFPDETSTGGLIGMVANGTKGG DNKVCINAECVDIERAYKSTNCSSKCKGHAV CDHELQCQCEEGWFPDCDDSSVYFHEISIVG CTELWGPGTEVANSKCKYNRNGGGSKYGYCR RVDDTLIPCKANDTMCGRLFCQAGSDNLPW KGNTYTFLCKTFTPDETSTGGLIGMVANGTKGG DNKVCINAECVDIERAYKSTNCSSKCKGHAV CDHELQCQCEEGWFPDCDDSSVYFHEISIVG VLFPMAVFVVVAMVIRHGSSREKQKEGDQP LSTTGTRPHKQRKRPQMVKAVQPGBMSQMK PHYDLPYCROPEPASHCDTNALPTYFKD	1		1			ľ	PYLDLAPYMPDYYKPQYLLDFEDRLPSSVHG
ASDLTSKASTRSTQRQNPPNEERAETYUS DTTPVHTTISQEKEAQALDPPDACTELEVURV TKKKKIGKKKKSSDEASPLIPACSQKKCA KQQDDSBNOSPSLGRSDFOTMLASPQEEG GPSSTTESSERSEPGLIPBMCDTSMERLGOPL SKVIDQLNGQLDPSTWCSRAEPPQOSPTROSP GRAPEPPLCDPSGLSAPMDPYRTYVESPST VTSGGGHIDPAGLGQPLLPYSSPSAAQGEE GGGGOTPRPLEDTTREAQELEAQLSI-VEE GGGGOTPRPLEDTTREAQELEAQLSI-VEE GGGGOTPRPLEDTTREAQELEAQLSI-VEE GGVSEPGTQEVLCQLKRQD-SPCLSSAEDS GVDEQQSFSEMVHSSEFRVDNNHLLLLMH VTRENEQLFKMRNSTGHMEGMLU-VILL TDCYVYLLRGATEKPYLVEEAVSYNELDY VSVGLDQOTVELVCTNRKKQFLDATDWAL AEFFLASIKSAMIKGCREPPYPSILTDAATMEK LALAKFVAQBSKCEASAVTVEPYGL-VHEED PTDESLGPTPCHCSPPEGTITIKEGMLHYKAGT SYLGKEHWKTCFVVLSNGIL-YQVPDRTDVP LISVNMGGCQCGCRRANTTDRHAFQVILS DEPCLELSASSAEMABWMQHLCQAVSKQIV PQOVAPSFCIPCL-UTDDRLFTCHBDCQTSF FRSLGTAKLGDISAVSTEPGKEYCVLEFSQDS QQLLPPWYIYLSCTSELDRLLSAINSGWKTIY QVDLPHTAIQRASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC- SPSLGTAKLGDISAVSTEPGKEYCVLEFSQDS QQLLPPWYIYLSCTSELDRLLSAINSGWKTIY QVDLPHTAIQRASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC- SARADTVLLESFSMLOGILPVSLLLSVAVSAI KELFOVKKYBVYPTRLHFLHKRAKEPEQQ EQFETLEKVMRTINGKAVL-JYLKANLAD- GYTETYYNSTGKEITTSPQIMDDCYYQGHLIN EKVSDASISTCRGLRGYFSQGDQRYFIERLSH HRDGGGHALFKVMPDEKNYDSTCGMDOVL WAHDLQQNIALPATTLLVALKDRKVQEHEKY EYYLVLDNGEFKKYNENQDEIKKYEMAN YVNMLYKKLNTHAUL-VAGEIWTDKDKIKTI PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVCLAFMSTMCSYLSRRKRHDIAQLITA TELAGTTVCLAFMSTMCSYLSRRKRHDIAQLITA TELAGTTVCLAFMSTMCSYLSRRKRHDIAQLITA TELAGTTVCLAFMSTMCSYLSRRKRHDIAQLITA TELAGTTVCLAFMSTMCSYLSRRKRHDIAQLITA TELAGTTVCLAFMSTMCSYLSRRKRHDIAQLITA TELAGTTVCLAFMSTMCSYLSRCKCKGMCRC TELWGPGTEVALARSCKKKTGCALGECCEK CQFKKAGMVCPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHBGKCHCLMGTCTTLQG GTSEECTNICCDAKTCKKATPCCALGECCEK CQFKKAGMVCPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHBGKCHCLMGTCTTLQG CTELWGPGTEVALARSCKYNREGGSSNGFYCC RVDDTLIPCKANDTMCGKLFCQGGSSNGFYCC RVDDTLIPCKANDTMCGKLFCQGGSSNGFYCC RVDDTLIPCKANDTMCGKLFCQGGSSNGFYCC RVDDTLIPCKANDTMCGKLFCQGGSSNGFYCC RVDDTLIPCKANDTMCGKLFCQGGSSNGFYCC RVDDTLIPCKANDTMCGKLFCQGGSSNGFYCC RVDDTLIPCKANDTMCGKLFCQGGSSNGFYCC RVDDTLIPCKANDTMANGTKCG DNKVCINAECVDEKAYKATOCSKCKGDRP LSTTGTRFHKQKKCPQMYAKAVQPGBMSQMK CDHELLC							SDSLSLNSFNSVTSTNLEWDDSAIAPSSEDYD
DTTP/HTTISGEREAQALDPPDACTELLEVIR TKKKKIGKKKKSBEASPLIPACSQKKCA KQGDGDSRIGSPSLGRDSPDTMLASPQEEGE GPSSTTESSERSEPGLLIPPMKDTSMERLGOP) SKVIDQLINGQLDPSTWCSRAEPPDQSFRTGISP GDAPERPILCDSEGLSAPMDFYRTVESSTI VISGGGHIDPAGLGOPLBYPSSEAAGQEEE GGGGGGOTPRPLEDTTREAQELEAQLSI.VRE. GPVSEPEPGTQEVLCQLKRDQPSPCLSSAEDS GVDEQQGSPSEMVHSSGFRVDNHSLLLMIH VFRENEQQLFKMRMSTGHMEGNLQLLYVLL TDCYVYLLRKGATEKPYLVEEAVTELDY VSVGLDQOTVKLVCTNRRKOPLLDTADVAL AEFFLASLKSAMIKGCREPPYPSILTDATWEL LALAKFVAQSSKCEASAVTNRYTGLVHWED PTDESLGPTPCHCSPPEGITIKEGMLHYKAGT SYLGKEHWKTCFVLSNGLTYOPPROTUPP LLSVNMGGEQGGGRRANTTDRPHAFQVLIS DPPCLELSASESEAMENWGHLOQAVSKGVI PQGVAPSPCIPCLVLTDDRLFTCHEDCQTSF FRSLGTAKLODISAVSTEPGKEYCVLEFSQB QQLLPPWYLYLSTSELDRLLSALNISGWTITY QVDLPHTAIQEASNKKKFEDALSLHISAWQR SDSLCRGASRPPWC*  ARRADTVLESSSMLQGLLPVSLLLSVAVSAI KELPGVKKYEVYYPIRLHHLHKREAKEPEQ EQFETELKYKMTINGKIAVLYLKKNKVLLAP GYTETYYNSTGKEITTSPQIMDDCYYQGHLIN EKVSDASISTCRGLRGYPGQGDRYFEPLSPI HRDGGEHALFKYNPDERKYDSTCGMDGVL WAHDLQQNIALPATKLVRLKDRKVQEHEKY ETYLVLDNGEFKKYNENDDEIKRKYFEWAN YVNMLYKKLNTHVALVGMEINTDRDKKKTI PNASFTLENSSKWRSVSLSRKRKFEDALGLITA TELAGTTVGLAFMSTMCSPYSVGVVQDDISD NLLRVAGTMAHEMGHNFOMFHDDYSCKCPS TICVMKALSFYLIPTSSSCSLSTDJKFTDKL SNCLFRAFLPTDIISTPICGRQLVEMGEDCDC GTSEECTNICCDAKTCKKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPBMCNGKSGNC PDDRFQVNGFPCHIGKGHCLMGTCPTLQQ CTELWGPGTEVADKSCVNRPEGGSSNGYGYC RVDDTLIFCKANDTMCGKLFCQGGSDNLFW GGRIVT-FICKATDPEDTSGEIGNYANGTKCG DDNKVCINABCVDIEKAYKSTNCSSKCKGMRY CDHELCQCCEGE WEPPCDDSSCKCYCOR RVDDTLIFCKANDTMCGKLFCQGGSDNLFW GCTELWGPGTEVADKSCVNRPEGGSKYGYCC RVDDTLIFCKANDTMCGKLFCQGGSDNLFW GCTELWGPGTEVADKSCVNRPEGGSKYGYCC RVDDTLIFCKANDTMCGKLFCQGGSDNLFW GCTELWGPGTEVADKSCVNRPEGGSKYGYCC RVDDTLIFCKANDTMCGKLFCQGGSDNLFWG CTELWGPGTEVADKSCVNRPEGGSKYGYCC RVDDTLIFCKANDTMCGKLFCQGGSDNLFW GCTELWGPGTEVADKSCVNRPEGGSKYGYCC RVDDTLIFCKANDTMCGKLFCQGGSDNLFW GCTELWGPGTEVADKSCVNRPEGGSKYGYCC RVDDTLIFCKANDTMCGKLFCQGGSDNLFW STGTTFTREKRQKKCPQMVAAVQPGEMSGMW HVYDLPVENDEPPASSFKHCDTMALDTFTVFKD CTELTGTRETHKQKKCPQMXAAVQPGEMSGMW HVYDLPVENDEPPASSFKHCDTMALDTFYFKD						l	FGDVFPAVPSVPSTDWEDGDLTDTVSGPRST
TKKKKIGKKKSRSDEASPLIPACSGKKCK KQGDGDSRNGSPLGRSPTMLASPQEEGG GPSTTTESSERSPGLLIPEMKDTSMERLGQPL SKVIDQLINGQLDSTWCSRAEPPDQSPRTGSS GDAPERPPLCDFSEGLSAFMDFYRTYCESPS GDAPERPPLCDFSEGLSAFMDFYRTYCESPS VTSGGGHIBPAGLGQPLBYPSSFEAAGGEE GGGGGTPRPLEDTTREAGELSGLS VRR GPVSEPPETGTVLCQLKRDQPSPCLSSAEDS GVDEGGSPSEMVHSSEPRVDNNHLLLLMIH VFRENEQLFKMIRMSTGHNEGRLQLLVYLL TDCYYYLLRGATEKPYLVEBAVSYNELDY VSVGLDQTVKLVCTNRKQPLDTADVAL AEFFLASIKSAMIKGCREPPYPSILTDATMEK LALAKFVAQSSKCEASAVTVREYLWBD PTDESLGPTPCHCSPPEGTITKEGMLHYKAGT SYLGKEHWKTCFVLSNGILYQYPDRTDVIP LLSVNMGGEQGGCRRANTTDRHARQVILS DPFCLELSASSAEMAEWMOHLOQAVSKOVI PQOVAPSPCPCCLVLTDRLFTCHEDCCTSF FRSLGTAKLGDISAVSTEPGKEYCVLEFSDD QQLPPWYVISCTSELDRLLSALNGSWKTIV QVDLPHTAIQEASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC* SDSLCRGRASRDPWC* ARRADTVLEESPSMLQGLPYSLLLSVAVSAI KELPGVKKYEVYPTRLHFLHKREAKEPEQ GOGGERALFKYNDFDSSMLGOLPYSELLSVAVSAI KELPGVKKYEVYPTRLHFLHKREAKEPEQ GOGGERALFKYNDPDERNYDSTCGMGVV WAHDLQQNIALPATTLLVKLKDRKVQEHERY EFYYLVLDNGEFKRYNENDQEIRKRYFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKTI PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKTI PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKTI PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKTI PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKTI PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKTI PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YVNMLYKKLNTHVALVGMEWTDKDKKRT PNASFTLENFSKWRSGVSLSRKRYPEMAN YNTH	1		l	1		1	ASDLTSSKASTRSPTQRQNPFNEEPAETVSSS
KQGGDSRNOSPSIGRSPDTMLASPÖREGEG GPSSTTESSERSPOLLPEMENTBELGOP) SKVIDOLAGOLDPSTWCSRAEPPDQSFRTGSP GDAPERPPLCDFSEGLSAPMDFYRFTVESPST VTSGGGHEDPAGLGQPLHYPSSPFAAGQEEE GGGGGGGTFRPLEDTTREAQELEAQLSI VRF. GPVSSPPEGTGVLOCLKARDPSCLSAEDS GVVEGQGSPSEMVHSSEFRVDNNHLLLLMIH VFRENEGLFKMIRMSTGFMEGNIQLLYVLL TDCYVYLLRKGATEKPYLVESAVSNELDY VSVGLDQQTVKLVCTNRRKQFLLDTADVAL AEFFLASLKSAMIKGGREPPTEAVSNELDY VSVGLDQQTVKLVCTNRRKQFLLDTADVAL AEFFLASLKSAMIKGGREPPTEAVSNNELDY VSVGLDQQTVKLVCTNRRKQFLLDTADVAL AEFFLASLKSAMIKGGREPPTEGTTTXEGMLHYKAGT SYLGKEHWKTCFVVLSNGILVQYPDRTDVIP LLSVMMGGEQCGGCRRANTTDRPHAFQVILS DPPCLELSABSEAEMAEWMOHLCQAVSKGVI PQQVAPSPCIPCCLVLTDDRLFFCHEDCOTSF FRSLGTAKLGDISAVSTEPGKEYVVLEFSQDS QQLLPPWVTLSCTSELDRLLSANSGWKTY QVDLPHTAIQEASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC* ARRADTVLLESPSMLQGILFVSLLLSVAVSAI KELPQVKKYEVVYPIRLHPLHKREAKEPEQQ EQFETELKYKMTINGKAVLYLKDRKVQEHEKY WAYDAYKKLNTHVALVGMEIWTDKDKIKT PRASSTLENESKWGSVLSRKFGDQRYFIEPISIT BRYDGGBHALFKYNPDEKNYDSTCGMDGVL WAYBDLQQNLALPATKLVKLKDRKVQEHEKY EYYLVLDNGEFKRYNENQDEIKKYFEMAN YVNMLYKKLNTHVALVGMEIWTDKJKKT PRASSTLENESKWGSVLSRKFMDAQCLTC GTSEECTNICCDAKTCKIKATFCALGECCEC CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQNVGFPCHHGKGHLONGTLOQQ CTELWGPGTEVADKSCYNKEGGSKYGYCR RVDDTLIPCKANDTNCGKLFCQGGSDNLPW KGRIVTFLICKTTPPEDTSGEIGMYANGTICQEQ CTELWGPGTEVADKSCYNKEGGSKYGYCR RVDDTLIPCKANDTNCGKLFCQGGSDNLPW KGRIVTFLICKTPPEDTSGEIGMYANGTICQE CTELWGPGTEVADKSCYNKEGGSKYGYCR RVDDTLIPCKANDTNCGKLFCQGGSDNLPW KGRIVTFLICKTPPEDTSGEIGMYANGTKCG DMKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWPPDCDDSGGMYANGTKCG DMKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWPPDCDDSGGMYANGTKCG DMKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWPPDCDDSGMYANGTKCG DMKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWPPDCDDSGMYANGTKCG DMKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWPPDCDDSGMYANGTKCG DMKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWPPDCDDSGMYANAVGPQEMSGMK PHVYDLPVENDEPASPHKDTNALPPTYFKD			l				DITPVHTISQEKEEAQALDPPDACTELEVIRV
GPSSTTESSERSEPGLIPPOGERTOSP SKVDPOLNGQLDPSTWCSRAEPPOGERTOSP GDAPERPPLCDFSEGLSAPMDFYRFTVESPST VTSGGGHHDPAGLGQPLHVPSSPEAAGGEE GGGGGGTPFLEDTTREAGLAQLSI-WER GPVSEPFBGTQEVLCQLKRDQPSPCLSAEDS GVDEGQGSPSEWVHSSEFRVDNNHLLLMHI VFRENEGLFKMIRMSTGHBEGNIQLLYVLL TDCYVYLLRKGATEKPYL-VEEAVSYNEELDY VSVGLDQQTVKLVCTNRRKQFLDTADVAL AEFFLASLKSAMIKGGREPYPSILTDATMEK LALAKFVAQESKCEASAVTVRFYGLVHWED PTDESLGPTPCHCSPFBGTTIKFGMLHYKAGT SYLGKEHWKTCFVVLSNGILVQYPDRTDVIP LLSVNMGGEGGCGRANTTDRPHAFOVILS DPPCLELSABSEAEMAEWMOHLCQAVSKGVI PQOVAFSPCIPCLVLTDDRLFTCHEDCOTSF FFRSLGTAKLGDISAVSTEPGKEVCVLEFSQDS QQLLPPWVTVLSCTSELDRLLSALNSGWKTIY QVDLPPTAIQLGASNKKFEFDALSLIHSAWQR SDSLCRGRASRDPWC*  ARRADTVLESFSMLQOLLFVSLLLSVAVSAI KELPOVKKYEVVYPRLIPFLHKREAKEPFQQ EQFETELKYKMTINGGIAVJYLKKNKNLAP GYTETYYNSTGKETTSPQMOGVYQGHILM EKVSDASISTCRGLRGYFSQGDQRYFIEFLSPI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WARIDLQONLAPATKLVKLKDRKVQEHEKY WAYMLYKKLNTHYALVGMEIWTDDKIKTT PNASFTLENFSKWRGSVLSRRKRIDIAQLITA TELAGTTVGLAFMSTMCSFYSVGVVQHBDD NLLRVAGTMAHEMGHNFOMFHDDYSCKCPS ICVMDKALSFYIPTDFSSCSRLSYDKFFEDKL SNCLFNAPLFTDIISTPICGNQLVEMGEDCO GTSEECTNICCDAKTCKKATTQCALGECCEK COFKKAGNVCRPAKDEGDLPEMCNGKSRNC PDDRFQNORFPCHIGKGHCLMGTCPTLQEQ CTELWGPOTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGRLFCQGGSDNLPW KGRIVTFLICKTPPEDTSGERGMYANOTIKCG DMKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELCQCCEEGWIPPDCDDSSVVFHFISTIVG CDKKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELCQCCEEGWIPPDCDDSSVVFHFISTIVG CDKKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELCQCCEEGWIPPDCDSSVVFHFISTIVG CDKKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELCQCCEEGWIPPDCDSSVVFHFISTIVG CDKKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELCQCCEEGWIPPDCDSSVVFHFISTIVG CDKKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELCQCCEEGWIPPDCDSSVVFHFISTIVG CDKKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELCQCCEEGWIPPDCDSSVVFHFISTIVG CDKKCPTTPTKQRKRCPMWKAVQPOEMSOMK PHVYDLPVENDEPASHKCHTNALPTVFKD						1	KOGDGDSPNGSPSI GPDSPDTA A SPOSESS
SKVIDQLNGQLDPSTVCSRAEPPDQSFRTGSF GDAPERPLCIPSEGLSAMPDFYRFTVESPST VTSGGGHHDPAGLGQPLHVPSSPEAAGQEEE GGGGGGTPRIEDTTREAQELEAQLINEF GPVSEPPBTQEVLCQLKERQESCLSSAEDS GVDEGGGSSEMVHISSEFRVDNNHLLLIMH VFRENEGLFKMIRMSTGHMEGNIQLLYVILL TDCYVYLLRKGATEKPYLVEEAVSYNELDY VSVGLDQTVKLVCVTNRKQFLLDTADVAL AEFFLASLKSAMIKGCREPPYSILTDATMEK LALAKRVAQESKCEASAVTVRFYGLVHWED PTDESLGPTECHCSPPEGITIKEGMLHYKAGT SYLGKEHWXTCRVVLSNGILYQYPDRTDVIP LLSVNMGGEQCGGCRRANTTDRHARGVILS DPPCLEISAISEAEMAEWMQHLCQAVSKGVI PQQVAPSCEPCLVLTDDRLFTCHEDCQTSF FRSLGTAKLGDISAVSTEPGKEVLFSQDS FRSLGTAKLGDISAVSTEPGKEVLFSQDS FRSLGTAKLGDISAVSTEPGKEVLFSQDS GQLLPPWVIVLSCTSELDRILSALNSGWKTIY QVDLPHTAIQEASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC*  ARRADTVILESPSMLGOLLPVSLLISVAVSAI KELPOVKSYEVVYPRIHPLIKIRSAKEPSQQ EQFETEILKYKNTINGKIAVLYLKKNKNLAP GYTETYYNSTGKEITTSQIMDDCYYGGHLN EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMGDVL WAAIDLQQNIALPATKLVKLKDRKVQEHEKY EYYLVLDNGEFKRYNENDDCHYGGHEKY EYYLVLDNGEFKRYNENDGURVENDEDDCC GTSEECTNICCDAKTCKRATTPCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSRCC PDDRRPNGPFFIGGNQLVEMGEDDCD GTSEECTNICCDAKTCKKATTPCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSRCC PDDRRPNGPFFIGGRGVANOTIKCG DMKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPDCDDSSKCKCHAV CDHELQCQCEEGWIPDCDDSSKCKGRNC PDDRRVNGFPCHHGKGHCLAGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTNAGRLFCQGGSDNLPW KGRIVTFLICKTTPPEDTSGEIGMVANOTIKCG DMKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELQCQCEEGWIPDCDDSSRCKCHFIESTUG CDHKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELQCQCEEGWIPDCDDSSRCKKPHIFSITUG CDHKVCINAECVDIEKAYKSTNCSSKCKCHAV CDHELQCQCEEGWIPDCDDSSCPTHSFISTUG CDHKVCINAECVDIEKAYKSTNCSSKCKCKDRP LSTTGTPRHKQRKRCMWKAVQPQEMSOMK PHVYDLIVEGNEPPASTHKDTNALPTTVFKD	1					l	GPSSTTESSERSEPGI LIPEMKINTEMEDI CODI
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TDCYVYLLRKGATEKPYLVEEAVSYNELDY VSVGLDQQTVKLVCTNRRKQFLLDTADVAL AEFFLASLKSAMIKGCREPPYPSILTDATMEK LALAKFVAQBSKCEASAVTVRFYGLVHIWED PTDESLGPIPCHCSPEPGTITKEGMLHYKAGT SYLGKEHWKTCFVVLSIGILYQYPDRTDVIP LLSVNMGGEQCGGCRRANTTDRPHAFQVILS DPPCLELSAESEAMABWMQHLCQAVSKGVI PQGVAPSPCIPCCLVLTDDRLFTCHEDCQTSF FRSLGTAKLGDISAVSTEPGREYCVLEFSQDS QQLLPPWVIVLSCTSELDRLLSALNSGWKTIY QVDLPHTAIQEASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC*  ARRADTVLESPSMLQGLLPVSLLLSVAVSAI KELPGVKKYEVVYPIRLHPLHKREAKEPEQQ EQFETELKYKMTINGKIAVLYJKKNKNLLAP GYTETYYNSTGKEITTSQIMDDCYYQGHILN EKVSDASISTCRGLRGYFSQGDQRYFIEPLSPI HRDGQEHALFKYNPDEKNYDSTCMDGVL WAHDLQQNIALPARKLYKLKDRXVQEHEKY IEFYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFILENFSKWRGSVLSRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGINFGMFHDDYSCKCPS TICVMMKALSFYPITDFSSSSRLSYDKFFEDKL SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRREGSKYGYCK RVDDTLIPCKANDTMCGKLFCQGGSDNLFW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWPPPDCDDSSVVFHRSIVVG VLFPMAVIFVVVAMVIRHOSSREKOKKDORP LSTTGTRPHKQKKKPQMYKAVQPQEMSQMK PHYDLLPVERNEPPSFFHKDINALPPTVFKD							GVDEGQGSPSEMVHSSEFRVDNNHLLLLMIH
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TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKL SNCLFNAPLPTDLISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSINCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD		]	]	j			TELAGTI VGLAFMSTMCSPYSVGVVQDHSD
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CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD	1		İ	- 1	J	ŀ	GTSEECTNICCDAKTCKIKATEOCAI GECCEK
PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD			1	ľ	į	į	CQFKKAGMVCRPAKDECDLPEMCNGKSGNC
CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD			J	ł		İ	PDDRFQVNGFPCHHGKGHCLMGTCPTLOEO
RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD			- 1	1	1	i	CTELWGPGTEVADKSCYNRNEGGSKYGYCR
KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD				-			RVDDTLIPCKANDTMCGKLFCOGGSDNLPW
CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHVYDLPVEGNEPPASFHKDTNALPPTVFKD				1		1	KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG
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PHVYDLPVEGNEPPASFHKDTNALPPTVFKD	1	1	- 1	.	1		LSTTGTRPHKOKRKPOMVKAVOPOEMSOMV
	1				1	1	PHVYDLPVEGNEPPASFHKDTNALPPTVFKD
	L						

OPO 12	OFC TO	14-4	l eco	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	поц	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	sed-	1	USSN	location	corresponding	I-Isoleucine, K-Lysine, L-Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	dellee		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uaice			] /**	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	ļ	peptide		/=possible nucleotide deletion, \=possible
			}	sequence	1	nucleotide insertion
950	2300	A	8100	1	1251	MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE
300		1		1 -		PPADEAARAGEGFRYIKPVPGLLLREYLYGG
			1	Í	ĺ	GRDEEPSGAAPEGGATPTAAPETPAPPTRETC
		İ	]			YFLNATILFLFRELRDTALTRRWVTKKIKVEF
			1	Į	}	EBLLQTKTAGRLLEGLSLRDVFLGETVPFIKTI
		1	}	l	)	RLVRPVVPSATGEPDGPEGEALPAACPEELAF
				1		EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS
			1			RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV
			1	Į	1	RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY
	·		1		1	KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE
			1			GRLKVTLLECSRLLIFGSYDREANVHCTLELS
				1		SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE
		1		!	i	AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ
		<u> </u>			<u></u>	CPG
951	2301	A	8108	1612	839	EVALFCFEMAAGMYLEHYLDSIENLPFELQR
		1	1	1		NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR
		1			1	SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL
	ł	ł		ł	ì	AMQTYEMVDKHIRRLDTDLARFEADLKEKQI
				•		ESSDYDSSSSKGKKKGRTQKEKKAARARSKG
					•	KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE
		}	l		1	MIGCONPOCSIEWFHFACVGLTTKPRGKWFC
		1				1 · · · · · · · · · · · · · · · · ·
		<b></b>	0110		201	PRCSQERKKK PSVASLARRFSGRALWPPSHSVPGNRALCPRL
952	2302	A	8112	595	291	LHGTTLPGGNQRELARQKNMKKQSDSVKGK
		1	}	ł	1	RRDDGLSAAARKQRDSTPRDSEIMQQKQKK
		ŀ	]			ANEKKEEPK
953	2303	A	8118	1	669	VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG
900	2505	^	0110	1.	1005	LETNILKMTTPNKTPPGADPKQLERTGTVREI
		1	,	1		GSOAVWSLSSCKPGFGVDQLRDDNLETYWQ
			1	i		SDGSQPHLVNIQFRRKTTVKTLCIYADYKSDE
				l	1	SYTPSKISVRVGNNFHNLQEIRQLELVEPSGW
•	Į.		ł	1		IHVPLTDNHKKPTRTFMIQIAVLANHQNGRD
			1			THMRQIKIYTPVEESSIGKFPRCTTIDFMMYRS
			ļ			IR
954	2304	A	8133	66	1015	PPLPPRSFPNLFSRPEPLPEPGRRGCNRSREPA
				1		ARAPSPPPPFEGAPGRAMVKVTFNSALAQKE
				1		AKKDEPKSGEEALIIPPDAVAVDCKDPDDVV
		1				PVGQRRAWCWCMCFGLAFMLAGVILGGAY
		l		1	1	LYKYFALQPDDVYYCGIKYIKDDVILNEPSAD
	1	J	1	1		APAALYQTIEENIKIFEEEEVEFISVPVPEFADS
				1		DPANIVHDFNKKLTAYLDLNLDKCYVIPLNT
		1				SIVMPPRNLLELLINIKAGTYLPQSYLIHEHMV
	1	1		1		ITDRIENIDHLGFFIYRLCHDKETYKLQRRETI
1		1		1		KGIQKREASNCFAIRHFENKFAVETLICS
955	2305	A	8143	35	1171	VESRSAWHEGEDQIDRLDFIRNQMNLLTLDV
						KKKIKEVTEEVANKVSCAMTDEICRLSVLVD
	1	1			!	EFCSEFHPNPDVLKIYKSELNKHIEDGMGRNL
		1		1	i	ADRCTDEVNALVLQTQQEIIENLKPLLPAGIQ
		1		1		DKLITTLIPCKKFDLSYNLNYHKLCSDFQEDIV
	]		1	i	1	FRFSLGWSSLVHRFLGPRNAQRVLLGLSEPIF
		1	1	1		QLPRSLASTPTAPTTPATPDNASQEELMITLVT
			1	1	1	GLASVTSRTSMGIIIVGGVIWKTIGWKLLSVS
l		1	1		1	LTMYGALYLYERLSWTTHAKERAFKQQFVN
	1					
						YATEKLRMIVSSTSANCSHQVKQQIATTFARL
1						CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS
						CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS KLLRNKAVQLENELENFTKQFLPSSNEES
956	2306	A	8157	1854	798	CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS

	SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	
	NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
	nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	eotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq-	uence	J	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
- 1	uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
- 1		ł	1	}	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ			1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
			1	1	peptide	1	/=possible nucleotide deletion, \=possible
ŀ		-	<del> </del>	ļ	sequence		nucleotide insertion
ļ		ļ	ļ	1	!	!	DRYTTSRRLDPIPQLKCVGGTAGCDSYTPKVI
.			1		l	İ	QCQNKGWDGYDVQWECKTDLDIAYKFGKT
- 1		İ	1	1 :		{ ·	VVSCEGYESSEDQYVLRGSCGLEYNLDYTEL
-			1	ļ			GLQKLKESGKQHGFASFSDYYYKWSSADSC
-1		ľ	1				NMSGLITIVVLLGIAFVVYKLFLSDGQYSPPP
1			1				YSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQ
1		ļ	1	J :		1	NTGHGATSGFGSAFTGQQGYENSGPGFWTGL
			1				GTGGILGYLFGSNRAATPFSDSWYYPSYPPSY PGTWNRAYSPLHGGSGSYSVCSNSDTKTRTA
ı			1		•		SGYGGTRRR
ı	957	2307	A	8159	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSL
1						1	VYSMPSRNLSLRLEGLQEKDSGPYSCSVNVQ
i			j				DKQGKSRGHSIKTLELNVLVPPAPPSCRLQGV
1			l			1	PHVGANVTLSCQSPRSKPAVQYQWDRQLPSF
ı			ĺ			*	QTFFAPALDVIRGSLSLTNLSSSMAGVYVCKA
1						i	HNEVGTAQCNVTLEVSTGPGAAVVAGAVVG
1		}	l	1			TLVGLGLLAGLVLLYHRRGKALEEPANDIKE
			l			,	DAIAPRTLPWPKSSDTISKNGTLSSVTSARAL
1			İ	!			RPPHGPPRPGALTPTPSLSSQALPSPRLPTTDG
ı					-		AHPQPISPIPGGVSSSGLSRMGAVPVMVPAQS
r	958	2308	A	8161	2340	1100	QAGSLV
۱	100	2000	, n	0101	2340	1192	ELARRPKQQSSEKSRNMIRNWLTIFILFPLKLV
			Ì	1			EKCESSVSLTVPPVVKLENGSSTNVSLTLRPP
							LNATLVITFEITFRSKNITILELPDEVVVPPGVT NSSFQVTSQNVGQLTVYLHGNHSNQTGPRIR
1				1			FLVIRSSAISIINQVIGWIYFVAWSISFYPQVIM
					į		NWRRKSVIGLSFDFVALNLTGFVAYSVFNIGL
1							LWVPYIKEQFLLKYPNGVNPVNSNDVFFSLH
							AVVLTLIIIVQCCLYERGGQRVSWPAIGFLVL
l	- 1						AWLFAFVTMIVAAVGVITWLQFLFCFSYIKL
l							AVTLVKYFPQAYMNFYYKSTEGWSIGNVLL
							DFTGGSFSLLQMFLQSYNNDQWTLIFGDPTK
1	959	2309	A	8163	501	10.15	FGLGVFSIVFDVVFFIQHFCLYRKRPGYDQLN
Ι.		2307	л	0103	521	1345	OERAGRRGRLGVWAQPQPLLPRPVGSRRE
l					•		MQPPGPPPAYAPTNGDFTFVSSADAEDLSGSI
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					ŀ		LEVEDDDPEDNKPLLEELDIDLKDIYYKIRCV LMPMPSLGFNRQVVRDNPDFWGPLAVVLFFS
ļ	- 1				. 1		MISLYGQFRVVSWIITIWIFGSLTIFLLARVLG
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۱	60	2310	A	8167	1	2921	MTCFKGQKGEQRSHAFEANKDHKAKVPSPN
	- 1	l		)	1	j	LYSQLNALQFTVDERSILWLNOFLLDLKOSL
							NOFMAVYKLNDNSKSDEHVDVRVDGLMLK
	1		i				FVIPSEVKSECHQDQPRAISIQSSEMIATNTRH
	1		1	ł	1	1	CPNCRHSDLEALFQDFKDCDFFSKTYTSFPKS
	- 1	.			- 1	j	CDNFNLLHPIFQRHAHEQDTKMHEIYKGNITP
	- 1				i	1	QLNKNTLKTSAATDVWAVYFSQFWIDYEGM
	- 1		}	1	1	ļ	KSGKGRPISFVDSFPLSIWICQPTRYAESQKEP
	j	-					QTCNQVSLNTSQSESSDLAGRLKRKKLLKEY YSTESEPLTNGGQKPSSSDTFFRFSPSSSEADI
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	- 1		ĺ		[		KKDSFYTDSSSVLNYREDSNILSFDSDGNONI
	L						LSSTLTSKGNETIESIFKAEDLLPEAASLSENL

					<b>1</b>	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	:	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
achiec			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1		sequence	/=possible nucleotide deletion, \=possible
	İ	<b> </b>		peptide		
				sequence		nucleotide insertion
						DISKEETPPVRTLKSQSSLSGKPKERCPPNLAP
Ì						LCVSYKNMKRSSSQMSLDTISLDSMILEEQLL
	i .	1	İ			ESDGSDSHMFLEKGNKKNSTTNYRGTAESVN
						AGANLQNYGETSPDAISTNSEGAQENHDDLM
		·		1	1	SVVVFKITGVNGEIDIRGEDTEICLQVNQVTP
	İ		İ		ì	DQLGNISLRHYLCNRPVGSDQKAVIHSKSSPE
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		1		l		ISLRFESGPGAVIHSLLAEKNGFLQCHIENFST
					!	EFL'ISSLMNIQHFLEDETVATVMPMKIQVSNT
	ļ	1	1		•	KINLKDDSPRSSTVSLEPAPVTVHIDHLVVER
	i .	ļ		İ	Į.	SDDGSFHIRDSHMLNTGNDLKENVKSDSVLL
	1				1	TSGKYDLKKQRSVTQATQTSPGVPWPSQSAN
ł	İ	1	1			FPEFSFDFTREQLMEENESLKQELAKAKMAL
			<u> </u>			AEAHLEKDALLHHIKKMTVE
961	2311	Α	8172	1442	682	TAAMSIFTPTNQIRLTNVAVVRMKRAGKRFEI
í		1			i .	ACYKNKVVGWRSGVEKDLDEVLQTHSVFVN
	ļ	1.				VSKGOVAKKEDLISAFGTDDQTEICKQILTKG
	1		1			EVQVSDKERHTQLEQMFRDIATIVADKCVNP
			i		1	FTKRPYTVILIFRAMKDIHYSVKTNKSTKQQA
	ļ		1	l		LEVIKOLKEKMKIERAHMRLRFILPVNEGKKL
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		i	1			KEKLKPLIKVIESEDYGQQLEIVCLIDPGCFREI
l			<u> </u>			DELIKKETKGKGSLEVLNLKDVEEGDEKFE
962	2312	Α	8175	286	587	NISNKAEVSSHPSVISHSMDSFGQPRPEDNQS
			1	ł	}	VLRRMOKKYWKTKQVFIKATGKKEDEHLVA
i				1		SDAELDAKLEVFHSVQETCTELLKIEKYQLR
1		1		1	l	LNGMKS
	0010	<del>  </del>	0101	13	2215	AEGCAERRGTEPVVELSMSWESGAGPGLGSQ
963	2313	ļ Ņ.	8181	13	2213	
1	į		İ		1	GMDLVWSAWYGKCVKGKGSLPLSAHGIVV
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1	1	1	1		ì	TVWRSRSGNELPLAVASTADLIRCKLLDVTG
	1		1			GLGTDELRLLYGMALVRFVNLISERKTKFAK
1	1		1	1	1	VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI
i		1	1		1	NDCRRGCYFVLDWLQKTYWCRQLENSLRET
		1	1	1		WELEEFREGIEEEDQEEDKNIVVDDITEQKPE
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			j	}	]	PQDDGKSTESDVKADGDSKGSEEVDSHCKK
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYBEBQFTVLEKFRYL
						PODDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYBEBQFTVLEKFRYL
						PODDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGOWEARRGWRLFNCSASLDWP
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEBNVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEBNVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEBNVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEBNVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDDRMEVGPFSTGQESSTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEKEEKEVLPDQVEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS
						PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEDEDDDDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEKEEKEVLPDQVEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEDEDDDDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEDEDDDDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYBRARELLVSYBEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYBENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDREWGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYBRARELLVSYBEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYBENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFPFCTIDPNESR
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEDDRMEVGPFSTGGESFTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEKEEKEVLPDQVEEEEENDDQE EEEDEDDDDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF EPRRNFRDDSTRPRTRGRTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGFFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTINSQASAENPFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEENDDQE EEEDEDDEDDDEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGLHGLKTGLQLF EPRRNFRDDSTRPTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFPFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGLHGLKTGLQLF EPRRNFRDDSTRPTTRGTTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDTTHVEGSVDPIRDIEIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGLHGLKTGLQLF EPRRNFRDDSTRPTTRGTTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDTTHVEGSVDPIRDIEIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGLHGLKTGLQLF EPRRNFRDDSTRPTTRGTTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFPFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS
964	2314	A	8184	6	1393	PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEBQFTVLEKFRYL PKAIKAWNNPSPRVECVLABLKGVTCENREA VLDAFLDDGFLVPTFEQLAALQIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQQEEQ GSVNDVKEEEKEEKEVLPDQVEEEEENDDQE EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGLHGLKTGLQLF EPRRNFRDDSTRPTTRGTTRGRRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFFFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDTTHVEGSVDPIRDIEIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS

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peptide colide sequence   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN   USSN							Amino acid sequence (A=Alanine C=Cysteine,
Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Soci	nucl-	peptide		1			F=Phenylalanine G=Glycine H=Histidine
Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept	eotide	seq-		USSN			I=Isoleucine K=Lysine L=Leucine
914 an to first amino acid peptide sequence de peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide pep	seq-	uence	i	09/496	correspondi		M=Methionine, N=Asparagine, P=Proline
amino acid peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	uence		Ī	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
Persidue of peptide   Sequence   Y=Tyrosine, X=Usinown, *=Sigo podon, / Peptide sequence   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Pep						of peptide	T=Threonine, V=Valine, W=Tryptophan.
	1			1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
AMMTOSAJEKIRKAPÇAACKIHTDEKKOFIMAEV   RAWTEKGTKAPÇAACKIHTDEKKOFIMAEV   MYEDPYEEGGBNAVKAAGKYRQQGKNY    SPENJESPELSPERMALCAAGATRVFVAMV   AAALGOHPILOVSATINSVINSNAINNI.PPI   GOAAGHPILOVSATINSVINSNAINNI.PPI   GOAAGHPILOVSATINSVINSNAINNI.PPI   GOAAGHPILOVSATINSVINSNAINNI.PPI   GOAAGHPILOVSATINSVINSNAINNI.PPI   GOAAGHPILOVSATINSVINSNAINNI.PPI   GOAAGHPILOVSATINSVINSNAINNI.PPI   GOAAGHPICOSAVSAAPOILI.YGGNXY.VOIDOVSATINSVINSNAINNI.PPI   LSSKMYHTKOGGGSVILSSBOCASILOVSCHIP   CXCYGGGI SCRIOKCHHQASISSRI.HTCQRH   FWSKICKPVI.KGGQVCTKHERKGSISOLEIPQ   RCYCGGGI SCRIOKCHHQASISSRI.HTCQRH   FWSKICKPVI.KGGQVCTKHERKGSISOLEIPQ   RCYCGGGI SCRIOKCHHQASISSRI.HTCQRH   FWSKICKPVI.KGGQVCTKHERKGSISOLEIPQ   RCYCGGGI SCRIOKCHHQASISSRI.HTCQRH   FWSKICKPVI.KGGQVCTKHERKGSISOLEIPQ   RCYCGGGI SCRIOKCHHQASISSRI.HTCQRH   FWSVICKPVI.KGGGRV.CVIEKNASG   AMINIMISEVI.VIVDAGAGNISHI   LISAKYPANVAVDPVERIFIWSSEVAGSI.Y   RABIDOVGKALLETISEKTIAVSI.DVI.KGGRV.CVIEKNASG   AMINIMISEVI.VIVDAGAGNISHI   LISAKYPANVAVDPVERIFIWSSEVAGSI.Y   RABIDOVGKALLETISEKTIAVSI.DVI.KGG.KGG.CVCPIL.HTCGRICLU.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HTCGGCI.CVC.HT	ļ			ł		ł	
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RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIBMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVTVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM		1 1		1 1	1		SLIGRSDLNGKRSKIITIENISOPRGIAVHPMAK
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DLKWWELRHAGHGQQQKVIVVAVCVVVLV MILLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIJESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM			[			l	HDGVCMYIEALDKYACNCVVGYIGERCOYR
MILLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM							DLKWWELRHAGHGOOOKVIVVAVCVVVI.V
RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ DPHQMELTQ SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQPFKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	- 1	:	1	1		J	MLLLLSLWGAHYYRTOKLLSKNPKNPYEESS
LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQPFKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	1	1	j	- 1	1		RDVRSRRPADTEDGMSSCPOPWFVVIKEHOD
967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIJESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	1	!	i	ļ		İ	LKNGGQPVAGEDGQAADGSMOPTSWROEPO
967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM		}		j		l	MESVOTOTI POOLININGS CPQVMERSFH
967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	- 1	Ì			[	1	DEBHOME TO
RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	967	2317	$\overline{\mathbf{A}}$	8210	3	601	
NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	İ		-				BI HHRED ALD DINKY CALCULATION OF COLORS
VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	- 1	ł	1	1	!	}	NPLGDRIESFFPDGSOPVDEDGEVDVI ATTEST
DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM		.			i	ļ	VEDEDTETODPKK PEPI NGB DNIKI LIVAROL V
ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	-		}			I	DLDRDGKISRHEMLOVI.RI.MVGVOVTERO
DVEHKMSIRILK	l	l		1		1	ENIADRTVQEADEDGDGAVSFVEFTKSLEKM
							DVEHKMSIRILK

		r =				Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, B=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
Ì	ļ			peptide	sequence	/=possible nucleotide deletion, \=possible
			Ì	sequence		nucleotide insertion
968	2318	A	8211	2.	409	ISSCPHTAYEGSMSTLSNFTQTLEDVFRRIFIT
906	2310	^	0211	2	100	YMDNWRQNITAEQEALQAKVDAENFYYVIL
	<b>j</b>	]	1	j	)	YLMVMIGMFSFIIVAILVSTVKSKRREHSNDP
	1		ļ			YHQYIVEDWQEKYKSQILNLEESKATIHENIG
	Ì	1		i		AAGFKMSP
969	2319	A	8215	<u> </u>	1938	GMPRSRGGRAAPGPPPPPPPPGQAPRWSRWR
909	4319	Α	0213	<b>'</b>	1 1330	VPGRLLLLLPALCCLPGAARAAAAAAGAGN
				İ	ļ	RAAVAVAVARADEAEAPFAGQNWLKSYGY
l		1				LLPYDSRASALHSAKALQSAVSTMQQFYGIP
	ł	l	1	ł		VTGVLDQTTIEWMKKPRCGVPDHPHLSRRRR
		l	1		ľ	NKRYALTGQKWRQKHITYSIHNYTPKVGELD
		l				TRKAIRQAFDVWQKVTPLTFEEVPYHEIKSDR
1		1	İ		1	KEADIMIFFASGFHGDSSPFDGEGGFLAHAYF
	i	İ		1		PGPGIGGDTHFDSDEPWTLGNANHDGNDLFL
1	l			· ·		VAVHELGHALGLEHSSDPSAIMAPFYQYMET
l	}					HNFKLPQDDLQGIQKIYGPPAEPLEPTRPLPTL
i .						PVRRIHSPSERKHEROPRPPRPPLGDRPSTPGT
ł i		1	1		İ	KPNICDGNFNTVALFRGEMFVFKDRWFWRL
1	Ì			ļ		RNNRVQEGYPMQIEQFWKGLPARIDAAYER
}	ļ	1	ļ			ADGRFVFFKGDKYWVFKEVTVEPGYPHSLG
	ļ	l .	1			ELGSCLPREGIDTALRWEPVGKTYFFKGERY
	ļ		1	1		WRYSEERRATDPGYPKPITVWKGIPQAPQGA
				1		FISKEGYYTYFYKGRDYWKFDNQKLSVEPGY
]	)	1		Į		PRNILRDWMGCNQKEVERRKERRLPQDDVDI
		ì	1			MVTINDVPGSVNAVAVVIPCILSLCILVLVYTI
1		1		l		FQFKNKTGPQPVTYYKRPVQEWV
970	2320	A	8216	1235	2223	SRLSLQFYVSFRRTGLFTCKLIVEIFFRNYMN
		1	1		İ	DSLRTNVFVRFQPETIACACIYLAARALQIPLP
	1					TRPHWFLLFGTTEEEIQEICIETLRLYTRKKPN
1	1	1		1.	ŀ	YELLEKEVEKRKVALQEAKLKAKGLNPDGTP
1		1		1		ALSTLGGFSPASKPSSPREVKAEEKSPISINVK
		1		1		TVKKEPEDRQQASKSPYNGVRKDSKRSRNSR
	1	1	1			SASRSRSRTRSRSRSHTPRRHYNNRRSRSGTY
	1	Į.				SSRSRSRSRSHSESPRRHHNHGSPHLKAKHTR
		•		j	1	DDLKSSNRHGHKRKKSRSRSQSKSRDHSDAA
				1		KKHRHERGHHRDRRERSRSFERSHKSKHHGG
	<u> </u>		1	<u> </u>		SRSGHGRHRR
971	2321	Α	8217	3	3274	DCRLQAAMPTNFTVVPVEAHADGGGDETAE
		1		1		RTEAPGTPEGPEPERPSPGDGNPRENSPFLNN
		1		1	1	VEVEQESFFEGKNMALFEEEMDSNPMVSSLL NKLANYTNLSQGVVEHEEDEESRRREAKAPR
		1		Į	ì	
		1			į	MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG VLESPLIVAMCCTCTMLTAISMSAIATNGVVP
1	1	i	1			AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA
I	1	1	1			
		1	1	1		GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCILVLMALVVFVGVKYVN
1	1	1	1	1	i	KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV
	1		1	1		CLLGNRTLSRRSFDACVKAYGIHNNSATSAL
	1	1	1	1		
İ	1	1		1		WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV
1	1	1		1		ASGVILENLWSTYAHAGAFVERRGVPSVPV
1	1	i	1			
	i	1	1		1.	IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM
1	1	1			<u>'</u>	LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL
		1	1 .	1		QAIARDGIVPFLQVFGHGKANGEPTWALLLT
	1	1		1	]	VLICETGILIASLDSVAPILSMFFLMCYLFVNL
	1	1		1		ACAVOTLLRTPNWRPRFKFYHWTLSFLGMSL
			1	ſ		CLALMFICSWYYALSAMLIAGCIYKYIEYRG
		1	1	Į.		AEKEWGDGIRGLSLNAARYALLRVEHGPPHT
		1		1		KNWRPQVLVMLNLDAEQAMKHPRLLSFTSQ
	1	1	1	1	1	THE WILL GALLATERING CONTINUE LONG 196

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LKAGKGLTIVGSVLEGTYLDKHMEAQRAEE NIRSLMSTEKTKGFCQLVVSSSLRDGMSHLIQ SAGLGGLKHNTVLMAWPASWKQEDNPFSW KNFVDTVRDTTAAHQALLVAKNVDSFPQNQ ERFGGGHIDVWWIVHDGGMLMLLPFLLRQH KVWRKCRMRIFTVAQVDDNSIQMKKDLQMF LYHLRISAEVEVVEMVENDISAFTYERTLMM EQRSQMLKQMQLSKNEQEREAQLIHDRNTAS HTAAAARTQAPPTPDKVQMTWTREKLIAEK YRSRDTSLSGFKDLFSMKPDQSNVRRMHTAV KLNGVVLNKSQDAQLVLLNMPGPPKNRQG
972	2322	A	8224	701	246	ENYMEFLEVLTEGLNRVLLVRGGGREVITIYS TSRRVTMKFNPFVISDRSKNRKRHFNAPSHV
					2.0	RRKIMSSPLSKELRQKYNVRSMPIRKDDEVQ VVRGHYKGQQIGKVVQVYRKKYVIYIERVQ REKANGTTVHVGIHPSKVVTTRLKLDKDRKKI LERKAKSRQVGKEKGKYKEELIEKMQE
973	2323		8237	873		GCPHAGGKGRVPTGGLTGGRTWSPSAAPRSC PRPGPTPAPGAMDKLPPSMRKRLYSLPQQVG AKAWIMDEEDAEEGAGGRQDPSRRSIRLR PLPSPSPSAAAGGTESRSSALGAADSEGPARG AGKSSTNGDCRRFRGSLASLGSRGGSGGTG SGSSHGHLHDSAEERRLIAEGDASPGEDRTPP GLAAEPERPGASAQPAASPPPPQQPPQPASAS CEQPSVDTAIKVEGGAAAGDQILPEAEVRLG QAGFMQRQFGAMLQPGVNKFSLRMFGSQKA VEREQERVKSAGFWIIHPYSDFRFYWDLTML LLMVGNLIIIPVGITFFKDENTTPWIVFNVVSD TFFLIDLVLNFRTGIVVEDNTEIILDPQRIKMK YLKSWFMYDFISSIPVDYIFLIVETRIDSEVYK TARALRIVRFTKILSLLILILRLSRLIRYHHQWE EIFHMTYDLASAVVRIVNLIGMMLLLCHWDG CLQFLVPMLQDFPDDCWVSINNMVNNSWGK QYSYALFKAMSIMLCIGYGRQAPVGMSDV WLTMLSMIVGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPPDTRQRIHD YYEHRYQGKMFDESSILGELSEPLREEIINFNC RKLVASMPLFANADPNFVTSMLTKLRFEVFQ PGDYIIREGTIGKKMYFIQHGVVSVLTKGNKE TKLADGSYFGEICLLTRGRRTASVRADTYCR LYSLSVDNFNEVLEEYPMMRRAFETVALDRL DRIGKKNSILLHKVQHDLNSGVFNYQENEIIQ QIVQHDREMAHCAHRVQAAASATPTPTPVIW TPLIQAPLQAAAAATTSVAIALTHHPRLPAAIFR PPPGSGLGNLGAGGGTPRHLKRLQSLIPSALGS ASPASSPSQVDTPSSSSFHIQQLAGFSAPAGLS PLLPSSSSSPPPGACGSPSAFTPSAGVAATTIA GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGLPEHFLPPPPSSRSPSS SPGQLGQPPGBLSLGLATGPLSTPETTPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFFRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNIL
974	2324	A	8247	279	468	EYKQWERRFLSCQNRNDLGYGKPRKGGGLL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL G

						(A-Almino CarCartaino
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Hisidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
1				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
ł		l	1	residue of	sequence	/=possible nucleotide deletion, \=possible
ł				peptide	•	
		<u> </u>	0040	sequence	1831	nucleotide insertion  LVALKNWKPKGTNIPAPQSPVFGEAVSGVYM
975	2325	Α	8249	62	1571	MTKVLGMAPVLGPRPPQEQVGPLMVKVEEK
						EEKGKYLPSLEMFRQRFRQFGYHDTPGPREA
1		Ì				LSQLRVLCCEWLRPEIHTKEQILELLVLEQFLT
1	Ì		1		ł	ILPQELQAWVQEHCPESAEEAVTLLEDLEREL
1	)		}	1		DEPGHQVSTPPNEQKPVWEKISSSGTAKESPS
			ŀ	i		SMQPQPLETSHKYESWGPLYIQESGEEQEFAQ
1				İ	i	DPRKVRDCRLSTQHEESADEQKGSEAEGLKG
1				1		DIISVIIANKPEASLEROCVNLENEKGTKPPLQ
l	ł	ľ	<b>!</b>	Ì	Ĭ	EAGSKKGRESVPTKPTPGERRYICAECGKAFS
	1	1	Ì	İ	1 '	NSSNLTKHRRTHTGEKPYVCTKCGKAFSHSS
1		1			1	NLTLHYRTHLVDRPYDCKCGKAFGQSSDLLK
1	]	1		J	]	HORMHTEEAPYOCKDCGKAFSGKGSLIRHYR
1		1	1	1	1	IHTGEKPYQCNECGKSFSQHAGLSSHQRLHT
		1				GEKPYKCKECGKAFNHSSNFNKHHRIHTGEK
		1				PYWCHHCGKTFCSKSNLSKHQRVHTGEGEA
1		!		ł	1.	P
976	2326	A	8257	298	7086	GNMACWPQLRLLLWKNLTFRRRQTCQLLLE
'						VAWPLFIFLILISVRLSYPPYEQHECHFPNKAM
		'			] .	PSAGTLPWVQGIICNANNPCFRYPTPGEAPGV
	1	1	İ		1	VGNFNKSIVARLFSDARRLLLYSQKDTSMKD
		l	ļ			MRKVLRTLQQIKKSSSNLKLQDFLVDNETFS
	1	ł	Ì	1	ľ	GFLYHNLSLPKSTVDKMLRADVILHKVFLQG
				1		YQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP
		1	1	1		REKLAAAERVLRSNMDILKPILRTLNSTSPFPS
				j		KELAEATKTLLHSLGTLAQELFSMRSWSDMR
1	1			ŀ		QEVMFLTNVNSSSSSTQIYQAVSRIVCGHPEG
		1	1	1		GGLKIKSLNWYEDNNYKALFGONGTEEDAE
1			1	1		TFYDNSTTPYCNDLMKNLESSPLSRIIWKALK
1		1	ļ	i	İ	PLLVGKILYTPDTPATRQVMAEVNKTFQELA VFHDLEGMWEELSPKIWTFMENSQEMDLVR
Ì			1		<u> </u>	MLLDSRDNDHFWEQQLDGLDWTAQDIVAFL
			1	1 .		AKHPEDVQSSNGSVYTWREAFNETNQAIRTIS
1		1.	ļ			RFMECVNLNKLEPIATEVWLINKSMELLDER
1	1	[				KFWAGIVFTGITPGSIELPHHVKYKIRMGIDN
-	į					VERTNKIKDGYWDPGPRADPFEDMRYVWGG
1				1	i	FAYLQDVVEQAIIRVLTGTEKKTGVYMQQMP
1	ļ	l	1	1	1	YPCYVDDIFLRVMSRSMPLFMTLAWIYSVAV
'	1			1		IIKGIVYEKEARLKETMRIMGLDNSILWFSWFI
1				1	1	SSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV
				1		FLSVFAVVTILQCFLISTLFSRANLAAACGGII
1	1	1	1	1	1	YFTLYLPYVLCVAWQDYVGFTLKIFASLLSP
1					1	VAFGFGCEYFALFEEQGIGVQWDNLFESPVE
			}	1	1	EDGFNLTTSVSMMLFDTFLYGVMTWYIEAVF
1	}				1	PGQYGIPRPWYFPCTKSYWFGEESDEKSHPGS
1		1				NQKRISEICMEEEPTHLKLGVSIQNLVKVYRD
1		1		1	1	GMKVAVDGLALNFYEGQITSFLGHNGAGKT
		1		1		TTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQ
1	1	1	1	1	1	NLGVCPQHNVLFDMLTVEEHIWFYARLKGLS
i		1		1		EKHVKAEMEQMALDVGLPSSKLKSKTSQLS
	}	1			1	GGMQRKLSVALAFVGGSKVVILDEPTAGVDP
1						YSRRGIWELLLKYRQGRTIILSTHHMDEADVL
ſ	[	1	[			GDRIAIISHGKLCCVGSSLFLKNQLGTGYYLT
	1					LVKKDVESSLSSCRNSSSTVSYLKKEDSVSQS
	}	1		1		SSDAGLGSDHESDTLTIDVSAISNLIRKHVSEA
		]		1	1	RLVEDIGHELTYVLPYEAAKEGAFVELFHEID
	1	1				DRLSDLGISSYGISETTLEBIFLKVABESGVDA
	1	1				ETSDGTLPARRNRRAFGDKQSCLRPFTEDDA
		1				ADPNDSDIDPESRETDLLSGMDGKGSYQVKG
L	1	1	1	<u></u>	<u> </u>	WKLTQQQFVALLWKRLLIARRSRKGFFAQIV

SEQ II	SEQID	Met	SEQ	Predicted	Dendinted and	I A single distribution of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
NO: of		hod	ID NO:		Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-		USSN	location	corresponding	Franciscon, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
1		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		Į		peptide	1	/=possible nucleotide deletion, \=possible
	,		1	sequence	1	nucleotide insertion
			<b>———</b>			LPAVFVCIALVFSLIVPPFGKYPSLELQPWMY
İ	İ	Ì	İ	İ	į	NEQYTFVSNDAPEDTGTLELLNALTKDPGFG
		1		ļ	İ	TRCMEGNPIPDTPCQAGEEEWTTAPVPQTIM
		1	{	i	!	DLFQNGNWTMQNPSPACQCSSDKIKKMLPV
	1		İ			CPPGAGGLPPPQRKQNTADILQDLTGRNISDY
	1		1	ĺ	1	LVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVS
1	1					NTQALPPSQEVNDATKQMKKHLKLAKDSSA
}		]	1		<b>i</b> .	DRFLNSLGRFMTGLDTRNNVKVWFNNKGW
		İ			<u> </u>	HAISSFLNVINNAILRANLQKGENPSHYGITAF
1		1				NHPLNLTKQQLSEVAPMTTSVDVLVSICVIFA
İ		į				MSFVPASFVVFLIQERVSKAKHLQFISGVKPVI
						YWLSNFVWDMCNYVVPATLVIIIFICFQQKSY
						VSSTNLPVI.ALLLLLYGWSITPI.MYPASFVFK
	,	1				IPSTAYVVLTSVNLFIGINGSVATFVLELFTDN
	1			· ·		KLNNINDILKSVFLIFPHFCLGRGLIDMVKNQ
	1	1				AMADALERFGENRFVSPLSWDLVGRNLFAM
			,			AVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLN DEDEDVRRERQRILDGGGQNDILEIKELTKIY
1		ł				RRKRKPAVDRICVGIPPGECFGLLGVNGAGK
			1.			SSTFKMLTGDTTVTRGDAFLNRNSILSNIHEV
						HQNMGYCPQFDAITELLTGREHVEFFALLRG
						VPEKEVGKVGEWAIRKLGLVKYGEKYAGNY
1 .	ļ	1				SGGNKRKLSTAMALIGGPPVVFLDEPTTGMD
İ	1					PKARRFLWNCALSVVKEGRSVVLTSHSMEEC
	1	İ	l i			EALCTRMAIMVNGRFRCLGSVQHLKNRFGD
1		l				GYTIVVRIAGSNPDLKPVQDFFGLAFPGSVPK
1		j				EKHRNMLQYQLPSSLSSLARIFSILSQSKKRLH
					٠	IEDYSVSQTTLDQVFVNFAKDQSDDDHLKDL
977	0205		00.50			SLIIKNQTVVDVAVLTSFLQDEKVKESYV
"'	2327	A	8260	3	1567	IPGSTISFSLCFIFPPCVPTMVRKPVVSTISKGG
1						YLQGNVNGRLPSLGNKEPPGQEKVQLKRKV
		1			ĺ	TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSVGM
				İ		SLTIWTVCGVLSLFGALSYAELGTTIKKSGGH
	1					YTYILEVFGPLPAFVRVWVELLIIRPAATAVIS
			1			LAFGRYILEPFFIQCEIPELAIKLITAVGITVVM
1	1			l	l	VLNSMSVSWSARIQIFLTFCKLTAILIIIVPGV MQLIKGQTQNFKDAFSGRDSSITRLPLAFYYG
1						MYAYAGWFYLNFVTEEVENPEKTIPLAICISM
1					j	AIVTIGYVLTNVAYFTTINAEELLLSNAVAVT
						FSERLLGNFSLAVPIFVALSCFGSMNGGVFAV
						SRLFYVASREGHLPEILSMIHVRKHTPLPAVIV
1						LHPLTMIMLFSGDLDSLLNFLSFARWLFIGLA
					j	VAGLIYLRYKCPDMHRPFKVPLFIPALFSFTC
			1			LFMVALSLYSDPFSTGIGFVITLTGVPAYYLFII
050	احججا					WDKKPRWFRIMSEKITRTLQIILEVVPEEDKL
978	2328	Α	8261	2	2165	RGGSLRCVLGKLLGQLLCFOSERCVRFPEGLL
					l	RHRGCGLLSSRLSAGKPPLRTSFFGSWGVLPP
1		ļ			1	LADAASMSGVRAVRISIESACEKOVHEVGLD
		j	<u> </u>		l	GTETYLPPLSMSQNLARLAQRIDFSQGSGSEE
			f		[	EEAAGTEGDAQEWPGAGSSADODDEEGVVK
				l	1	FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI
	1	l	-		1	VRDKKFMTLDPVSQDALPPKQNPQTLQLISK
			1	ĺ	1	KKSLAGAAQILLKGAERLTKSVTENOENKLO
1	[	1	ľ		1	RDFNSELLRLRQHWKLRKYGDKILGDLSYRS
1			i	İ		AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL
		[	ŀ	ļ	- 1	DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN
1				1	ĺ	LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI
1		1	- 1	ļ	ļ	FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ
		ł	1		.	LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE
l						HNLHLLIREFHKQTLSSIMMPHPASAPFGHKR

	<del></del>					Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	]	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence	Ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	]	ļ	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		peptide	sequence	/=possible nucleotide deletion, \-possible
	l	l	1	sequence		nucleotide insertion
		<del> </del>	<del></del>	504		MRLSGPQAFDKNEINSLQSSEGLLEKIIKQAK
		1			}	HIFLRSRAAATIDSLASRIEDPQIQAHWSNIND
		1		-	1	VYESSVKVLITSQGYEQICKSIQLQLNIGVEQI
						RVVHRDGRVITLSYQEQELQDFLLSQMSQHQ
	Ì	ł		l		VHAVQQLAKVMGWQVLSFSNHVGLGPIESIG
		}	1	ļ		NASAITVASPSGDYAISVRNGPESGSKIMVQF
	1	[		ļ		PRNQCKDLPKSDVLQDNKWSHLRGPFKEVQ
					1	WNKMEGRNFVYKMELLMSALSPCLL
979	2329	A	8289	2	1053	FVWNPRGGRKRRRQAAVTQAATRASGTPSP
					]	RDGTMTQGKLSVANKAPGTEGQQQVHGEKK
	ļ	1				EAPAVPSAPPSYEEATSGEGMKAGAFPPAPTA
		1				VPLHPSWAYVDPSSSSSYDNGFPTGDHELFTT
		İ				FSWDDQKVRRVFVRKVYTILLIQLI.VTI.AVV
						ALFTFCDPVKDYVQANPGWYWASYAVFFAT
	1		1		·	YLTLACCSGPRRHFPWNLILLTVFTLSMAYLT
	1	Ì	1			GMLSSYYNTTSVLLCLGITALVCLSVTVFSFQ
		1				TKFDFTSCQGVLFVLLMTLFFSGLILAILLPFQ
		i				YVPWLHAVYAALGAGVFTLFLALDTQLLMG
		1	(	.!		NRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFG
	1	1				TNRE
980	2330	Α	8305	59	857	ASQLPDYSISPPSLPPRISFHPSPTLARVAMAEP
l		ł			ŀ	SEATQSHSISSSSFGAEPSAPGGGGSPGACPAL
İ		(	ĺ			GTKSCSSSCAVHDLIFWRDVKKTGFVFGTTLI
		1	1			MLLSLAAFSVISVVSYLILALLSVTISFRIYKSV
1		j	)	į	)	IQAVQKSEEGHPFKAYLDVDITLSSEAFHNY
i		l				MNAAMVHINRALKLIIRLFLVEDLVDSLKLA
ļ		1	ļ		1	VFMWLMTYVGAVFNGITLLILAELLIFSVPIV
		ł	}	i	l	YEKYKTQIDHYVGIARDQTKSIVEKIQAKLPG
		<u> </u>	<u> </u>		<u> </u>	IAKKKAE
981	2331	A	8308	186	1337	TRMSRHEGVSCDACLKGNFRGRRYKCLICYD
1		1	i		ļ	YDLCASCYESGATTTRHTTDHPMQCILTRVD FDLYYGGEAFSVEQPQSFTCPYCGKMGYTET
		1 .	. }	1 .	<b>}</b> -	
		1	1			SLQEHVTSEHAETSTEVICPICAALPGGDPNH VTDDFAAHLTLEHRAPRDLDESSGVRIIVRR
			1		ľ	MFHPGRGLGGPRARRSNMHFTSSSTGGLSSS
		İ	İ			OSSYSPSNREAMDPIAELLSQLSGVRRSAGGQ
]		1		1	1	LNSSGPSASQLQQLQMQLQLERQHAQAARQ
1		1		1	1	QLETARNATRRINTSSVITTITQSTATINIAN
1		1	1	1	1	TESSQQTLQNSQFLLTRLNDPKMSETERQSM
			1		1	ESERADRSLFVQELLLSTLVREESSSSDEDDR
	1		1			GEMADFGAMGCVDIMPLDVALENLNLKESN
		ł	1		1	KGNEPPPPL
000	2222	+	9215	1	1004	GSTHASADAWAQWFCTEALVMGAPVWYLV
982	2332	A	8315	1 1	1004	AAALLVGFILFLTRSRGRAASAGQEPLHNEEL
1		1		1	1	AGAGRVAOPGPLEPEEPRAGGRPRRRRDLGS
1	1			1	İ	RLQAQRRAQRVAWAEADENEEEAVILAQEE
		1	1		1	EGVEKPAETHLSGKIGAKKLRKLEEKQARKA
l	1		1	1	ì	OREAEEAEREERKRLESOREAEWKKEEERLR
		1		1	1	LEEEQKEEEERKAREEQAQREHEEYLKLKEA
	1	1	1.			FVVBEEGVGETMTEEQSQSFLTEFINYIKQSK
	1				1	VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT
Į.			1	1	1	GVIDDRGKFIYITPEELAAVANFIRQRGRVSIA
1		1	1	1	1	
L		4	1-0000	1	1.00	ELAQASNSLIAWGRESPAQAPA
983	2333	A	8320	244	1420	RRRWRARGGLVPTLAWAEATGAYVPGRDKP
		1				DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD
		1	1	1		PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD
[		1	1	1		TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP
1	1					CPQPLRSPSLDNPTPFPNLGPSENPLKRLLVPG EEWEFEVTAFYRGRQVFQQTISCPEGLRLVGS

SEO ID	SEO ID	l Afet	CEO	D	18.0.0	I 4
		Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine,
NO: of	NO: of peptide	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
			in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ı		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i		1	1	peptide	1	/=possible nucleotide deletion, \=possible
		ļ	ļ	sequence		nucleotide insertion
1		1	!	!	!	EVGDRTLPGWPVTLPDPGMSLTDRGVMSYV
		1	1	]	1	RHVLSCLGGGLALWRAGQWLWAQRLGHCH
						TYWAVSEELLPNSGHGPDGEVPKDKEGGVF
1		l			l	DLGPFIVGSLGPPDLITFTEGSGRSPRYALWFC
		١.	!		1	VGESWPQDQPWTKRLVMVKVVPTCLRALVE
ı		1	İ			MARVGGASSLENTVDLHISNSHPLSLTSDQY
						KAYLQDLVEGMDFQGPGES
984	2334	A	8321	1	1243	ANMAPVEHVVADAGAFLRHAALQDIGKNIY
i		ł	1.		l	TIREVVTEIRDKATRRRLAVLPYELRFKEPLPE
		1	1		1	YVRLVTEFSKKTGDYPSLSATDIQVLALTYQL
İ	1	1			İ	EAEFVGVSHLKQEPQKVKVSSSIQHPETPLHIS
						GFHLPYKPKPPQETEKGHSACEPENLEFSSFM
ļ		Ì				FWRNPLPNIDHELQELLIDRGEDVPSEEEEEE
1		1	1			NGFEDRKDDSDDDGGGWITPSNIKOIOOELE
l		1			ŀ	QCDVPEDVRVGCLTTDFAMQNVLLQMGLHV
		1	1 .			LAVNGMLIREARSYILRCHGCFKTTSDMSRV
		1				FCSHCGNKTLKKVSVTVSDDGTLHMHFSRNP
	1	ŀ				KVLNPRGLRYSLPTPKGGKYAINPHLTEDQRF
1	İ					PQLRLSQKARQKTNVFAPDYIAGVSPFVENDI
İ	į.	1	1			SSRSATLQVRDSTLGAGRRRLNPNASRKKFV
	ł	1				KKR
985	2335	A	8322	352	529	RRNNIRQFIMKVCISGQARWLTPVVPVLWET
"		1		, 552	327	EAGRSLELKSLRPAWATWGNPISTKINK
986	2336	A	8325	89	1172	KMNPTDIADTTLDESIYSNYYLYESIPKPCTKE
1			0323	0,	1172	GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL
						CYCALOEDLELLE ISEAL ALOTFOWAY AAFAF
1		1				FKYKRLRSMTDVYLLNLAISDLLFVFSLPFWG
		l				YYAADQWVFGLGLCKMISWMYLVGFYSGIF
			İ			FVMLMSIDRYLAIVHAVFSLRARTLTYGVITS
	-					LATWSVAVFASLPGFLFSTCYTERNHTYCKT
Ï	i	1	1 1			KYSLNSTTWKVLSSLEINILGLVIPLGIMLFCY
			1			SMIRTLQHCKNEKKNKAVKMIFAVVVLFLG
						FWTPYNIVLFLETLVELEVLQDCTFERYLDYA
						IQATETLAFVHCCLNPIIYFFLGEKFRKYILQL
						FKTCRGLFVLCQYCGLLQIYSADTPSSSYTQS
987	2337	A	8326	3	470	TMDHDLHDAL
~ '	2331	Γ^	0320	,	4/0	SLSAMRFLAATFLLLALSTAAQAEPVQFKDC
			]	ł		GSVDGVIKEVNVSPCPTQPCQLSKGQSYSVN
	!					VTFTSNIQSKSSKAVVHGILMGVPVPFPIPEPD
				Į	ļ	GCKSGINCPIQKDKTYSYLNKLPVKSEYPSIK
988	2338	<u> </u>	9225	1005	202	LVVEWQLQDDKNQSLFCWEIPVQIVSHL
700	2338	A	8335	1205	323	VIKMALAARLLPQFLHSRSLPCGAVRLRTPA
			] [	{		VAEVRLPSATLCYFCRCRLGLGAALFPRSAR
					-	ALAASALPAQGSRWPVLSSPGLPAAFASFPAC
				ļ		PQRSYSTEEKPQQHQKTKMIVLGFSNPINWV
			l·	l		RTRIKAFLIWAYFDKEFSITEFSEGAKQAFAH
J I					*	VSKLLSQCKFDLLEELVAKEVLHALKEKVTS
				ľ	ļ	LPDNHKNALAANIDEIVFTSTGDISIYYDEKG
						RKFVNILMCFWYLTSANIPSETLRGASVFQVK
				1		LGNQNVETKQLLSASYEFQREFTQGVKPDWT
L			L		[	IARIEHSKLLE .
989	2339	A	8349	67	185	MSGFIHQLLIQNLFCVYHTRLKTSQGLCLLSL
			L 1		ľ	KSLHPMS
990	2340	A	8361	210	1115	ASPPLRPQGHDSGEREPFSQTPGLMQPFSIPVQ
				1		ITLQGSRRRQGRTAFPASGKKRETDYSDGDPL
			<b> </b>	- 1	ļ	DVHKRLPSSTGEDRAVMLGFAMMGFSVLMF
				1	. 1	FLLGTTILKPFMLSIQREESTCTAIHTDIMDDW
				ł	i	LDCAFTCGVHCHGQGKYPCLQVFVNLSHPG
				l	į	QKALLHYNEEAVQINPKCFYTPKCHODRNDL
			Ì	l	ŀ	LNSALDIKEFFDHKNGTPFSCFYSPASQSEDVI
						2. VOLUMENTA DIRECTOR TO LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CO

SEQ ID No. of nucleotide peptide control of the period of peptide sequence (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market Sequence) (Market S							
mucle celidide seq- uence    14	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
entide  ### 1058/10			hod				D=Aspartic Acid, E=Glutamic Acid,
991 2341 A 8369 9 921 Saverence Profiles, Perfolics, Columnia, Revagnine, Sescine, Thronise, Valaine, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling, Walling,	nucl-	peptide	i				F=Phenylalanine, G=Glycine, H=Histidine,
uenec    Page	eotide	seq-	[				I=Isoleucine, K=Lysine, L=Leucine,
amino acid residue of peptide residue of peptide residue of peptide sequence peptide sequence peptide sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequenc	seq-	uence		1		1 '	
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peptide sequence    Possible muleotide deletion, prossible nucleotide insertion			1	į			
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TQDEILKMRNTFAELKNSLEALSSRMDQAEE RIGTQAGVQWRDHGSLQPQPPEFKQCFHLSL PSSWDYRACLS	994	2344	A	8385	231	644	
RIGTQAGVQWRDHGSLQPQPPEFKQCFHLSL PSSWDYRACLS			1	1	1		
PSSWDYRACLS	}		1		Į	ł	TQDEILKMRNTFAELKNSLEALSSRMDQAEE
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995   2345   A   8390   194   3421   AWRKSSVVPPRGTRRGEKSDQDKSGQKNKR	<u></u>	1	1		<u>                                     </u>	<u> </u>	
	995	2345	A	8390	194	3421	AWRKSSVVPPRGTRRGEKSDQDKSGQKNKR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C-Cysteine.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	""	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		l .	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1			J	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ŀ				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \=possible
1		1	ļ	sequence	ļ	nucleotide insertion
			<del> </del>	sequence	<del></del>	DFLSMKQSPALAPEERGRRAGSPKPVLRADD
	1			1	1	
1		l	1		l	NNMGNGCSQKLATANLLRFLLLVLIPCICALV
				ı		LLLEILLSYVGTLQKVYFKSNGSEPLVTDGEI
				•		QGSDVILTNTIYNQSTVVSTAHPDQHVPAWT
1	i	l	l	Į	1	TDASLPGDQSHRNTSACMNITHSQCQMLPYH
1	1	1				ATLTPLLSVVRNMEMEKFLKFFTYLHRLSCY
1		1				QHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCE
						AAKEGCESVLGMVNYSWPDFLRCSQFRNQT
1		l				ESSNVSRICFSPQQENGKQLLCGRGENFLCAS
1			1		i :	GICIPGKLQCNGYNDCDDWSDEAHCNCSENL
						FHCHTGKCLNYSLVCDGYDDCGDLSDEQNC
1						DCNPTTEHRCGDGRCIAMEWVCDGDHDCVD
			1		-	KSDEVNCSCHSQGLVECRNGQCIPSTFQCDG
					i	DEDCKDGSDEENCSVIQTSCQEGDQRCLYNP
1 .						CLDSCGGSSLCDPNNSLNNCSQCEPITLELCM
1						NLPYNSTSYPNYFGHRTQKEASISWESSLFPA
ļ						LVQTNCYKYLMFFSCTILVPKCDVNTGEHIPP
						CRALCEHSKERCESVLGJVGLQWPEDTDCSQ
						FPEENSDNQTCLMPDEYVEECSPSHFKCRSGQ
						CVLASRRCDGQADCDDDSDEENCGCKERDL
1		i				WECPSNKQCLKHTVICDGFPDCPDYMDEKN
1 :		i				CSFCQDDELECANHACVSRDLWCDGEADCS
						DSSDEWDCVTLSINVNSSSFLMVHRAATEHH
1						VCADGWQEILSQLACKQMGLGEPSVTKLIQE
						QEKEPRWLTLHSNWESLNGTTLHELLVNGQS
						CESRSKISLLCTKQDCGRRPAARMNKRILGGR
1						TSRPGRWPWQCSLQSEPSGHICGCVLIAKKW
1						VLTVAHCFEGRENAAVWKVVLGINNLDHPS VFMQTRFVKTIILHPRYSRAVVDYDISIVELSE
			!		ļ	DISETGYVRPVCLPNPEQWLEPDTYCYITGW GUMGNYMPEYLOEGEVERING
1						GHMGNKMPFKLQEGEVRIISLEHCQSYFDMK TITTRMICAGYESGTVDSCMGDSGGPLVCEK
		- 1			-	PGGRWTLFGLTSWGSVCFSKVLGPGVYSNVS
	.	- 1				YFVEWIKRQIYIQTFLLN
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		İ				ASESSKPWPDATYGTGSASRASAVSELSPRER
1 [						SPALKSPLQSVVVRRRSPRPSPVPKPSPPLSST
1				i		SQMGSTLPSGAGYQSGTHQGQFDIIGSGSLSP
					1	SKKSPVGKSPPSTGSTYGSSQKEESAASGGAA
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	ŀ	1	ļ		1	DKAKGRKESEFDDEPKFMSKVIGANKNQEEE
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		- 1	1	ľ	ł	RSKKEDRGKRSEGGHRGFVPEKNFRVTAYK
[					l	AVQEKSSSPPPRKTSESRDKLGAKGDFPTGKS
	1			1	l	SFSITREAQVNVRMDSFDEDLARPSGLLAQER
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[				1	ĺ	KYLKRGTEQEAAKNKKSPEIHRRIDISPSTFRK
			. }	1	· {	HGLAHDEMKSPREPGYKAEGKYKDDPVDLR
		İ	.	ı	i	LDIERRKKHKERDLKRGKSRESVDSRDSSHSR FRSAEKTEVTUKGSVKOVKUDBARDBSRSSS
		- 1		ļ	l	ERSAEKTEKTHKGSKKQKKHRRARDRSRSSS
L						SSSQSSHSYKAEEYTEETEEREESTTGFDKSRL

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion GTKDFVGPSERGGGRARGTFQFRARGRGWGRGNYSGNNNNSNNDFQKRNREEEWDPEYTPKSKKYYLHDDREGEGSDKWVSRGRGRGAFPRGRGRFMFRKSSTSPKWAHDKFSGEEGEIE
997	2347	A	8398	202	552	DDESGTENREEKDNIQPTTE  CPALGGRQDLQGTRLLWAHDSGVGGQKAKS KQENLESLEATGREEEGGGGPPVTTKGVLLA LLMAGLALQPGTALLCYSCKAQVSNEDCLQ VENCTQLGEQCWTARIREWGDDSRQA
998	2348	A	8400	697	301	NPPSACTPGSCDSCSGRGRDLAFDSVWSTNN MSDPRRPNKVLRYKPPPSECNPALDDPTPDY MNLLGMIFSMCGLMLKLKWCAWVAVYCSFI SFANSRSSEDTKQMMSSFMLSISAVVMSYLQ NPQPMTPPW
999	2349	A	8401	93	1126	ASASHITSGHLRCFPGSEGVGTMARCFSLVLL LTSIWTTRLLVQGSLRAEELSIQVSCRIMGITL VSKKANQQLNFTEAKEACRLLGLSLAGKDQ VETALKASFETCSYGWVGDGFVVISRISPNPK CGKNGVGVLIWKVPVSRQFAAYCYNSSDTW TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYS VASPYSTIPAPTTTPPAPASTSIPRRKKLICVTE VFMETSTMSTETEPFVENKAAFKNEAAGFGG VPTALLVLALLFFGAAAGLGFCYVKRYVKAF PFTNKNQQKEMIETKVVKEEKANDSNPNEES KKTDKNPEESKSPSKTTMRCLEAEV
1000	2350	A	8406	2	777	KERCQFVVKPMLSTVGSFLQDLQNEDKGIKT AAIFTADGNMISASTLMDILLMNDFKLVINKI AYDVQCPKREKPSNEHTAEMEHMKSLVHRL FTILHLEESQKKREHHLLEKIDHLKEQLQPLE QVKAGIEAHSEAKTSGLLWAGLALLSIQGGA LAWLTWWVYSWDIMEPVTYFITFANSMVFF AYFIVTRQDYTYSAVKSRQFLQFFHKKSKQQ HFDVQQYNKLKEDLAKAKESLKQARHSLCL QMQVEELNEKN
1001	2351	A	8410	1400	264	VGFWERPLRSSRWFRRSLRRWEMLARAARG TGALLLRGSLLASGRAPRASSGLPRNTVVLF VPQQEAWVVERMGRFHRILEPGLNILIPVLDR IRYVQSLKEIVINVPEQSAVTLDNVTLQIDGV LYLRIMDPYKASYGVEDPEYAVTQLAQTTM RSELGKLSLDKVFRERESLNASIVDAINQAAD CWGIRCLRYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKKQAQILAS EAEKAEQINQAAGEASAVLAKAKAKAEAIRI LAAALTQHNGDAAASLTVAEQYVSAFSKLA KDSNTILLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTDASLDEELDR VKMS
1002	2352	A	8421	134	941	NRENLLESRMMDPCSVGVQLRTTNECHKTY YTRHTGFKTLQELSSNDMLLLQLRTGMTLSG NNTICFHHVKIYIDRFEDLQKSCCDPFNIHKKL AKKNLHVIDLDDATFLSAKFGRQLVPGWKLC PKCTQIINGSVDVDTEDRQKRKPESDGRTAK ALRSLQFTNPGRQTEFAPETGKREKRRLTKN ATAGSDRQVIPAKSKVYDSQGLLIFSGMDLC DCLDEDCLGCTYACPACGSTKCGAECRCDRK WLYEQIBIEGGEIIHNKHAG
1003	2353	A	8427	3	1416	TEWGLSGSCPGCSPLEPGSRGRGAAAWRILR CRRLPEPSPFLTQPNLAQSQPPAPVPVTDPSVT MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEIT

SEQ ID	SEQID	1 1/1-4	Topo	Deadles	10.00	
NO: of	NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in NO:	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-		USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	1	914	ng to first	acid residue	Q=Glutamine, N=Asparagine, P=Proine,
	1	1	1214	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1	1	1	peptide	sequence	/=possible nucleotide deletion, \=possible
	1			sequence		nucleotide insertion
	<del>                                     </del>	<del>                                     </del>		1-3-4	<del></del>	SLDTENIDELLINADVALVNFYADWCRFSOM
1	1	1	1		1	LHPIFEEASDVIKEEFPNENQVVFARVDCDQH
1						SDIAQRYRISKYPTLKLFRNGMMMKREYRGQ
	-			ŀ		RSVKALADYIRQQKSDPIQEIRDLAEITTLDRS
	1			ļ	İ	KRNIIGYFEQKDSDNYRVFERVANILHDDCAF
1	1	i	1	ĺ	t	LSAFGDVSKPERYSGDNIIYKPPGHSAPDMVY
İ		ľ	1			LGAMTNFDVTYNWIQDKCVPLVREITFENGE
1 .		1		ļ		ELTEEGLPFLILFHMKEDTESLEIFQNEVARQL
		1	-		İ	ISEKGTINFLHADCDKFRHPLLHIOKTPADCP
İ		ŀ				VIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDL
}	1	ł		[	l	HSGKLHREFHHGPDPTDTAPGEQAQDVASSP
						PESSFQKLAPSEYRYTLLRDRDEL
1004	2354.	Λ	8432	910	387	GLSRKLRAGFLPGFCRVSPCGSWVVETLVKM
	1	ł		ł	1	ACAAARSPADQDRFICIYPAYLNNKKTIAEGR
		1	}			RIPISKAVENPTATEIQDVCSAVGLNVFLEKN
	1			j		KMYSREWNRDVQYRGRVRVQLKQEDGSLC
		ĺ	1			LVQFPSRKSVMLYAAEMIPKLKTRTQKTGGA
1005	0000	<del> </del>				DQSLQQGEGSKKGKGKKKK
1005	2355	A	8453	90	530	QSHETKMQSGTHWRVLGLCLLSVGVWGQD
1						GNEEMGGITQTPYKVSISGTTVILTCPQYPGSE
	1	1	,		1	ILWQHNDKNIGGDEDDKNIGSDEDHLSLKEF
		]				SELEQSGYYVCYPRGSKPEDANFYLYLRARG
1006	2356	<del>                                     </del>	0450		205	NPGLQNRYHRLFREDHSKGHSQ
1000	2330	A	8458	3	307	AVQRIRHEMNIFRLTGDLSHLAAIVILLLKIW
						KTRSCAGISGKSQLLFALVFTTRYLDLFTSFIS
	ļ	1	}			LYNTSMKVWYAIHRNVFHLQCTGLWTLNLC
1007	2357	A	8459	43	553	QLCIFN
100,	1237	\ \frac{1}{2}	0435	43	333	GAGAGGDWAAMDKLKKVLSGQDTEDRSGL .
l		{	1		,	SEVVEASSLSWSTRIKGFIACFAIGILCSLLGT VLLWVPRKGLHLFAVFYTFGNIASIGSTIFLM
1		l				GPVKQLKRMFEPTRLIATIMVLLCFALTLCSA
		ì				FWWHNKGLALIFCILQSLALTWYSLSFIPFAR
						DAVKKCFAVCLA
1008	2358	A	8462	487	150	AQDIRSVHSLGQKSTFVKHFRTLSHLHGLPDP
ļ		j				PPHWPPQERSPPSHPCMPSHRPQIPQLSNSGPS
1						DPRWGCVGPSMPTSTCLPGAVEASTTKASLP
L	<u>L</u>	1				KCPVDSSLPTPEACFL
1009	2359	A	8465	134	954	ETRVKTSLELLRTQLEPTGTVGNTIMTSQPVP
1		1				NETIIVLPSNVINFSQAEKPEPTNQGQDSLKKH
1						LHAEIKVIGTIQILCGMMVLSLGIILASASFSPN
		Ì	1		Ì	FTQVTSTLLNSAYPFIGPFFFIISGSLSIATEKRL
					ļ	TKLLVHSSLVGSILSALSALVGFIILSVKQATL
				İ		NPASLQCELDKNNIPTRSYVSYFYHDSLYTTD
			•			CYTAKASLAGTLSLMLICTLLEFCLAVLTAVL
			1	ļ		RWKQAYSDFPGSVLFLPHSYIGNSGMSSKMT
						HDCGYEELLTS
1010	2360	A	8468	2	473	KYRYRRPYPVMRKICQVGPAGLAFILNISPVA
				ł	}	HRVALCHLAGCQEQAAWYHTLQILFFLVSAY
	ŀ				ì	FFSCPVPEKYFPGSCDIVGHGHQIFHAFLSICT
					ļ	LSQLEAILLDYQGRQEIFLQRHGPLSVHMACL
	<u> </u>		<u> </u>		1	SFFFLAACSAATAALLRHKVKARLTKKDS
1011	2361	A	8478	5	409	TELSQLEKAHPPADMGRRKSKRKPPPKKKMT
				Ţ		GTLETQFTCPFCNHEKSCDVKMDRARNTGVI
				ļ	1	SCTVCLEEFQTPITCLLGNLGFFQRVGRGLESG
				1	1	PCSSGPLCALVQGQSRPEEQVPPSDFCGVRRC
			<u> </u>		1	RAGFQCQ
1012	2362	A	8481	2810	1652	RTSTQKWQSVFNDSQEHLERFYCNPENDRM
	[ [			·	i	RMKYGGQEFWADLNAMNVYETTEFDOLRR
L	L					LSTPPSSNVNSIYHTVWKFFCRDHFGWREYPE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	İ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
<b>!</b>	!	İ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	İ			peptide		/-possible nucleotide deletion, \-possible
<b>j</b>	]	ļ	}	sequence		nucleotide insertion
						SVIRLIEEANSRGLKEVRFMMWNNHYILHNS
	!	i	ľ			FFRREIKRRPLFRSCFILLPYLQTLGGVPTQAP
Į į		l	1		1	PPLEATSSSQIICPDGVTSANFYPETWVYMHP
1			1	·		SQDFIQVPVSAEDKSYRIIYNLFHKTVPEFKYR
		l	ľ			ILQILRVQNQFLWEKYKRKKEYMNRKMFGR
				]	1	DRIINERHLFHGTSQDVVDGICKHNFDPRVCG
1		ł	1	1	l	KHATMFGQGSYFAKKASYSHNFSKKSSKGV
	ĺ		1		1 '	HFMFLAKVLTGRYTMGSHGMRRPPPVNPGS
	1		i	1		VTSDLYDSCVDNFFEPQIFVIFNDDQSYPYFVI
[	1		<u> </u>	1	1	QYEEVSNTVSI
1013	2363	A	8488	2	517	IENCRTRLRQAWHEVCGNKMAAPIPQGFSCL
	1	1	1	I	I	SRFLGWWFRQPVLVTQSAAIVPVRTKKRFTP
		1		1	1	PIYQPKFKTEKEFMQHARKAGLVIPPEKSDRS
1	1	ł		į .		IHLACTAGIFDAYVPPEGDARISSLSKEGLIER
			1	1		TERMKKTMASQVSIRRIKDYDANFKIKDFPE
					]	KAKDIFIEGSPLY
1014	2364	A	8501	363	17	YIRTGYVYICIIYAQLMYTYYIRTAYVYICILY
101,	250.	1		500	[	AOLMYTYVLYTHSLCIHMYSIRTAYVYICIIY
ļ	,	ľ	1	1	·	AQIMYTYVFYTHRLCIHMYSIRTDYVYICILY
J			1	ļ	Į	AQLMYTYVFYTHSYMSDE
1015	2365	A	8504	3	2190	NSSEHFSQAPQRLSFYSWYGSARLFRFRVPPD
10.5	2505	1 1	000.	1		AVLLRWLLOVSRESGAACTDAEITVHFRSGA
Ī	i					PPVINPLGTSFPDDTAVQPSFQVGVPLSTTPRS
	İ		]			NASVNVSHPAPGDWFVAAHLPPSSQKIELKG
1	1		İ			LAPTCAYVFQPELLVTRVVEISIMEPDVPLPQ
ŀ		1			1	TLLSHPSYLKVFVPDYTRELLLELRDCVSNGS
1	l	1			ł	LGCPVRLTVGPVTLPSNFQKVLTCTGAPWPC
1		1				RLLLPSPPWDRWLQVTAESLVGPLGTVAFSA
<u> </u>	-		1			VAALTACRPRSVTIQPLLQSSQNQSFNASSGL
1	1		İ	ł	ł	LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRED
ł		1	ļ	ł	}	MDVVSVHFQPLDRVSVRVCSDTPSVMRLRL
	1	1	Ì			NTGMDSGGSLTISLRANKTEMRNETVVVACV
		j	1	ļ		NAASPFLGFNTSLNCTTAFFQGYPLSLSAWSR
ł	i	i	İ	ĺ	i	RANLIPYPETDNWYLSLQLMCPENAEDCEQ
	Ĭ		Ì	ļ		AVVHVETTLYLVPCLNDCGPYGQCLLLRRHS
Į.				1	İ	YLYASCSCKAGWRGWSCTDNSTAQTVAQQR
İ			1	1		AATLLLTLSNLMFLAPIAVSVRRFFLVEASVY
i •	l .		1	ĺ	Ì	AYTMFFSTFYHACDQPGEAVLCILSYDTLQY
1	İ				1	CDFLGSGAAIWYTILCMARLKTVLKYVLFLL
1	1	1	1	į		GTLVIAMSLOLDRRGMWNMLGPCLFAFVIM
1		1	1	1		ASMWAYRCGHRRQCYPTSWQRWAFYLLPG
		1	1	1		VSMASVGIAIYTSMMTSDNYYYTHSIWHILL
1		1	1	1	1	AGSAALLLPPPDQPAEPWACSQKFPCHYQIC
}	1	1	1	!	1	KNDREELYAVT
1015	10000	<del>   </del>	9511	<del>                                     </del>	453	KWYPSOPVRIPGRFYYKLPAGHRRCRMAPAK
1016	2366	Α	8511	1.	455	
1	1	1	1	1	ł	KGGEKKKGRSAINEVVTREYTINIHKRIHGVG
<b>!</b> .	1	1		1		FKKRAPRALKEIRKFAMKEMGTPDVRIDTRL
1		1	1	l .	1	NKAVWAKGIRNVPYRIRVRLSRKRNEDEDSP
		1	1	<del> </del>	<u> </u>	NKLYTLVTYVPVTTFKNLQTVNVDEN
1017	2367	A	8513	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINT
1		1			1	LSAKWADNFMAEGCGGSKEHSFQHPFLQAV
	1	1		1	1	GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPQ
	(	1	1	1		QPFNPLLFLPPALCDMTGTSLMYVALNMTSA
	1	1	Į.	1		SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL
	1					
		1	1		1	GILATIAGLVVVGLADLLSKIIDSQHKLSEVIT
					1	GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR
						GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR AVGTEGLFGFVILSLLLVPMYYIPAGSFSGNP
						GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D-Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion SLALGWEAFHALQULGFLULLIGTALYNGLHR PLLGRLSRGRPLAEESEQERLLGGTRTPINDA S
1018	2368	A	8518	324	694	SPFWTEKRRMEKPLFPLVPLHWPGFGYTALV VSGGIVGYVKTGSVPSLAAGLLFGSLAGLGA YQLYQDPRNVWGFLAATSVTFVGVMGMRS YYYGKFMPVGLIAGASLLMAAKVGVRMLM TSD
1019	2369	A	8526	2	1787	VSAAAVNMEPPDAPAQARGAPRLILLAVIL AAHPDAQAEVRLSVPPLVEVMRGKSVILDCT PTGTHDHYMLEWFLTDRSGARPRLASAEMQ GSELQVTMHDTRGRSPPYQLDSQGRLVLAEA QVGDERDYVCVVRAGAAGTAEAAARLNVF AKPEATEVSPNKGTLSVMEDSAQEIATSNSRN GNPAPKITWYRNGQRLEVPVEMNPEGYMTS RTVREASGLLSLTSTLYLRLRKDDRDASFHC AAHYSLPEGRHGRLDSPTFHLTLHYPTEHVQ FWVGSPSTPAGWVREGDITVQLLCRGDGSPSP EYTLFRLQDEQEEVLNVNLEGNLTLEGVTRG QSGTYGCRVEDYDAADDVQLSKTLELRVAY LDPLELSEGKVLSLPLNSRAVVNCSVHGLPTP ALRWTKDSTPLGDGPMLSLSSITPDSNGTYVC EASLPTVPVLSRTQNFTLLVQGSPELKTAEIEP KADGSWREGDEVTLICSARGHPDPKLSWSQL GGSPAEPIPGRQGWVSSSLTLKVTSALSRDGI SCEASNPHGNKRHVFHFGTVSPQTSQAGVAV MAVAVSVGLLLLVVAVFYCVRRKGGPCCRQ RREKGAP
1020	2370	A	8530	2	1200	PRVRLIRPSRSRSCRGLLSTRAPGPSPFRSLHS SPLLPHAMKSPFYRCQNITTSVEKGNSAVMGG VLFSTGLLGNLLALGLLARSGLGWCSRRPLR PLPSVFYMLVCGLTVTDLLGKCLLSPVVLAA YAQNRSLRVLAPALDNSLCQAFAFFMSFFGL SSTLQLLAMALECWLSLGHPFFYRRHITLRLG ALVAPVVSAFSLAFCALPFMGFGKFVQYCPG TWCFIQMVHEEGSLSVLGYSVLYSSLMALLV LATVLCNLGAMRNLYAMHRRLQRHPRSCTR DCAEPRADGREASPQPLEELDHLLLALMTV LFTMCSLPVIYRAYYGAFKDVKEKNRTSEEA EDLRALRFLSVISIVDPWIFIFFSPVFRIFFHKI FIRPLRYRSRCSNSTNMESSL
1021	2371	A	8536	1	237	RRGEIDMATEGDVELELETETSGPERPPEKPR KHDSGAADLERVTDYAEEKEIQSSNLETAMS VIGDRRSREQKAKQER
1022	2372	A	8537	94	541	RKERRRRRMEAVFVFSLLDCCALIFLSV YFITLSDLECDYINARSCCSKLNKWVIPELIG HTIVTVLLLMSLHWFIFLLNLPVATWNIYRYI MVPSGNMGVFDPTEIHNRGQLKSHMKEAMI KLGFHLLCFFMYLYSMILALIND
1023	2373	A	8540	26	431	RMMKCPQALLAIFWLLLSWYSSEDKVVQSPL SLVVHEGDTVTLNCSYEVTNFRSLLWYKQEK KAPTFLFMLTSSGIEKKSGRLSSILDKKELSSIL NITATQTGDSAIYLCAVEAQCSLVTCSLYSNS TAEALOL
1024	2374	A	8544	1731	743	GVRLRYSPIAVVMVGEAGRDLRRRRAVAVT AEKMAVLAPLIALVYSVPRLSRWLAQPYYLL SALLSAAFLLVRKLPPLCHGLPTQREDGNPCD FDWREVEILMFLSAIVMMKNRRSITVEQHIGN IFMFSKVANTILFFRLDIRMGLLYITLCIVFLM

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F-Phenylalanine, G-Glycine, H-Histidine,
cotide	seq-		USSN 09/496	location	corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
seq- uence	uence		914	correspondi ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	}		714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
			ļ	sequence		nucleotide insertion
	ł	Ì			ĺ	TCKPPLYMGPEYIKYFNDKTIDEELERDKRVT WIVEFFANWSNDCQSFAPIYADLSLKYNCTG
	İ					LNFGKVDVGRYTDVSTRYKVSTSPLTKQLPT
			]			LILFOGGKEAMRRPOIDKKGRAVSWTFSEEN
			İ			VIREFNLNELYQRAKKLSKAGDNIPEEQPVAS
					l	TPTTVSDGENKKDK
1025	2375	Α	8546	2194	1707	TVSFHKTMASLKCSTVVCVICLEKPKYRCPA
				l	ľ	CRVPYCSVVCFRKHKEQCNPETRPVEKKIRS
			}		]	ALPTKTVKPVENKDDDDSIADFLNSDEEEDR VSLONLKNLGESATLRSLLLNPHLRQLMVNL
Ì						DOGEDKAKLMRAYMQEPLFVEFADCCLGIV
						EPSQNEES
1026	2376	Α	8547	1078	594	VGMELPAVNLKVILLGHWLLTTWGCIVFSGS
1	ŀ	1	1		1	YAWANFTILALGVWAVAQRDSIDAISMFLGG
1						LLATIFLDIVHISIFYPRVSLTDTGRFGVGMAIL
			1		]	SLLLKPLSCCFVYHMYRERGGELLVHTGFLG SSQDRSAYQTIDSAEAPADPFAVPEGRSQDAR
		į				GY
1027	2377	A	8557	1	340	DFLGPASPQEEGGSESSTMTELETAMGMIIDV
		- "		_		FSRYSGSEGSTQTLTKGELKVLMEKELPGFLQ
						SGKDKDAVDKLLKDLDANGDAQVDFSEFIVF
						VAAITSACHKYFEKAGLK
1028	2378	A	8569	20	963	KMAATLGPLGSWQQWRRCLSARDGSRRLLL
						LLLLGSGQGPQQVGAGQTFEYLKREHSLSKP YQGEAPRPCFLRDWELQVHFKIHGQGKKNL
ļ						HGDGLAIWYTKDRMQPGPVFGNMDKFVGLG
						VFVDTYPNEEKQQERVFPYISAMYNNGSLSY
İ		1				DHERDGRPTELGGCTAIVRNLHYDTFLVIRY
1						VKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
1						YYFGTSSITGDLSDNHDVISLKLFELTVERTPE
		j		]	1	EEKLHRDVFLPSVDNMKLPEMTAPLPPLSGL ALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK
			1	1		RFY
1029	2379	A	8572	1	578	AAAASHRSRARSRPRRVSSGPAPRRAQSSAG
						RVASGLDSAPLCTMARALCRLPRRGLWLLLA
	}			1		HHLFMTTACQEANYGALLRELCLTQFQVDM
		İ				EAVGETLWCDWGRTIRSYRELADCTWHMAE
		ì				KLGCFWPNAEVDRFFLAVHGRYFRSCPISGR   AVRDPPGSILYPFIVVPITVTLLVTALVVWQS
	į		1			KRTEGIV
1030	2380	A	8574	1352	372	DSSTVKGGSESRHLCLIPDLKGKARTREASSG
					1	SRTCGRRTSLCTSAKSSWTYRSGRLSWQSIKG
		1				THLTITQALRQPLHRAPLLPGQLCWSPRPLEK
						NKAMGRPLLLPLLLLQPAFLQPGGSTGSGP
		1	1	{		SYLYGVTQPKHLSASMGGSVEIPFSFYYPWEL AIVPNVRISWRRGHFHGOSFYSTRPPSIHKDY
-	,	}	1			VNRLFLNWTEGQESGFLRISNLRKEDQSVYF
					1	CRVELDTRRSGRQQLQSIKGTKLTITQAVTIT
		1				TTWRPSSTTTIAGLRVTESKGHSESWHLSLDT
						AIRVALAVAVLKTVILGLLCLLLLWWRRRKG
		<u> </u>	<u> </u>		<u> </u>	SRAPSSDF
1031	2381	A	8580	905	340	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQL
	1	1		]		AFDDFQESCAMMWQKYAGSRRSMPLGARIL FHGVFYAGGFAIVYYLIOKFHSRALYYKLAV
	1			1		EQLQSHPEAQEALGPPLNIHYLKLIDRENFVDI
	1					VDAKLKIPVSGSKSEGLLYVHSSRGGPFQRW
					1	HLDEVFLELKDGQQIPVFKLSGENGDEVKKE
1032	2382	A	8593	2558	961	RRRPRLLPGAEPCEPRVGPRRADMGCSAKAR
	<u> </u>	<u> </u>	<u></u>	<u> </u>	L	WAAGALGVAGLLCAVLGAVMIVMVPSLIKQ

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, B=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  QVLKNVRIDPSSLSFNMWKEIPIPFYLSVYFPD  VMNPSEILKGEKPQVRERGPYVYREFRHKSNI
1022	7307		9606	606		TFNNNDTVSFLEYRTFQFQPSKSHGSESDYIV MPNILVLGAAVMMENKPMTLKLIMTLAFTTL GERAFMNRTVGEIMWGYKDPLVNLINKYFP GMFPFKDKFGLFAELNNSDSGLFTGFTGVQNI SRIHLVDKWNGLSKVDFWHSDQCNMINGTS GQMWPFPMTPESSLEFYSPŁACRSMKLMYKE SGVFEGIPTYRFVAPKTLFANGSIYPPNEGFCP CLESGIQNVSTCRFSAPLFLSHPHFLNADPVL AEAVTGLHPNQEAHSLFLDHPVTGIPMNCSV KLQLSLYMKSVAGIGQTGKIEPVVLPLLWFA ESGAMEGETLHTFYTQLVLMPKVMIHYAQYV LLALGCVLLLVPVICQIRSQEKCYLFWSSSKK GSKDKEAIQAYSESLMTSAPKGSVLQEAKL
1033	2383	A	8595	595	767	AHLPDTLLLPPHSPTVPTPKSFQCSQKACFSRS FCLLLSLVSSSLVSLSLCPPLTQA
1034	2384	Α	8597	640	164	VTTSCIIPFAFGLGVRASERLAEIDMPYLLKYQ PMMQTIGQKYCMDPAVIAGVLSRKSPGDKIL VNMGDRTSMVQDPGSQAPTSWISESQVFQTT EVLTTRITELQRRFPTWTPDQYLRGGLCAYSG GAGYVRSSQDLSCDFCNDVLARAKYLKRHG F
1035	2385	A	8603	936	204	AMASTLEYSPSPLRRLVGPAAGFSRAARADL SWDPMAFFTGLWGPFTCVSRVLSHHCFSTTG SLSAIQKMTRVRVVDNSALGNSPYHRAPRCI HVYKKNGVGKVGDQILLAIKGQKKKALIVG HCMPGPRMTPRFDSNNVVLIEDNGNPVGTRI KTPIPTSLRKREGEYSKVLAIAQNFV
1036	2386	Α	8606	1	562	PTRAHSFDLCCSPCRRRLLGREEAGEEPTSPV TQYLQPRSPEECKMFACAKLACTPSLIRAGSR VAYRPISASVLSRPEASRTGEGSTVFNGAQNG VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLILFAM
1037	2387	A	8615	2	2364	SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDIINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNIHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT GHICLSLEQVLGEGWEGICRIAPACPSTPPPPS

WO 01/57188 PCT/US01/03800

CODOTO	SEQ ID	Mai	T C D A	Dendicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	Met hod	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1		[	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ		İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide		/=possible nucleotide deletion, \=possible
				sequence	ł	nucleotide insertion
				<del>                                     </del>		SDVPGPASCPRLFPPWDLLPVSTVAADDHVGI
			ļ		İ	EAL
1038	2388	A	8621	3	1494	RSRMARAPLGVLLLLGLLGRGVGKNEELRLY
		_		_	-	HHLFNNYDPGSRPVREPEDTVTISLKVTLTNL
		ļ				ISLNEKEETLTTSVWIGIDWQDYRLNYSKDDF
		İ		ŀ		GGIETLRVPSELVWLPEIVLENNIDGQFGVAY
	1	l	}		į	DANVLVYEGGSVTWLPPAIYRSVCAVEVTYF
1				1		PFDWQNCSLIFRSQTYNAEEVEFTFAVDNDG
						KTINKIDIDTEAYTENGEWAIDFCPGVIRRHH
ĺ	1		ĺ	[	1	GGATDGPGETDVIYSLIIRRKPLFYVINIIVPCV
ŀ			1		]	LISGLVLLAYFLPAQAGGQKCTVSINVLLAQT
}			Ì			VFLFLIAQKIPETSLSVPLLGRFLIFVMVVATLI
ĺ		l		1		VMNCVIVLNVSQRTPTTHAMSPRLRHVLLEL
1	1			1		LPRLLGSPPPPEAPRAASPPRRASSVGLLLRAE
			ľ			ELILKKPRSELVFEGQRHRQGTWTAAFCQSL
		ļ	}			GAAAPEVRCCVDAVNFVAESTRDQEATGEE
		1		,		VSDWVRMGNALDNICFWAALVLFSVGSSLIF
<u> </u>		<u>L</u>	1			LGAYFNRVPDLPYAPCIQP
1039	2389	A	8636	1	900	PGRERPGGGGARRRPQHLPALLPSERPDCATL
		l	1	1		QAMENELPVPHTSSSACATSSTSGASSSSGCN
		1	ĺ		·	NSSSGGSGRPTGPQISVYSGIPDRQTVQVIQQ
		1	İ	l .	ļ	ALHRQPSTAAQYLQQMYAAQQQHLMLQTA
		1			i	ALQQHLSSAQLQSLAAVQQASLVSNRQGST
ł	1	ľ	ł		ĺ	SGSNVSAQAPAQSSSINLAASPAAAQLLNRA
				ł		QSVNSAAASGIAQQAVLLGNTSSPALTASQA   QMYLRAQMLIFTPTATVATVQPELGTGSPAR
		]		j	ļ	PPTPAQVQNLTLRTQQTPAAAASGPTPTQPVL
			ľ		İ	PSLALKPTPGGSQPLPTPA
1040	2390	Α	8645	98	1388	ASQLAFGGKLTSTPSRDFQGCGRGAVTCCSF
1010	2370	1	0043	"	1500	HEHRHOSGRCLSTGMAPNLKGRPRKKKPCPO
l		1	1	1		RRDSFSGVKDSNNNSDGKAVAKVKCEARSA
						LTKPKNNHNCKKVSNEEKPKVAIGEECRADE
			1			QAFLVALYKYMKERKTPIERIPYLGFKQINLW
1		ĺ				TMFOAAOKLGGYETITARROWKHIYDELGG
1						NPGSTSAATCTRRHYERLILPYERFIKGEEDKP
	Ì	1				LPPIKPRKQENSSQENENKTKVSGTKRIKHEIP
				1		KSKKEKENAPKPQDAAEVSSEQEKEQETLISQ
1	1	1		[	[	KSIPEPLPAADMKKKIEGYQEFSAKPLASRVD
-		1	1	1		PEKDNETDQGSNSEKVAEEAGEKGPTPPLPSA
}	1	1	l	1		PLAPEKDSALVPGASKQPLTSPSALVDSKQES
	1					KLCCFTESPESEPQEASFPRLPHHTGHRWQTR
		L				MRRRMTNCPPWQITLPTAP
1041	2391	A	8646	113	1492	LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYP
1	1	1	}	1		GIKARITQRALDYGVQAGMKMIEQMLKEKK
		1		1		LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP
				1		NTSLAFVPGVGIKALTNHGTANISTDWGFESP
	1	ſ	1	<b>[</b>	!	LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVK
			1		ĺ	ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE
		1	ĺ	1		NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER
		}	J	J		SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS
	1	[				TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM
		l	-		1	VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK
	ł	l		1		NSTVETIVSMDFVASTSVGLVILGQRLVCSLS
				1	1	LNRFRLALPESNRSNIEVLRFENILSSILHFGVL
				1		PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF
		1				LLISTDLKYETSSKQQPSFHVWEGLNLISRQW
			<u> </u>	L		RGKSAP
1042	2392	A	8672	538	170	ARRIARTRESKAAVSQDNVPALQPGKKKKLR
	1	L	1		1	LGGKKKKFKFFRLPKEFKKQLMYSPSNFKKM

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  TSLAGNTVQCLNKLKYVIYSAQYPAYGNITT LDMITSTDHVLEQDFWICFTFYSVKERQI
1043	2393	·A	8688	359	17	GLKTRAPATPITPQREVLGPAKQDMQRRCPRI GLMTSLLKPIKRRWRDYKRWKSGGFTGESC HHADTLGDRGGLQGDHSELLQWQKRILRTE GEPSPKYISKNIPPICSYITGFL
1044	2394		8718	292	1490	GTVKTSVATPITAGHSCSSGGVLQVKSPATQS GFKFTSKMEDFNMESDSFEDFWKGEDLSNYS YSSTLPPFLLDAAPCEPESLEINKYFVVIIYAL VFLLSLLGNSLVMLVILYSRVGRSVTDVYLL NLALADLLFALTLPIWAASKVNGWIFGTFLC KVVSLLKEVNFYSGILLACISVDRYLAIVHA TRILTQKRYLVKFICLSIWGLSLLLALPVLLFR RTYYSSNVSPACYEDMGNNTANWRMLLRIL POSFGFIVPLLIMLFCYGFTLRTLFKAHMGQK HRAMRVIFAVVLIFLLCWLPYNLVLLADTLM RTQVIQETCERRNHIDRALDATEILGILHSCLN PLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDS
1045	2395	A	8724	254	·	RPSFVGSSSGHTSTIL  FRANLAITVANRRGAQGKMHTCCPPVTLEQ DLHRKMHSWMLQTLAFAVTSLVLSCAETIDY YGEICDNACPCEEKDGILTVSCENRGIISLSEIS PPRFPIYHLLLSGNLLNRLYPNEFVNYTGASIL HLGSNVIQDIETGAFHGLRGLRR.HILNNNKL ELLRDDTFLGLENLEYLQVDYNYISVIEPNAF GKLHLLQVLILNDNLLSSLPNNLFRFVPLTHL DLRGNRLKLLPYVGLLQHMDKVVELQLEEN PWNCSCELISLKDWLDSISYSALVGDVVCETP FRLHGRDLDEVSKQELCPRRLISDYEMRPQTP LSTTGYLHTTPASVNSVATSSSAVYKPPLKPP KGTRQPNKPRVRPTSRQPSKDLGYSNYGPSIA YQTKSPVPLECPTACSCNLQISDLGLNVNCQE RKIESIAELQPKPYNPKKMYLTENYIAVVRRT DLLEATGLDLLHLGNNRISMIQDRAFGDLTN LRRLYLNGNRIERLSPELFYGLQSLQYLFLQY NLIREIQSGTFDPVPNLQLLFLNNNLLQAMPS GVFSGLTLLRLNLRSNHFTSLPVSGVLDQLKS LIQIDLHDNPWDCTCDIVGMKLWVEQLKVG VLVDEVICKAPKKFAETDMRSIKSELLCPDYS DVVVSTPTPSSIQVPARTSAVTPAVRLNSTGA PASLGAGGGASSVPLSVLILSLLLVFIMSVFVA AGLFVLVMKRRKKNQSDHTSTNNSDVSSFN MQYSVYGGGGGTGGHPHAHVHHRGPALPK VKTPAGHVYEYIPHPLGHMCKNPIYRSREGN SVEDYKDLHELKVTYSSNHHLQQQQQPPPPP QQPQQPPPQLQLQPGEEERRESHHLRSPAYS VSTIEPREDLLSPVQDADRFYRGILEPDKHCST TPAGNSLPEYPKFPCSPAAYTFSPNYDLRPH QYLHPGAGDSRLREPVLYSPNSAVFVEPNRNE
1046	2396	A	8736	28	452	YLELKAKLNVEPDYLEVLEKQTTFSQF SPSAAGGLAWVSLALGSGSRGRDHSGSGVGT AMAGALVRKAADYVRSKDFRDYLMSTHFW GPVANWGLPIAAINDMKKSPEIISGRMTFALC CYSLTFMRFAYKVQPRIWLLFACHATNEVA
1047		A		673	924	QLIQGGRLIKHEMTKTASA  ALPGTPQQTVTLNTDGKVKSFTSPHSNPNLPP AKFFTSLQSLNWSSHLPPSPATESVGKRGNAK PPTTKLLHSSPLWNFFAQQL
1048	2398	A	8747	3	5054	PEVTKPSLSQPTAASPIGSSPSPPVNGGNNAKR

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq-uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, B=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide deletion, \=possible nucleotide deletion, \=possible nucleotide insertion VAVPNGGPFSAARYMPREVPPRFRCQQDHK VLLKRGQPPPPSCMLLGGGAGPPPCTAPGAN PNNAQVTGALLQSESGTAPDSTLGGAAASNY ANSTWGSGASSNNGTSPNPHHIWDKVIVDGS DMBEWPCIASKDTESSENTTDNNSASNPGSE KSTLPGSTTSNKGKGSQCQSASSGNECNLGV WKSDPKAKSVQSSNSTTENNNGLGNWRNVS GQDRIGPGSGFSNFNPNSNPSAWPALVQEGTS RKGALETDNSNSSAQVSTVGGTSRQQSKME NAGVNFVVSGREQAQHHNTDGPKNGNTNSL NLSSPNPMENKGMPFGMGLGNTSRSTDAPSQ STGDRKTGSVGSWGAARGPSGTDTVSGQSNS GNNGNNGKEREDSWKGASVQKSTGSKNDS WDNNNRSTGGSWNFGPQDSNDNKWGEGNK MTSGVSQGEWKQPTGSDELKIGEWSGPNQPN SSTGAWDNQKGHPLLENQGNAQAPCWGRSS SSTGSEVEGQSTGSNHKAGSSDSHNSGRSY RPTHPDCQAVLQTLLSRTDLDPRVLSNTGWG QTQIKQDTVWDIEEVPRPEGKSDKGTEGWES AATQTKNSGGWGDAPSQSNQMKSGWGELS ASTEWKDPKNTGGWNDYKNNSSNWGGGR PPEKTPSSWNENPSKDQGWGGGRQPNQGWS SGKNGWGEEVDQTKNSNWESSASKPVSGWG EGQNEIGTWGNGGNASLASKGGWEDCKRS, PAWNETGRQPNSWNKQHQQQQPPQQPPPQ PPASGSWGGPPPPPGNVRPSNSSWSSGPQPA TPKDEEPSGWEEPSPQSISRKMDIDDGTSAWG DPNSYNYKNVNLWDKNSQGGPAPREPNLPTP MTSKSASDSKSMQDGWGESDCPYTGARHPS WEEEEDGGVWNTTGSQGSASSHNSASWGQG GKKQMKCSLKGGNNDSWMNPLAKQFSNMG LLSQTEDNPSSKMDLSVGSLSDKKFDVPKRA MNLIGDFNDIMRKDRSGFRPPNSSDWSSGPPP SSPLRAQVPPQFISPQVSASMLKQFPNSGLSP GLFNVGPQLSPQQLAMLSQLPQIPGFQLACQL LLQQQQQLLQNQRKGSQSNCPYSGLPP SSPLRAQVPPQFISPQVSASMLKQFPNSGLSP GLFNVGPQLSPQQAMPGKSGASTHNSASWGQG GKKQMKCSLKGGNNDSWMNPLAKQFSNMG LLSQTEDNPSSKMDLSVGSLSDKKFDVFRA MNLGDFNDIMRKDRSGFRPPNSKDMGTTDS GPYFEKGSHGLFGNSTAQSRGLHTPVQPLN SSPSLRAQVPPQFISPQVSASMLKQFPNSGLSP GLFNVGPQLSPQQAPQFGMKHSPSHPVGFK PHLDNMVPNALNVGLPDLQTKGPIPGYGSGF SSGGMDYGMVGGKEAGTESRFKQWTSMME GLPSVATQEANMHKNGAIVAPGSPSYWLVLHN LTPQIDGSTLRTICMQHGFLLTFHLNLTQGTA LIRYSTKQEAAKAQTALHMCVLGNTTILAEF ATDDEVSRFLAQAQPPTPAATPSAPAAGWQS
						LTPQIDGSTLRTICMQHGPLLTFHLNLTQGTA LIRYSTKQEAAKAQTALHMCVLGNTTILAEF ATDDEVSRFLAQAQPPTPAATPSAPAAGWQS LETGQNQSDPVGPALNLFGGSTGLGQWSSSA
						GGSSGADLAGASLWGPPNYSSSLWGVPTVED PHRMGSPAPLLPGDLLGGGSDSI
1049	2399	A	8748	200	1387	VPWKRQDEQLSLQVETLYLDSPAVIHLLSPTF LPPSSLPPFLQIVDSSSSACTLDSFFPFLAPWDS PQDCGFKDHQPLTLQALTVELARWTLMLLLS TAMYGAHAPLLALCHVDGRVPFRPSSAVLLT ELTKLLLCAFSLLVGWQAWPQGPPPWRQAA PFALSALLYGANNNLVIYLQRYMDPSTYQVL

	SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	
	NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
	nucl-	peptide	1105	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid,
	eotide	seq-	1	USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
	seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
	uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
					residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ			1		peptide		/=possible nucleotide deletion, \=possible
			1	1	sequence	[	nucleotide insertion
ı						<del> </del>	SNLKIGSTAVLYCLCLRHRLSVRQGLALLLL
ļ		!	1.	<b>!</b> .	!	}	MAAGACYAAGGLQVPGNTLPSPPPAAAASP
-							MPLHITPLGLLLLILYCLISGLSSVYTELLMKR
-			ŀ	i			QRLPLALQNLFLYTFGVLLNLGLHAGGGSGP
-			1			•	GLLEGFSGWAALVVLSQALNGLLMSAVMKH
- 1		ļ	j			}	GSSITRLFVVSCSLVVNAVLSAVLLRLQLTAA
l			1			ļ	FFLATLLIGLAMRLYYGSR
	1050	2400	A	8758	3	1660	WVSSMGFEELLEQVGGFGPFQLRNVALLALP
- 1			l			1	RVLLPLHFLLPIFLAAVPAHRCALPGAPANFS
			İ				HQDVWLEAHLPREPDGTLSSCLRFAYPQALP
١							NTTLGEERQSRGELEDEPATVPCSQGWEYDH
-			1				SEFSSTIATESQWDLVCEQKGLNRAASTFFFA
1			l			l	GVLVGAVAFGYLSDRFGRRRLLLVAYVSTLV
- {			l	1		1	LGLASAASVSYVMFAITRTLTGSALAGFTIIV
- [							MPLELEWLDVEHRTVAGVLSSTFWTGGVML
- 1			1	1		1 -	LALVGYLIRDWRWLLLAVTLPCAPGILSLWW
ļ						ĺ	VPESARWLLTQGHVKEAHRYLLHCARLNGR
							PVCEDSFSQEAVSKVAAGERVVRRPSYLDLF
-			[	[			RTPRLRHISLCCVVVWFGVNFSYYGLSLDVS
-			l	] :		İ	GLGLNVYQTQLLFGAVELPSKLLVYLSVRYA
-	•					ŀ	GRRLTQAGTLLGTALAFGTRLLVSSDMKSWS
	:						TVLAVMGKAFSEAAFTTAYLFTSELYPTVLR
Í			[	1 1			QTGMGLTALVGRLGGSLAPLAALLDGVWLS
			İ				LPKLTYGGIALLAAGTALLLPETRQAQLPETI
L						ľ	QDVERKSAPTSLQEEEMPMKQVQN
	1051	2401	A	8759	515	1625	EIRTPVAVSSAPSGDSEGDEEETTQDEVSSHTS
1							EEDGGVVKVEKELENTEQPVGGNEVVEHEV
1	i		}	1.			TGNLNSDPLLELCQCPLCQLDCGSREQLIAHV
1							YQHTAAVVSAKSYMCPVCGRALSSPGSLGR
1	1						HLLIHSEDQRSNCAVCGARFTSHATFNSEKLP
	ĺ						EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYP
1	1						AGILLVCNNCAAYRKLLEAQTPSVRKWALRR
1	· 1						QNEPLEVRLQRLERERTAKKSRRDNETPEERE
1							VRRMRDREAKRLQRMQETDEQRARRLQRDR
1	- 1						EAMRLKRANETPEKROARLIREREAKRLKRR
	1			1 1			LEKMDMMLRAQFGQDPSAMAALAAEMNFF
1	1052	2402	A	970	110/		QLPVSGVELDSQLLGKMAFEEQNSSSLH
1	1032	2402	A	8763	1106	70	RHGHGGRDRRGGGRVARPGGLGRYPGRGAA
1	- 1						ASLVFVPTRRRSGPSGTASVAAMAYHSGYGA
				]			HGSKHRARAAPDPPPLFDDTSGGYSSQPGGY
1	l						PATGADVAFSVNHLLGDPMANVAMAYGSSI
1	ļ	l				ĺ	ASHGKDMVHKELHRFVSVSKLKYFFAVDTA
						ļ	YVAKKLGLLVFPYTHQNWEVQYSRDAPLPP
	}	ł				ļ	RQDLNAPDLYIPTMAFITYVLLAGMALGIQK
1	ĺ	l				1	RFSPEVLGLCASTALVWVVMEVLALLLGLYL
ļ		I				1	ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL
1		ľ				1	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL
1	1	l					GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY
H	1053	2403	A	8768	<del></del>	712	WLTFHLVR
		2703	'n	0/00	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVF
	- 1	i				!	YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW
1	- 1	- 1					PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE
1		1				- 1	VLMDCAHLVKANSIQGCKMNNVNVVYTPW
1		ſ				i	SNLKKTADMDVGQIGFHRQKDVKIVTVEKK
1	- 1	ļ	1			j	VNEILNRLEKTKVERFPDLAABKECRDREER
1		- 1	Į		ļ	1	NEKKAQIQEMKKREKEEMKKKREMDELRSY
F	1054	2404	A	8769	344	527	SSLMKVENMSSNQDGNDSDEFM
ı		1- <del>1</del> 01	^	0/03	J <del>44</del>	527	REATTLACRNSCWVFSRCSLGACKPTVCSMP
Ļ		J.					SLSRQGSQTLCLRLAEYCMESVDSQRLLLS

- OTO 17	T OF C TO	111	LODO	Dundietad	Dendisted and	Amino acid sequence (A=Alanine O=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	denoc		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
denoc	ļ	Į	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
j	i .	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		peptide	1 •	/=possible nucleotide deletion, \=possible
Ì		1		sequence		nucleotide insertion
1055	2405	A	8770	430	1104	QQESPAAGAARMNCKEGTDSSCGCRGNDEK
				[		KMLKCVVVGDGAVGKTCLLMSYANDAFPEE
İ			1			YVPTVFDHYAVTVTVGGKQHLLGLYDTAGQ
			1	İ		EDYNQLRPLSYPNTDVFLICFSVVNPASYHNV
<u> </u>	ļ	,				QEEWVPELKDCMPHVPYVLIGTQIDLRDDPK
Ì		1			1	TLARLLYMKEKPLTYEHGVKLAKAIGAQCYL
ł	1			1		<b>ECSALTQKGLKAVFDEAILTIFHPKKKKKKRCS</b>
	1	ļ	Ì	İ		EGHSCCSII
1056	2406	Α	8773	261	332	NPRIQLSGNSCCAGSCRVWLSEQ
1057	2407	A	8778	3	477	PAGIRHEQARGADRMGKCRGLRTARKLRSH
1		l			1	RRDQKWHDKQYKKAHLGTALKANPFGGAS
	]					HAKGIVLEKVGVEAKQPNSAIRKCVRVQLIK
1		1				NGKKITAFVPNDGCLNFIEENDEVLVAGFGR
İ		1	1	1	1	KGHAVGDIPGVRFKVVKVANVSLLALYKGK
	<u> </u>	<u> </u>				KERPRS
1058	2408	A	8808	171	881	PGLSQEPSGSMETVVIVAIGVLATIFLASFAAL
Į		-				VLVCRQRYCRPRDLLQRYDSKPIVDLIGAME
			1 .		İ	TQSEPSELELDDVVITNPHIEAILENEDWIEDA
1	ĺ	1	1	1		SGLMSHCIAILKICHTLTEKLVAMTMGSGAK
	1					MKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
	1	1	}	,		DPKLLDARTTALLLSVSHLVLVTRNACHLTG
1					1	GLDWIDQSLSAAEEHLEVLREAALASEPDKG
						LPGPEGFLQEQSAI
1059	2409	A	8809	246	757	MRLQGAIFVLLPHLGPILVWLFTRDHMSGWC
		1	1 .			EGPRMLSWCPFYKVLLLVQTAIYSVVGYASY
İ		1		1		LVWKDLGGGLGWPLALPLGLYAVQLTISWT
ļ	1	l	ļ		1	VLVLFFTVHNPGLALLHLLLLYGLVVSTALI
			Ī			WHPINKLAALLLLPYLAWLTVTSALTYHLWR
1000-	2410	<del>  </del>	8810	304	381	DSLCPVHQPQPTEKSD PKLSVYPLQSHHCLSEPFQSLVCCLA
1060 1061	2410	A	8820	1673	848	SCKTENLLEMWWFQQGLSFLPSALVIWTSAA
1001	2411	^	0020	10/3	1 646	FIFSYITAVTLHHIDPALPYISDTGTVAPEKCLF
						GAMLNIAAVLCIATIYVRYKQVHALSPEENVI
1			1	İ		IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA
						HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH
ļ			]	-		GKOVFWIRLLLVIWCGVSALSMLTCSSVLHS
ł		1		l		GNFGTDLEQKLHWNPEDKGYVLHMITTAAE
		1				WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL
1						TLYDTAPCPINNERTRLLSRDI
1062	2412	A	8824	1	763	GGAPPASVPARESPVSGAOGSSRTRGHKRAA
1002		1	1	1.	'	GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA
1		1	1	1		YSLAPATPEVKVACSEDVDLPCTAPWDPOVP
		i				YTVSWVKLLEGGEERMETPOEDHLRGOHYH
1	1			1		OKGONGSFDAPNERPYSLKIRNTTSCNSGTYR
J	]	1	1	j .		CTLODPDGQRNLSGKVILRVTGCPAQRKEET
				ļ		FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI
	1	1	1		1	FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT
1						ELV
1063	2413	A	8826	147	627	CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE
	1 2713	1	3323	1	1	HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT
	1	1		Ì		AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ
	1	1				KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH
1		1				CVLSKEMKSVORSLGLSRIHLOSKRKIIHFVL
}	1	1	1	1		TR
1064	2414	A	8835	2982	1869	LKDTLKSQMTQEASDEAEDMKEAMNRMIDE
1 ****	~~.~	^	1 3033	1 -732		LNKQVSELSQLYKEAQAELEDYRKRKSLEDV
1	1	1				TAEYIHKAEHEKLMQLTNVSRAKAEDALSE
l						MKSQYSKVLNELTQLKQLVDAQKENSVSITE
ſ	1	1		1	i	HLOVITTLRTAAKEMBEKISNLKEHLASKEVE
	1	1	1	1	1	

No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   N	SEQ ID	SEQ ID	Met	Leeo	I Durdings	18	
nucice colide solutions of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the c				SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Section			1.00	1 .			
1062   1063   2415   A   8841   3   3806   2204   1066   2416   A   8853   3806   2204   1067   2417   A   8855   1372   1513   2421   A   8866   293   1675   2422   A   8866   2   358   2487   2422   A   8866   2   358   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8866   2   358   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   A   8870   33   663   3880   2487   2422   2422   A   8870   33   663   3880   2487   2422   2422   A   8870   33   663   3880   2422   2422   A   8870   33   663   3880   2422   2422   A   8870   33   6	1		İ				
uenice   914   ng to first agains acid estidue of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence   of peptide sequence							
anino acid residue of peptide sequence	1 .		1	. 1			
Peptide   Sequence			1				TeThreonine V=Voline W=Tryntonhan
Popsible sequence	i						Y=Tymsine X=Inknown *=Ston coden
			1	İ	peptide		
VAKIEROLLERK AMTDANVIRSSYELLOK				İ			
SLSSYSYLASKLKESVKEKKYHSEVQYRELQKFQ   AGREIAEMKRYSESSKLEEDKDKKMEMS   EVSQVKKEKEMIVILLKSKEQSVHELLQKFQ   CAGEILAEMKRYSESSSKLEEDKDKKMEMS   KEVYKLKEKAINSLOGLYSYTSSKKRQSQLEA    LQQVKQLQNQLAECKKQHQEVISYYRMHL    LYAVQQQMDEDVQKVLKQILTMCKNQSQK    K		· ·		1		<del> </del>	
BVSQVKREKENQITLLKSKLØEVNELLQKFQ   QAQEELAMKYSESSKLEBENDKKNESS	1	i	1	1	i	ł	SLESEVSVLASKI, KESVKEKEK VHSEVVOIRS
1065   2415   A   8841   3   663				ļ		i ·	EVSOVKREKENIOTLLKSKFOEVNELLOKFO
1065   2415   A				İ	i		OAOEELAEMKRYSESSSKLEEDKDKKINEMS
LQQQYKQLQNQLAECKKQHQEVISYYRMHL   LYAYQGQMDEDYQKVLKQILTMCKNQSQK   K			1	1	1	ł	KEVTKLKEALNSLSOLSYSTSSSKROSOOLEA
LYAVQGQMDEDYGKVLKQILTMCKNQSQK   K		1				1	LQQQVKQLQNOLAECKKQHQEVISYYRMHI
1065	1	Į.		J	]	1	LYAVQGQMDEDVOKVLKOILTMCKNOSOK
1066		<u> </u>	L			1	
AFLTIGRAQMSPSGRLCLLTIVGLILTIVGCULT	1065	2415	A	8841	3	663	AAATAASLSPRGCRLRTPSSDVGPSRAPPPSA
KDTTSSSSADATIMDIQVTTRAPPAVYTELQT   TSPIPTWPADETPQPQTQTQQLGGTDGPLVT	} .	ļ		}			APLPTGRAQMSPSGRLCLLTIVGLILPTRGOTL
1066	}		1			}	KDTTSSSSADATIMDIQVPTRAPDAVYTELOP
DPETHIKSTKAAHPTIDITTLISERPSPIDVOT			l				
DPQTILKPSGPHEIDDPFYDEHTILRKRGLIVA	1						DPETHKSTKAAHPTDDTTTLSERPSPSTDVOT
AVLFITGIILTSGKCRQLSRLCRNHCR			1			ļ	DPQTLKPSGFHEDDPFFYDEHTLRKRGLLVA
1066						}	AVLFITGIILTSGKCRQLSRLCRNHCR
RRRRGGVYSRKKMSLSERRGIHVDQSDLL   CKKGCGYYGNPAWQGFCSKCWEYHKAR   QKQIQEDWELAERLQREEEAFASSQSSQGA   QSLTFSKFEEKKTNEKTTVKKFFSASSR   VGKKELQEAKAPSPINRQTEDWSKEPIE   ELKTFHKTGQEIYKQTKLFLEGMHYKRDLSIE   EQSECAQDPYHNVAERMQTRGKYPFERVEKI   MDQIEKYMTRLYKYVFCETDDEKKDLAI   QKRIRALIWVTPQMLCVPVNEDIPEVSDMVV   KAITDIEMDSKRVPPDKLACITKCSKHIPINAI   KITKNEPASADDFLPTLIVIVLGNPPRLQSNI   QYTIRFCNPSRLMTGEDGYYFTNLCCAVAPIE   KLDAQSLNLSQEDFDR YMSQGTSPRQEAES   WSPDACLOVKQMYKNDLLSQLNERQERIM   NEAKKLERDLDWTDGIAREVQDIVEKYPLEI   KPPNQFLAAIDSENVEDNKLPPLQPQVYAG   SNMREVGCWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKKK   LRQAWATKQDPISKKKK   LRQAWATKQDPISKKKK   LRQAWATKQDPISKKKK   LRQAWATKQDPISKKKK   LRQAWATKQDPISKAKKKK   LRQAWATKQDPISKKKK   LRQAWATKQDPISKKKKK   LRQAWATKQDPISKKKKK   LRQAWATKQDPISKKKKKKK   L	1066	2416	A	8853	3806	2204	FVGEQEGGCEAGAGRGAOTYPGEAGERWFG
CKKGCGYYGNPAWQGFCSKCWREEYHKAR   QKQIQEDWELAERLQRIEEEAFASSQSSQGA   QSLTISKFEEKKINEKTRKVTIVKKPFSASSR   QSKITSKFEEKKINEKTRKVTIVKKPFSASSR   VGSKKEIQEAKAPSPSINRQTSIETDRVSKEFIE   FLKTFIKTGQETYKQTKLFLEGMHYKRDLSIE   EQSECAQDFYHNVAERMQTRGKVPPERVEKI   MDQIERYIMTRLYKYVFCPETTDDEKXDLAI   QKRIRALRWYTPQMC_VEVPNEDIPEVSDMVV   KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI   KITKNEPASADDFLPTLIYTULKGNPPRLQSNI   QYITIFCPPSRLMTGEBGYFTNLCCAVAFIE   KLDAQSLNLSQEDFDRYMSQQTSPRKQEAES   WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKKLEKOLDWTDGIARBVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGCWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKKK   KPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGCWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK   LRQAWATKQDPISK		1	}				RRRRGRVVSRKKMSLKSERRGIHVDOSDLL
QKQIQEDWELARELQREEEEAFASSQSSQGA QSLTFSKFEEKKTNEKTVTVKKFFSASSR VGSKKEIQEAKAPPSPNRKQTSIETDRYSKEFIE FILKTFHKTGQETYKQTKLFLEGMHYKRDLSIE EQSECAQDFYHNVAERMQTRGKVPPERVEKI MDQIERYIMTRLYKYVFCPETTDDEKKDLAI QKRIRALRWVTPQMLCVPYNEDIPEVSDMVV KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE KLDAQSLNLSQEDFDRYMSGGTSCRKQERISM NEAKKLEKDLDWTDGIAREVQDIVEKYPLEI KPPNQPLAAIDSENVENDKLPPPLQPQVYAG  1067 2417 A 8855 1372 1513 SIMREVGCGWLVPVIPAFWEAEVGGSLEARS LRQAWATKQDPISKKK  1068 2418 A 8856 1530 1583 PCRFGMECNSMISVHCNL 1069 2419 A 8857 1330 1583 PCRFGMECNSMISVHCNL 1070 2420 A 8866 293 1675 PYPQGGYPQGPYPQGGYPQGP YQSPFPNPYQGPQVPFQOPDPSSPGHONYQ EEGPPSYYTDMOPPATINDDKSIRQAFIRKVP LVLTLQLSVTLSTVSVFTPVAEVKGFVRENV WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL VALSVLTASLSYMVGMLASPYNTEAVIMAVG IITAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFFAILCFIRNRILEIVYASLGALLFTCFLA VDTQLLIGMKQLSLSPEEYPYAALNLYTDINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPTGTGGSTRSRGEGISQ EVRYHYFPPVAPCPGYEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNITLYFLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVCADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVCADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVCADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVCADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVCADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVCADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVCADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVPRPTASII LNGEKLKVFPVRSGT*QGGSVWP GGGTGPSSDAGWGCMLRCGGMMAQALCCH		•					CKKGCGYYGNPAWQGFCSKCWREEYHKAR
QSLTPSKFEEKKTNEKTRKVTTVKKFFSASSR							QKQIQEDWELAERLOREEEEAFASSOSSOGA
VGSKKEIQEAKAPSPSINRQTSIETDRVSKEFIE   FLKTFHKTGQEIYKQTKLFLEIGMHYKRDLSIE   EQSECAQDFYHNVAERMQTRGKVPPERVEKI     MDQIEKYTMTRLYKYVPCPETTDDEKKDLAI     QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV     KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI     KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI     QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE     KLDAQSLNLSQEDFRYMSGQTSPRKQEAES     WSPDACLGVKQMYKNLDLLSQLNERQERIM     NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI     KLDAQSLNLSQEDFRYMSGQTSPRKQEAES     WSPDACLGVKQMYKNLDLLSQLNERQERIM     NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI     KLDAQSLNLSQEDFRYMSGQTSPRKQEAES     WSPDACLGVKQMYKNLDLLSQLNERQERIM     NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI     KLDAQSLNLSQEDFRYMSGQTSPRKQEAES     WSPDACLGVKQMYKNLDLLSQLNERQERIM     NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI     KLDAQSLNLSQEDFRYMSGQTSPRKQERIM     NEAKKLEKDLIDWTDGIAREVGGSLEARS     LRQAWATKQPPISKKK     LRQAWATKQPPISKKK     DROWNENGLENSMINSVHCNL     DROWNENGLENSMINSVHCNL     LRQAWATKQPPISKKK     DROWNENGLENSMINSVHCNL     DROWNENGLENSMINSVHCNL     1069   2419   A 8857   1530   1583   PCRPGMECNSMINSVHCNL     PYPQGGYPQQPYPQGGYPQQPYPQGGYPQQP     YPQSPPPPNYQQPYPQGGYPQQP     YPQSPPPPNYGQPQVPPQGGYPQQP     YPQSPPPPNYGQPQVPPQGGYPQQP     YPQSPPPPNYGQPQVPPQGGYPQQP     YPQSPPPPNYGQPQVPPQGGYPQQP     YPQSPPPPNYGQPQVPPQGGYPQQP     YPQSPPPPNYGQPQVPPQGGYPQQP     YPQSPPPPNYGQPQVPPQGYPQGYPQGPVPQGYPQQP     YPQSPPPPNYGQPQVPPQGYPQGYPQGPVPQGPVPQGYPQQP     YPQSPPPPNYGQPQVPPQGYPQGYPQGPVPQGPVPQGPVPQGPPQQP     YPQSPPPPNYGQPQVPPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPVPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPQVPPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPQVPPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPQVPPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPYPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPYPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPYPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPYPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPYPQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPYPQGYPQGPYPQGYPQQP     YPQSPPPPYGQPYPQGYPQGPYPQGYPQQP     YPQSPPPPYQQPPYQGYPQGPYPQGYPQQP     YPQSPPPPNYGQPYPQGYPQGPYPQGPYPQGP     YPQSPPPPYGQPPQQPPQGP     YPQSPPPNYGQPYPQGYPQGP     YPQSPPPNYGQPYQQP     YPQSPPPNYGQP     YPQSPPNYGQP     YPQSPPNYGQP     YPQSPPNY							QSLTFSKFEEKKTNEKTRKVTTVKKFFSASSR
FLKTFHKTGGEIYKQTKLFLEGMHYKRDLSIE   EQSECAQDFYHNVAERMQTRGKVPPERVEKI   MDQIEKYMTRJKYKYVFCPETTDDEKKDLAI   QKRRALRWYTPQMLCYPVNEDIPEVSDMVV   KAITDIEMDSKRVPRDKLACITKCSKHIPNAI   KITKNEPASADDFLFTLYIVLKGNPPRLQSNI   QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE   KLDAQSLNLSQEDFDRYMSOGTSPRKQEAES   WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKKLEKDLDWTDGIAKEVQDIVEKYPLEI   KPPNQFLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGCGWLVPVIPAFWAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   SPORGWLVPVIPAFWAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISPQOPPPQGGYPQGPYPQGPYPQGPYPQGPYPQGPYPQGPY		]					VGSKKEIQEAKAPSPSINROTSIETDRVSKEFIE
EQSECAQDFYHNVAERMQTRGKVPPERVEKI   MDQIEKYIMTRLYKYVFCPETTDDEKKDLAI   QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV   KAITDIEMDSKR VPROKLACITKCSKHIFNAI   KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI   QYITIRFCNPSRLMTGEDGYYFTNLCCAVAFIE   KLDAQSLNLSQEDFDRYMSQQTSPRKQEAES   WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKELEKBLID WTDGIAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGGGWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQPEISKEK   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGGWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK   LRQAWATKQPEISKEK							FLKTFHKTGQEIYKQTKLFLEGMHYKRDLSIE
MDQIEKYIMTRL YKYYPCPETTDDEKKDLAI   QKRIRALR WVTPQMLCVPVNEDIPE VSDMVV   KAITDIEMDSKR VPRDKLACITKCSKHIFNAI   KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI   QYITRICNPSRLMTGEDGYYPFINLCCAVAFIE   KLDAQSILN.SQEDFDR YMSGQTSPRKQEAES   WSPDACLGVKQMYKNLDLLSQLNERQRRIM   NEAKKLEKDLDWTDGIAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENKLPPPLQPQVYAG   SNMEREVGCWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKKK   ROPE   LRQAWATKQDPISKK   ROPE   LRQAWATKQDPISKK   ROPE   LRQAWATKQDPISKK   ROPE   LRQAWATKQDPISKK   ROPE   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWAT			ſ				EQSECAQDFYHNVAERMOTRGKVPPERVEKI
OKRIRALRWTPQMLCVPVNEDIPEVSDMVV   KAITDIEMDSKRVPRKQTKCSKHIFNAI   KITKINEPASADDFLPTLIVIVLKGNPPRLQSMI   QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE   KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES   WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKKLEKDLDWTDGIAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGCGWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKALLSDISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKALLSDISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAWATKQDPISKAK   LRQAW		ļ					MDQIEKYIMTRLYKYVFCPETTDDEKKDLAI
RAITDIEMDSKRYPRDKI.ACITKCSKHIFNAI   KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI   QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE   KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES   WSPDACLGVKQMYKNLDLSQLNERQRRIM   NEAKKLEKDLDWIDTGIAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGOGWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITKATA   LRQAWATKQDPITA   LRQAWATKQDPITKA   LRQAWATKQDPITKA   LRQAWATKQDPITKA   LRQAWATKQDPITKA   LRQAWATKQDPITKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQAWATKA   LRQA		Į		j j			QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV
RITKNEPASADDFLPTLIVIVLKGNPPRLQSNI QYITRFCNPSRLMTGEDGYFTNLCCAVAFIE KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES WSPDACLGVKQMYKNLDLLSQLNERQERIM NEAKKLEKDLDWTDGIAREVQDIVEKYPLEI KPPNQPLAAIDSENVENDKLPPPLQPQVYAG SNMREVGCGWLVPVIPAFWEAEVGGSLEARS LRQAWATKQDPISKKK LPRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKKK LRQAWATKQDPISKYD LRQAWATKQDPISKYD LRQAWATKQDPISKYD LRQAWATKQDPISKYD LRQAWATKQDPISKYD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWATKQD LRQAWAT		•	i				KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI
OYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE   KLDAQSLDFDRYMSGQTSPKQGAES   WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKKLEKDLDWTDGIAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGCGWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   DFFROMECNSMISVHCNL   LRQAWATKQDPISKKK   DFFROMECNSMISVHCNL   LRQAWATKQDPISKKK   DFFROMECNSMISVHCNL   LATER   LVALTIQLSVILSTSVFTPVABVE   LVALTIQLSVILSTSVFTPVABVE   LVALTIQLSVILSTVSVFTFVABVKGFVRENV   WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL   VALSVILTASLSYMVGMTASFYNTEAVIMAVG   HTTAVCFTVVIFSMQTRYDFTSCMGVLLVSM   VVLFFRAILCHFIRRILEIYYASLGALLFTCFLA   VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI   FLYLTIGRAKE*PSSSSLCPLRWHGWPGPCP   WHGSASCTSPLSCPQAQPREKDASLQPSCMY   TADTSIWTRCHSMAPLVIPPPPRGTKATFPC   HLLSTHCCMSPVCQFTPCTGGGSTRSRGEGLSQ   EVRYHVFPPVPAPQPGVEHPSPPPHPPGVLPS   GDMRSGGLPVLSPE   GDMRSGGLPVLSPE   GDMRSGGLPVLSPE   GDMRSGGLPVLSPE   LNGEKLKVFPVRSGT*QGCSVWP   LNGEKLKVFPVRSGT*QGCSVWP   LNGEKLKVFPVRSGT*QGCSVWP   GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI   GGTGPSSDAGWGCMLRCGOMMLAOALICRH   GKQHLKTEKSKLLSDISARLWFTYRRKFSPI   GGTGPSSDAGWGCMLRCGOMMLAOALICRH   GKQHLKTEKSKLLSDISARLWFTYRRKFSPI   GGTGPSSDAGWGCMLRCGOMMLAOALICRH   GKQHLKTEKSKLLSDISARLWFTYRRKFSPI   GGTGPSSDAGWGCMLRCGOMMLAOALICRH   GKQHLKTEKSKLLSDISARLWFTYRRKFSPI   GGTGPSSDAGWGCMLRCGOMMLAOALICRH   CYNTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CANTAC   CA				1 1			KITKNEPASADDFLPTLIYIVLKGNPPRLOSNI
WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKLEKDLIDWTDGIAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG							QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE
NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI	1			1 1			KLDAQSLNLSQEDFDRYMSGOTSPRKOEAES
NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI							WSPDACLGVKQMYKNLDLLSQLNERQERIM
1067   2417   A   8855   1372   1513   SNMREVGCGWLVPVIPAFWEAEVGGSLEARS LRQAWATKQDPISKKK     1068   2418   A   8856   1530   1583   PCRPGMECNSMISVHCNL     1070   2420   A   8866   293   1675   PYPOGGYPQGPYPQGGYPQGP YPQGPYPQGGYPQGP YPQGPYPQGYPQGPYPQGYPQGYPQGP YPQSPFPPNPYGQPQVFFQQPPDSPQHONYQ EEGPPSYYDNQDFPATNWDDKSIRQAFIRKVF LVLTLQLSVTLSTVSVFTFVAEVKGFVRENV WTYYVSYAVFTISLIVLSCCGDFRRKHPWNL VALSVLTASLSYMVGMIASFYNTEAVIMAVG IITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HILLSTHCCMSPVCQPTPGTGSTRSRGEGLSQ EVRVHVPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE GDMRSGGLIPVLSPE GDMRSGGLIPVLSPE     1071   2421   A   8868   2   358   ARGNILYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRIPFFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVSGT*QGCSVWP     1072   2422   A   8870   33   658   MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHMLAOALICRH	] .			] ]			NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI
1068   2418   A   8856   1530   1583   PCRPGMECNSMISVHCNL	10/7	0410		0077			KPPNQPLAAIDSENVENDKLPPPLQPQVYAG
1068	1007	2417	A	8855	1372	1513	SNMREVGCGWLVPVIPAFWEAEVGGSLEARS
1069   2419   A   8857   1530   1583   PCRPGMECNSMISVHCNL	1000	0//0					
1070 2420 A 8866 293 1675 PYPQGGYPQGYPQGPYPQGPYPQGPYPQGPYPQGPYPQG							PCRPGMECNSMISVHCNL
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EEGPPSYYDNQDFPATNWDDKSIRQAFIRKVF LVLTLQLSVTLSTVSVFTFVAEVKGFVRENV WTYYVSYAVFFISLIVLSCCGDFRKHPWNL VALSVLTASLSYMVGMIASFYNTEAVIMAVG ITTAVCFTVVIIFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSSPEEYVFAALNLYTDIINI FLYILTIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLV1PPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRYHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNILYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	10/0	2420	A	8866	293	1675	PYPQGGYPQGPYPQEGYPQGPYPQGGYPQGP
LVLTLQLSVTLSTVSVFTFVAEVKGFVRENV WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL VALSVLTASLSYMVGMIASFYNTEAVIMAVG ITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVIPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSGEGLSQ EVRYHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGGSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GGQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAOALICRH				l l			YPQSPFPPNPYGQPQVFPGQDPDSPQHGNYQ
LVLTLQLSVTLSTVSVFTFVAEVKGFVRENV WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL VALSVLTASLSYMVGMIASFYNTEAVIMAVG ITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVIPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSGEGLSQ EVRYHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGGSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GGQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAOALICRH						-	EEGPPSYYDNQDFPATNWDDKSIROAFIRKYF
WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL VALSVLTASLSYNVGMIASFYNTEAVIMAVG ITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFFFALCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSFEEYVFAALNLYTDIINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVVVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGGSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GGQTGPSSDAGWGCMLRCGQMMLAQALICRH						1	LVLTLQLSVTLSTVSVFTFVAEVKGFVRENV
VALSVLTASLSYMVGMIASFYNTEAVIMAVG IITAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRRRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFRRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAYYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH							WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL
VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIGRAKFPSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRYHVFPPVAPOPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAOALICRH							VALSVLTASLSYMVGMIASFYNTEAVIMAVG
VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKEPSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	1 1				1	ł	
VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKEPSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH							VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA
FLYILTIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH		J		]	i		VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI
WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVIPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGGSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAOALICRH					[	1	FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP
TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRYHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRIPFMI*S\RLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP LNGEKLKVFPVRSGT*QGCSVWP GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH		1			1		WHGSASCTSPLSCPQAQPREKDASLQPSCMY
HILSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLPVLSPE  1071 2421 A 8868 2 358 ARGNILYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNIFFKRNDCRYVMISCKADMAYDN VRHPFMI*SNKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH		i			1		TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC
EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNILYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNIFFKRNDCRYVMISCKADMAYDN VRHPFMI*SNKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH		j				. 1	HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSO
GDMRSGGLIPVLSPE					[	ĺ	EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS
DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFNI*S\RLIMEETYLNIIKAVYDRPTASII LNOEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	1007	246:	<u> </u>				GDMRSGGLIPVLSPE
DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAOALICRH	10/1	2421	A	8868	2	358	ARGNTLYHLPRLCRKLNLRWFSASTLYDVOH
VRHPFMI*SNKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGOMMLAOALICRH	) )	j		l		ļ	DDKMGSNTFFKRNDCRYVMISCKADMAYDN
1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGOMMLAOALICRH		ŀ	1	1	1	{	VRHPFMI*SI\KLIMEETYLNIIKAVYDRPTASII
10/2 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGOMMLAOALICRH	1000						LNGEKLKVFPVRSGT*QGCSVWP
GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGOMMLAOALICRH	1072	2422	A	8870	33	658	MESVLSKYEDOITIFTDYLEEYPDTDELVWII.
GGTGPSSDAGWGCMLRCGOMMLAOALICRH		j	- 1	}		]	GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI
LGRDWSWEKOKEOPKEYORII OCEI DRKTOC							GGTGPSSDAGWGCMLRCGQMMLAOALICRH
							LGRDWSWEKQKEQPKEYQRILQCFLDRKDC

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	Ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
į	L			sequence		nucleotide insertion
					i	CYSIHQMAQMGVGEGKSIGEWVLGPNTVAQ
	1		1			GV*KNLA\LFDEW\NSLGLVYVSM\DNPSGSIA
L			<u> </u>			RFPKKLCRVLPL\SADTAGLTGP
1073	2423	A	8879	146	412	DFSV*GDVDIEVTCPICLQLLTEPLSLNCGLRL
1						*QVCITA*IKESVIISGG*SSSPVCHTTFQPANL
			ļ		10.5	RTSRYLPT*SIKSLGPDEPQEG
1074	2424	A	8884	67	435	HLQGRSIRTLQLTGENEKNCEVSERIRRSGPW
1	i	İ	1	1		KEISFGDYICHTFQGDCWADRSPLHEAAAHG
ł			1	i		RLLALKTLIAQGVNVNLWTL/DRVSSLHEACL
	<del> </del>	<u> </u>	0000	1004	0.40	*GPVACAKPYWKMVPRHGGTVTGPPLLMV
1075	2425	Α	8896	1294	248	RSGDRNGLTHQLGGLSQGSRNQSYRSRSRSR SRERPSAPRGIPFASASSSVYYGSYSRPYGSDK
				!		PWPSLLDKEREESLRQKRLSERERIGELGAPE
1	ì	1	i	İ	l	VWGLSPKNPEPDSDEHTPVEDEEPKKSTTSAS
1.						TSEEEKKKKSSRSKERSKKRRKKKSSKRKHK
		ì	1	1		KYSEDSDSDSDSETDSSDEDNKRRAKKAKKK
						EKKKKHRSKKYKKKRSKKSRKESSDSSSKES
	1.	1	1			OEEFLENPWKDRTKAEEPSDLIGPEAPKTLTS
					i e	QDDKPLNYGHALLPGEGAAMAEYVKAGKRI
		j				PRRGEIGLTR*RNCHHLNAQVM**VVSRHRR
1	İ					MEAVRTAKREPESTVLMRREPLHPFNPRRET
	1			1		KERE
1076	2426	A	8899	146	789	GRSTEAEKEPAFDERTGKGRRLPRAGEFHG*E
1		1				*APGPGPRSFQVSRKMPEE\PPGARKHPFSGKS
1				İ		FYLDLPAGKNLQFLTGAIQQLGGVIEGFLSKE
						VSYIVSSRREVKAESSGKSHRGCPSPSPSEVR
İ	1	ĺ		i	[	VETSAMVDPKGSHPRPSRKPVDSVPLSRGKE
	}		1			LLQKAIRNQK**CTVQQL\$HCRLY\GEKTTAK
	1			i		RSQREHVQQQSQEHGKWPDLKGPR
1077	2427	A	8901	352	3	AKIGAYKYIQELWRKKQSDVMHFLLRVRCW
1	[	1	1	1		QYPALHRAGTEWQLSALHRAPRSTQPDKAC
1				1		RLGYKAKQGYIIYRICVRRGGWKCPVPKAVT
						\YGKPVHHGVN*LKFAQSLQSVAEEQ
1078	2428	A	8905	536	781	ACPAENREVPEMAAGQAPHAGPGAGPGQPA
	1			ľ	•	PALPFAATPGSRGQALCRGGRRRQHLHGPLH
10=0	10.00	1	10010	101	276	RP*QAAPALHAGCQLAPHPPT
1079	2429	A	8912	121	376	NLIWKLCVTERRLVILDNYDLASE/YEANKYI CNRIIOFKPGODKYFTLGLPTGSTPL*CYPKLI
	1		1	1	1	EYNKNGHLSFKYVKTFSMDEY
1000	12420	<del>  </del>	1 0000	201	1788	SSESPSDPGRMAMTWIVFSLWPLTVFMGHIG
1080	2430	Α	8920	381	1/00	GHSLFSCEPITLRMCQDLPYNTTFMPNLLNHY
		1				DOOTAALAMEPFHPMVNLDCSRDFRPFLCAL
İ	1	1				YAPICMEYGRVTLPCRRLCORAYSECSKLME
1	1	}	1	1	1	MFGVPWPEDMECSRFPDCDEPYPRLVDLNLA
1		1				GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY
1		1		1		SFLHVRDCSPPCPNMYFRREELSFARYFIGLIS
1	1	1	1	1		IICLSATLFTFVTFLIDVTRFRYPERPIKCYAV
		1		1	1.	WHMMVSLIFF\IGFLLEDRVACNA\SIPAQYKA
	1					STVTQGSHNKACTMLFMILYFFTMAGSVWW
			1	1	1	VILTITWFLAAVPKWGSEAIEKKALLFHASA
İ		1	1			WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD
1		1		1		VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR
1	1	1		1		VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL
	1	1		1		VVIGCYFYEQAYRGIWETTWIQERC
1081	2431	A	8922	56	420	EERTKMSTGPDVKATVGDISSDGNLNVAQEE
		1	1	1	1	CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG
1	1	1		1	1	TLANFVF\CSVRHGLALILQLCNFSIYTQQMN
		1	1		<u> </u>	LSIAIPAMVNNTAPPSQPNASTERPST
1082	2432	A	8923	355	1079	PFGTPSSTMAVVKNKCLMKGGKKGVKKKVV
				, <del></del>		

SEQ ID	SEQ ID	Met	Leco	I D 11-41	15.0	
NO: of	NO: of	Met hod	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	Dou	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-		1	nucleotide location	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	1	USSN 09/496		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
uence	uchec	ļ	914	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
201100	1		714	ng to first amino acid	acid residue of peptide	Q=Glutamine, R=Arginine, S=Serine,
			1	residue of	sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	sequence	/=possible nucleotide deletion, \=possible
	ł	1	ł	sequence	l	nucleotide insertion
		<del></del>		sequence	<del></del>	CONCENTRACTION
İ	İ	ĺ	Í	ĺ	Ì.	GPFSKKDQYDVKAPAMFNIRNTGK/TLVART
1		ļ				QGTQIASDGLKGLLFEVSLADLQNDEVAFRK FKLITEDVQDKNCLTNFYGMDLTCDKICSMV
	1	1				EKWSTMIEAHVDVKTTDGYFFHLFCVGFTKK
				ŀ		HNNQILKTSYA*HQQS/RQIQKKMMEIMT*EV
1						QTNDLKEVVNKLIPDNIGKDTEKV/CPIYPLH
		ĺ	1		ĺ	DVFIRKVKMLENPGFER\MELRGGGSSS
1083	2433	A	8948	28	385	LTWPQPHIPSCPAMSEETLQSKLAAAKKKLP
					1 -00	WGAVQGSRAMSDLLLLLDLTLLLLLMLLGF
	İ	l	]			AGYSGQLAGVAVSAGSPPLRYKFHVEPYGET
		ļ	i l			GWLLT/ESCSISPKLCSIAVH*DNPAWF
1084	2434	A	8950	156	318	HYTPINTDTIENSENNKCW*GY*E\VGLIHHW
	1	l				WGGKRVQPFWKRVWQKRTLNLRV
1085	2435	A	8956	16	413	HMGQLGYFIQCWWECKRLISF\WKTI*QSPAK
						*TIYTSYDTAIPIS/GI/YPKRMSSKCHQETCAR
			1			MFILAPFTATIKGKQLTCPLVEERIDY\MWYS
						HKYYIKVKRNL*VTITH\TWVNLNILMFEIILW
			٠			YSHKYY
1086	2436	A	8962	868	1026	H*KILQVGRAQRAHXSRL*SQLLRRLRHESHL
						NPGARGCSEARLHRCTPAWTT
1087	2437	Α	8985	58	330	LHVKHLGHFQLVFSEVICHCILMPVS*ELORL
}						*ERSVCAFHVCIQTYVCLQVYACMCVYYICM
						FVYSVYGCGLCTCVCMDVYICVCVQEFL,
1088	2438	A	8989	394	404	N*KWILHVNVRIQSIFF/IKRNQK/INSHELKLD
						KKFLDMMSNA*STKKHDKLD/LIKFKT/LCSA
ŀ						KYTVKRIKIHPTDLEKMLRNHLSDKD*YS/GV
						YKDLSKLNRRKTE/S*/VKKWVKDLSRYFIKE
1089	2439	•	9004			VISMENKHKKIFSTS
1009	2439	A	8991	60	329	MALTPESPSSFPGLAATGSSVPEPPGGPNATL
]						NSSWDSPTEPSSLEDLEATGTIGTLLSDMGVV
1090	2440	A	8996	2	351	GVEDNAYTLEVNSRYMRAVGIM*IHL
10,0	2110	•	0220	<b>'</b>	331	SNITITLT*MKKYDNTFCW*GCGQIG/T/LIYC
						WQESKFIQAFWSKIQQYLA*ISIHILFDPAFLFL GGYPGGTQSVFLTGVLVSSVFYNMKMLHTR
						LLIAALFIIVQYWKQSKDHYI
1091	2441	A	8997	97	456	YPLPVCSYLSGPRGEHWNSLGGKSSCPLPLPT
				·		LVSSRFKISKVIVVGDLSVGKTCLINR*GGAG
i						AELGRVGPSLARWAGSRSQHLVPSQ\VCKDS
1			- 1	,		FDKNYKAPIGADFEMERFEVLGIPF
1092	2442	A	8999	548	811	SSFIKRHILIFEDDWHQTTCCHHPHHP\F*RCQ
			[	i		FHIFYVSVQNSISPSLSVSSSHPDRPDHEVHQH
			į			RAAHHHQHGQGPLGHGLVARVG
1093	2443	A	9002	3	2745	ALLGLQQPAQSLILSRSSVMGVRGLQGFVGS
		ĺ	ļ			TCPHICTVVNFKELAEHHRSKYPGCTPTIVVD
	į					AMCCLRYWYTPESWICGGQWREYFSALRDF
		- 1				VKTFTAAGIKLIFFFDGMVEQDKRDEWVKRR
}	1		- 1		ļ	LKNNREISRIFHYIKSHKEQPGRNMFFIPSGLA
ĺ	l	1	1	1	1	VFTRFALKTLGQETLCSLQEADYEVASYGLQ
į	ļ	ĺ	1	I	ŀ	HNCLGILGEDTDYLIYDTCPYFSISELCLESLD
J	ì	J	}	1	l	TVMLCREKLCESLGLCVADLPLLACLLGNDII
	ļ			ļ	[	PEGMFESFRYKCLSSYTSVKENFDKKGNIILA
	ŀ		I	ļ	Ì	VSDHISKVLYLYQGEKKLEEILPL/VTKQSSFL
į	j	j		- 1	ŀ	*RNGIISFTRT/INLHGFSKNPKV**LWTNK*YP
1	1	1		İ		RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP
- 1		- 1	- 1	ļ	l l	GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTG
			1	į	1	PESRREVPMCSDPEPRQEVPMCTGPEPRQEVP
	ļ		į	İ	1	MCTGPEARQEVPMCTDSEPRQEVPMCTDSEP
	- 1	ł	-	1	j	RQEVPMYTGSEPRQEVPMYTGPESRQEVPMY
						TGPESRQEVLIRTDPESRQEIMCTGHESKQEV

SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
		noa				F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ	USSN	location	corresponding	
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
l .			i	amino acid	of peptide	T-Threonine, V-Valine, W-Tryptophan,
i		1	l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ſ		[	1	peptide	•	/=possible nucleotide deletion, \=possible
		l	ļ	sequence		nucleotide insertion
<b></b>		ļ	<del> </del>	Sequence		PICTOPISKQEDSMCTHAEINQKLPVATDFEFK
]	] .		1			LEALMCTNPEIKQEDPTNVGPEVKQQVTMVS
]	}	j		)	1	
		l	l			DTEILKVARTHHVQAESYLVYNIMSSGEIECS
		ļ	1	!	ĺ.	NTLEDELDQALPSQAFTYRPIRQRVYSLLLED
	ļ	l	ŀ		ŀ	CQDVTSTCLAVKEWFVYPGNPLRHPDLVRPL
ĺ		[	1	[		OMTIPGGTPSLKILWLNQEPEIQVRRLDTLLA
1			Ì			CFNLSSSREELQAVESPFQALCCLLIYLFVQV
					i	DTLCLEDLIIAFIAQALCLQCKSTSQLVNLQP
1	ľ	1	1	•	ĺ	DYINPRAVQLGSLLVRGLTTLVLVNSACGFP
l .		1			ŧ	
l .					1	WKTSDFMPWNVFDGKLFHQKYLQSEKGYA
l			1		1	VEVL/CRTK*ISAHQIPQPEGSRLQGLHEGEQT
			L		l	HHWPSPLGLTPRREVGKTGLQLPQDGLWV
1094	2444	Α	9021	97	834	AREACRAKTOFFGRRFRLWPSCCCRVIVGAE
İ	1	l	1			T*H\MAEPVSPLKHFVLAKKAITAIFDQLLEFV
	Ì			1 .	Ì	TEGSHFVEATYKNPELDRIATEDDLVEMQGY
						KDKLSIIGEVLSRRHMKVAFFGRTSSGKSSVI
l	1	1	1		ł	NAMLWDKVLPSGIGHITNCFLSVEGTDGDKA
	Ì					YLMTEGSDEKKSVKTVNQLAHALHMDKDLK
			Į.	l		AGCLVRVFWPKAKCALLRDDLVLVDGPGTD
1	1					1
	ļ					VTTELDSWIDKFCTKSSTREITNSGSDT
1095	2445	Α	9022	1	537	LVLNSRVEDFVPPEGAGRTLPFALRPLAACW
i		}		i		LLHRRARRSSALCPRPRSWGVSGGEGAGARE
l			1			P*ITSSSCCLSAA/SHLSIQSPNMAGARRRIRPQ
1	ł	1	I	1	i	LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF
ì		1			•	DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNATV
	İ			1	ł	FAYGQT\GAGKTYTMGTGFD
1096	2446	Α	9029	1	285	FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL
1050	2440	Ι ^ .	3023	1 1	203	GOHSETPSLKKK\LAGYSGMCL*SQVLRRLRQ
	1	i	i		٠.	EDCLSPGGGNCRES*SCPYTPAWITERDPV
			<b></b>		<u> </u>	
1097	2447	Α	9032	716	357	ARSTGFWGEILWCGFLKRSLALSPRVKCSGAI
İ		1	1	1		LAHCNFRHAGFPPLSCLSLPNRWEYRRPPARP
1	1	ļ	1	1	1	GKFFLVFLVETGFQC/G*DGLDLLTSRSACLG
İ		l			1	LPKCWDYRREPAASIIFQTTFFINSK
1098	2448	A	9038	230	652	KVVVMSCEDINISGSFYRNKLKYLAFLCKRTS
1	1		1		""	TNPSQGPYHLWVPSHIFWQTTCGRLPHKTKQ
	1	1				G*AALDHLKVFDRIPLPYDKKKQMAVSATLE
1	1	1		1		VVRPKP*RKFAYLGHWAQKVDWKYQAMTA
		1			1	
		<b> </b>	<del> </del>	<u> </u>	-	TMGEKRKVYYQKICYQKK
1099	2449	A	9043	185	372	IIFYSHQQCMRV/WQGCGDIETLIHCW*E*KII
1				1		HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP
					L	RKIKTCPQNSCTSMLINAIHNDQKWKKINI
1100	2450	A	9045	763	584	RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL
1	' ' '	1	1	l .		SLTSSWDYRRPPPHPANFLYFK*RRGF
1101	2451	A	9050	275	2	LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL
1101	24,71	^	3030	2/3	. ~	FLL/FEMESLPVA/RVECSGTISAHCNLCLPGSS
	1	1		1		
L	<u> </u>	<u> </u>		L		DSPASAS*VAGITDMCRYTQLILFHAS
1102	2452	A	9053	449	1224	KTSMFWKFDLHSSSHIDTLLEREDVTLKELM
	}	1				DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF
	1	1		1		I\*EEPPQDMDEKIRYKYPNISCELLTSDVSQM
1	[	i				NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF
·	ì	1	1		1	SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG
1		1		1	1	TSAIMDLLLRLLTCIEPPOPRODVLN/WFKVQ
	1	1		1	1	RNL*HST*NVMDISKYVNLHWGLNKSHSLL*
	}				1	
]	]	}	1	]		LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS
L	L	1	1		<u> </u>	SLV
1103	2453	A	9058	403	3	GLHVYDFQVYREHILTLNVKKCSVSFWGLRE
1	1	1	]	1	1	WLYLQMYEIIKSPRFPIIKMTDITKCW*GC\GA
1	1	[	1		1	AGMQI/H/CW\WCVNVGKFWEMS*YYLLKLSI
1	1	1	1	1	1	ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMLIA
	L	1	1	1		

SEQ ID	I GEO ID	13.64	1.000	Two	Y	
NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in NO.	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	1	USSN	location	corresponding	P=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	1	09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T-Threonine, V-Valine, W-Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		İ		peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
					1	APFVLAVNC
1104	2454	A	9064	75	393	KWLFSSLNITGRGDIIGHLKWLDCR\NCSSFPI
].					ľ	KRNRQTHSTESNKLKAGHSFGYN*LIH*NS\V
1		1	1			KTDCGCGANSKGVVVVMKV\KTAQQKQTTS
1105	2455	<del> </del>	-			YMQIGTTKNSRAT
1103	2455	A	9065	366	778	DLLILRNLAFPELKRRNCISRFYLAYHLHKIYS
		1		İ		RSILLCNNCSGFYILSL*QYDVFFFNYFFFRDR
		1		ļ		AWPCCPGWSAAWLTIVILAHYRRPGLERSCC
1		1	1	i	1	LSLSSSWDHRRVPPCPANF*/YFSMGFTAFPRL
1106	2456	A	9083	673	816	VLNS*TQGI
1	2130	1^	7003	0/3	810	ESGSLIH*WWENKPAQPLWWEI*QHVQKLPT
1107	2457	A	9086	580	18	HFPCDPAIPLLGICPED
,		1.	7000	300	10	KPSSGSFIRAIYIFLSTAHVPALFSVLVRTKLT*
1			]			AFSQSSVLWAHKQQKTSLSLVIR/ERLQIKTA
1		l			ŀ	VRENFLPIRLAKILKLDNVKCWQG/SGSNMSL I/HCWWEYNVIHIIWNSVTFPRKVEHVYITYA
	İ	1				PEISVR*IHGGLPTLVHQETHTSVFRGAPSVIP
<u></u>	ł	1			}	ETR/CRPTKESINKLLHIYTMEHYGDENK
1108	2458	A	9093	540	1	GGNDCSVTPTTEPGRKEIT*KRKF*EKTDRLP
		1				GA/PPSRTPPTPYPCPHGDRLLPPSRPLPAGPA
						SAFPPAERSRGHRRASL*RARWSAAVPRRSA
1						GSASEPVQSRWLRLPVGSDSPPAVPVRVCPAP
i		1				DSRPAAPGSRLPDPGLDSPAPSRTPSSSVD*GG
1100-	0.470					QRPPPPSGDSLSPPGCCRY
1109	2459	Α	9099	1255	1425	HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL
1110	2460		1000			GAVAHSCNPSTLVGRGGRITRGOELR
1110	2400	Α	9103	242	70	EEQFFFFAVGMFP*VDFLAPASGELWDRLRLT
1	1	1	ł l			CSRPFTRHQSFGLAFLRVCSSLDSLDDSVVGP
						SALLSSVL/NQGGRNVLEAREAAKHPTI*RQS
1111	2461	A	9110	189	121	LLRKQRNKRMAIP
1112	2462	A	9113	100	910	SFLSVRLECNGAIMAHCALPLPG
			''''	100	310	RRRGGGSRPRRTPVPAPGPGPSFGMDVRFYP
						AAAGDPASLDFAQCLGYYGYSKFGNNNNYM NMAFANNAFFAASEGFEITERG GDEITERDY
						NMAEANNAFFAASEQTFHTPSLGDEEFEIPPIT PPPESDPALGMPDVLLPFQALSDPLPSQGSEFT
						POFPPQSLDLPSITISRNLVEQDGVLHSSGLHM
					-	DQSHTQVSQYRQDPSLIMR\PSST*PDAARSG
						VMPPAQLTTINQSQLSAQLGLNLGGASMPHT
						SPSPPASKSATPSPSSSINEEDADEANRAIGEK
1110						RAAPDSGKKPKTPKK
1113	2463	A	9120	3452	3051	FLRPSFALVPQAGVQWCALSWLQPPSPRFK*F
						SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH
						VGQAGHEPLTSGDPPASASOSAGITGVSHOA
	1	-	1	ł	1	WPSFFIFSRDTVLLCCSGWSRTSGLKQSACLS
1114	2464	A	9122	150	355	LTKCMDA .
''''	~707	^	7144	152	377	NQLPLQQWTFFIYETGFCSVAQAGVQCRDHS
			- 1	İ	j	SLHP*PPG\SSDPPAPPS*VLGITGQRYHACLII
1115	2465	A	9124	553	001	YLYVQTVPQRV
			7147	223	981	QRPLLRQQLGSWPTCRSLEGDLASPW**RLPG
J	- 1	i	1		.	SPRMRRSGT/ATLNLPLSPQGTVRTAVEFQVM
- 1		- 1			1	TQTQSLSFLLGSSASLDCGFSMAPGLDLISVE
					j	WRLQHKGRGRGDLHLPDHHLSVPSSADHPA QQPSQFNGRNLYFLPLFR
1116	2466	A	9135	48 .	410	SASHEPAEHDGGADSLSASQPPRPAGRPAGA
	- 1	1				QHVHVPPWTDVLAGQDRRAPTAGDGAPWP
ļ			1		ļ	APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ
			- 1			PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA
	İ		- 1		1	GAGGP*GSPAGRACGAAGCRPRPPRPAASSA
					İ	*NSAGS*GLVEGT*PPGAGHGAPSPAVGARLS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  CPARTSVQGGTWTC*APAGRPAGLGGWEAE RESAPPSCSAGS*DAD*GAEPWGAGSRSWGS KSGHWAKECLQPRIPPRPCPICVGPHWKSDCP TCPGAVPRAPGTLPQGSLTDSFPDLLSLVAED *CCLMASEASWTITIELWVTLTVEGKSVP/CL
1118	2468	A	9154	471	2	NTEATHSTLPSFQGPVSLASITVVGIDGQASKP LKTPQLWCQLGQYSFMHYFLVIPTCPVPLLG* GILTKLSAFLTIPRLQPHLIAALSPSS AAGQVVVEVTSHLYLCITSDAAGLRLLPPAES
						ERGEGGHCPAEAPLPPRPQYCLAKHPLLRKLP EEKIKLDPYLTQHTKINSKQIKYLS/VRAKTTQ LVEGNIGVNLQNTELKQH*INGFLDTTPEAQE TKEKTNKLNFIKKVKRQLAEWEKIFQIA
1119	2469	A	9155	2	3187	ACPRLARRRRVRSLRRRRGWLRARWSRGQ NNMAARRITQETFDAVLQEKAKRYHMDASG EAVSETLQFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVFSGPSFR SSNPSISDDSYFRKECGRDLEFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHPGEADSV/LRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGVGKLVTL RNVSTKKIPTVNRITPKTQGTNQIQKNTPSPD VTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRR KMSFDIIDKSDVFSRFGIEIIKWAGFHTIKDDIK FSQLFQTLFELETETCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKAEPEPMREEEKMPPTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVTEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLPWQRRGLLRAQGLRGI WKARRANTTGTQTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPQTSSPCPSADIDMKT METAEKLARFVAQVGPEIEQFSIENSTDNPDL WFLHDQNSSAFKFYRKKVFELCPSICFTSSPH NLHTGGGDTTGSQESPVDLMEGEAEFEDEPP PREAELESPEVMPEEEDEDDEDGGEBAPAPG GAGKSEGSTPADGLPGEAAEDDLAGAPALSQ ASSGTCFPRKRISSKSLKVGMIPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRDRWR HFNPKEFCAPLQNVSRHSCFPVV
1120	2470	A	9163	124	207	PPRACRPCPRACPCPPT*KCSQPVSWPC
1121	2471	A	9166	272	523	PMSSLQGCFYTFKCIIFKGIFLLLISNLIAF**EK V/CSHITDSLKFIGKGWVGMVTHACNPGTLG G*GGWIA*VREFETSLGNM
1122	2472	С	9170	442	236	MNRRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRQN*
1123	2473	A	9171	10	423	MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC LTWINALGKFFG

SEQ ID	SEQ ID	Met	SEQ .	Predicted	Predicted end	Amino soid sequence (AmAlonine Co-Count
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in NO.	nucleotide	location	
eotide	1		USSN			F=Phenylalanine, G=Glycine, H=Histidine,
	seq- uence	l		location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1		l	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	ļ	į .	Î	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l		peptide		/=possible nucleotide deletion, \=possible
		<u> </u>		sequence		nucleotide insertion
1124	2474	A	9173	3	374	GPSPSLLVLLPQEPGGTGTPVRAGAGAGMWL
		1				WEDQGGLLGPFSFLMLMLLLETRNPVNACLL
ł						TGSLFVLLGVFSFEPVPSCRALQELKPRDRISA
1			1	1		IAHRGGRHDPPENTLGAIR/QGS**WSNRR
1125	2475	A	9179	704	188	ESSSGLLFQCFQGIHVQKLTLQARPTLFSWWL
1			1	1		CSKPPKETGELENAESGGDGGRRGGKQDNV
1		ŀ				AWWRRM\QKG\DFPWDDEDFPQSGPFGGOA
i						LPMGFFYLYFRDPGREITWKHFVQYYLARGL
1			]		·	VDRLEVVNKQSVRVIPAPGTSSEVRGEFKAE
ļ		1				YCRHKFISCKNVVFYFFQ
1126	2476	A	9183	153	233	TCMIATISCAIVVITIFQ
1127	2477	A	9185	1	321	MEYMAESTDRSPGHILCCECGVPISPN
11127	24//	Α.	9160	) <sup>1</sup>	321	LTGQLGSILLRYFSKSRAGLGARKLKAYRTM
		l	İ			EYMAESTDRSPGHILCCECGVPISPNPAQY\CV
				i '		ACLRSSFHIYHCIPKLFIHPFSKTSSSAFITPSHY
			<u> </u>			LTFFSTIS
1128	2478	Α _	9186	183	847	VLKFLLLQTMDEQSQGMQGPPVPQFQPQKAL
ł	·		l			RPDMGYNTLANFRIEKKIGRGQ\FSEVYRAAC
			1			L\LDGVPVALKKVQIFDLMDAKARADCIKEID
1	ĺ	l	1			LLKQLNHPNVIKYYASFIEDNELNIVLELADA
1		1				GDLSRMIKHFKKQKRLIPERTVWKYFVQLCS
i			1			ALEHMHSRRVMHRDIKPANVFITATGVVKLG
		1				DLGLGRFFSSKTTAAHSLVGTPYYMSPERIHD
1						NG
1129	2479	Α	9190	1	370	GTSWKIPSAAVSESSPNGAAYASGLPCGVRG
1				•	3,0	PPWAGLALLPSPTLMALLRRPTVSSDLDNIDT
i						RATT\KIRVVATITRARIEDMRHSATALTRPD
1130	2480	A	9194	131	487	ATTAQIPKLPVTTVCNRRANPGIPPSVL
1150	2700	Λ.	7134	131	40/	AYLKRLPVPESITGFARLTVSEWLRLLPFLGV
1						LALLGYLAVRPFLPKKKQQKDSLINLKIQKEN
1			1 1			PKVVNEINIEDLCLTKAAYCRCWRSKTFPAC
1121	2401		0000			DGSHNKHNELTGDNVGPLILKKKE
1131	2481	A	9201	184	605	KELVDEKSERGRAMDPVSQLASAGTFRVLKE
						PLAFLRALELLFAIFAFATCGGYSGGLRLSVD
						CVNKTESNLSIDIAFAYPFRLHQVTFEG\PTCE
		,	•	ŀ		GKERHKLALIGDSSSSAEFFGTVAGFAFLYSL
110			<u> </u>			AATGVYIFFQNKY
1132	2482	A	9206	1	852	GGGRAGAGSRDMGSTDSKLNFRKAVIQLTTK
						TQPVEATDDAFWDQFWADTATSVQDVFALV
					į	PAAEIRAVREESPSNLATLCYKAVEKLYOGA
						ESGCHSEKEKQIVLNCSRLLTRVLPYIFEDPD
			}			WRGFFWSTVPGAGRGGGGEEDDEHARPLAE
	1			*		SLILAIADLLFCPDFTVQSHRRSTVDSAEDVH
						SLDSCEYIWEAGVGFAHSPOPNYIHDMNRME
						LLKLLLTCFSEAMYLPPAPESWQH/RTHWFSS
1 1						EVECENDUAL DI ETCLI ATTUCATORI ETCLI
						FVSSENRHALPLFTSLLNTVCAYDPVEYGIPY NHLY
1133	2483	A	9208	1165	1463	
1	4403	Λ.	7400	1165	1463	GPRARVQGFSGADIVKFMALGSMYLVLTLIV
1 1	- 1			1		AKVLRGAEPCCGPLKNRVLRPCPLP/VPLPPP
1			l		j	HPQPSRGNPVGCLPTYKVVYKLLSWPLHSNS
		_,				NVYFIV
1134	2484	A	9210	66	1586	MAGAGPKRRALSAPVAEEKEEAREKIMAAK
1 1	1		l i	l	1	RADGAAPAGEGEGVTLQGNITLLKGVAVIVV
	İ			1	1	AIMGSGIFVTPTGVLKEAGSPGLALVVWAAC
			İ	1		GVFSIVGALCYAELGTTISKSGGDYAYMLDV
					J	YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL
1 1	I			1	1	LKPLFPTCPVPEEAAKLVACLCVLLLTAVNC
	1	i			ŀ	YSVKAATRVQDAFAAAKLLALALIILLGFVQI
1	ļ			l	l	GKGDVSNLDPNFSFEGTKLDVGNIVLALYSG
	1	l		l	l	LFAY.GGWNYLNFVTEEMINPYRNLPLAIIISLP
L						LIA LOG WINTENEY LEEMINF I KINLPLAIIISLP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
			<u> </u>	sequence		nucleotide insertion
			1			IVTLVYVLTNLAYFTTLSTEQMLSSEAVAVDF
		ł				GNYHLGVMSWIIPVFVGLSCFGSVNGSLFTSS
		i	İ			RLFFVGSREGHLPSILSMIHPQLLTPVPSLVFT
	1			ļ		CVMTLFYAFSKDIFSVINFFSFFNWLCVALAII
				j	}	GMIWLRHRKPELERPIKVNLALPVFFILACLF
		1	[		1	LIAVSFWKTTPWSVASDFTIILSGLPVYFFGV
						WWKNKPKWAPPGHLSPRPSCVRSSCMVVPQ
1135	2485	Α	9216	40	410	RDRLPPAYFCRPVVCVVTALDVG\SPESQEM
		1	}	1	İ	DLVAFEDVAVNFTQEEWSLLDPSQKNLYREV
	ļ		1			MQETLRNLASIGEKWKDQNIEDQYKNPRNNL
	L	<u> </u>	1	L		RSLLGERVDENTEENHCGETSSQIPDDTLNK
1136	2486	A	9223	3	983	RRRRSRYRRCSRFPRPGPLAVSMPHAFKPG
			İ			DLVFAKMKGYPHWPARIDDIADGAVKPPPN
						KYPIFFFGTHETAFLGPKDLFPYDKCKDKYGK
		]	]	1		PNKRKGFNEGLWEIQNNPHASYSAPPPVSSSD
						SEAPEANPADGSDADEDDEG\RGVMAVTAVT
	1	1	1	1		ATAASDRMESDSDSDKSSDNSGLKRKTPALK
		1	1			MSVSKRARKASSDLDQASVSPSEEENSESSSE
						SEKTSDQDFTPEKKAAVRAPRRGPLGGRKKK
		1	1	ĺ		APSASDSDSKADSDGAKPEPVAMARSASSSSS
	1	1				SSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRK
	1	1				PKPERPPSSSSSD
1137	2487	A	9229	21	239	LFPRLECRDPVTVNCTLNLPGSKNAPTTASQV
		1				GSTWNYRGGLPHPTNFFVKTGFRCSQAGLKL
		1				RGSREPPAWA
1138	2488	A	9231	1664	2	TRSVGVNTCEVGVVTEPECLGPCEPGTSVNL
	1	1	į		1	EGIVWHETEEGVLVVNVTWRNKTYVGTLLD
				1		CTKHDWAPPRFCESPTSDLEMRGGRGRGKR
		1				ARSAAAAPGSEASFTESRGLQNKNRGGANGK
	1			1		GRRGSLNASGRRTPPNCAAEDIKASPSSTNKR
			1		ł	KNKPPMELDLNSSSEDNKPGKRVRTNSRSTP
		İ				TTPQGKPETTFLDQGCSSPVLIDCPHPNCNKK
				ļ		YKHINGLRYHQAHAHLDPENKLEFEPDSEDK
		1	1			ISDCEEGLSNVALECSEPSTSVSAYDQLKAPA
		1		1		SPGAGNPPGTPKGKRELMSNGPGSIIGAKAGK
	1			1		NSGKKKGLNNELNNLPVISNMTAALDSCSAA
				[		DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK
	1					ANNCKTDKN\PSKLKSARPIAPAPAPTPPQLIA
		1	1	1		IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL
		1	1			KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR
		-		١ ،		KLKDKEGKETGSPKMDAKLGKLEDSKGASK
		1		1	1	DLPGHFLKDHLNKNEGLANGLSESQESRMAS
		1	1		1	IKAEADKVYTFTDNAPSPSIGS
1139	2489	A	9234	207	443	TRRGQPWRRRAAAAGILPGREAAACLPSC/AS
1	,	1 -	1	1		VTAAVSGLLVGYELGIISGALLQIKTLLALSC
		1	1			HEQEMGVSSLVIGALL
1140	2490	A	9238	248	328	MAQGNNYGQTSNGVADESPNMLVYRKV
1141	2491	$\frac{1}{A}$	9242	2	535	FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP
1177	4771	1^	1242	1	"""	TLRGHGGASGRNVTTGSLGEPQWLRVATGG
			1	1		RPGTSPALFSGRGAATGGRQGGRFDTKCLAA
				I		ATWGRLPGPEETLPGQDSWNGVPSRAGLGM\
				I	1	WPWAAALVVHCYSKSPSNKDAALLEAARAQ
	1			1		NMQEVSRNRCALLHSAAVQEYGYGN
1176	12402	+	0245	157	466	HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD
1142	2492	A	9245	157	400	FALGNDFLNITTKAQA/TKEKLDKLDFIKIKTC
	1	1	1			CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF
	1		1		1	
<del> </del>	<del></del>	<u> </u>	1	1	<del>                                      </del>	GICKEYSRQ
1143	2493	A	9247	264	115	GLPQQTSTIQPPGTPDGARDFTSTIQPPGAPDG
l	1	1	1	l	i	ARDSTSIIRMGPEIPPP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	}	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	İ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence	1	09/496 914	ng to first	to last amino	M=Methionine, N=Asparagine, P=Proline,
l delice		1	714	amino acid	of peptide	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
	ŀ	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		1	peptide		/=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
1144	2494	A	9260	[ 1	401	KKVPGRLSEMSFSLNFTLPANTTSSPVT\DCGP
	1	1			İ	SLGLAAGIPLLVATALLVALLFTLIHRRRSSIE
						AMEESDRPCEISEIDDNPKISENPRRSPTHEKN
						TMGAQEAHIYVKTVAGSEEPVHDRYRPTIEM ERRR
1145	2495	Α	9264	175	411	METIWIYQFRLIEIGDSTVGKSCLLHRFTQGRF
	1	١.	1	!		PGLRSPACDPTVGVDFFSRLLEIEPGKRIKLLL
		<u> L</u>				WDTAGQERFISIT
1146	2496	Α	9277	592	814	MFTYLEGREGIKSQPKMEPHSVT\RLECSGMI
1						SAHCSLNLPGTSDSPASASR/VAGTTGMRHHA
1147	2497	A	9279	1255	2	WLIFAFLVETGF
1	1 2.57		7217	1233	*	FRRGRRGEBEKEEEEEEEGWYNGMENSHPP HHHHQQPPPQPGPSGERRNHHWRSYKLMIDP
1						ALKKGHHKLYRYDGQHFSLAMSSNRPVEIVE
ľ		1				DPRVVGIWTKNKE\LELSVPKFKIDEFYVDQV
1				,	]	PPKQVTFAKLNDNIRENFLRDMCKKYGEVEE
j	1					VEILYNPKTKKHLGIAKVVFATVRGAKDAVQ
		1			!	HLIISTSVMGNIIIIVELDTKGETRMRFYELLLV
		i .				TGRYTPQTLPVGELDAVSPIVNETLQLSDALK RLKDGGLSAGCGSGSSSVTPNSGGTPFSQDTA
				. ,		YSSCRLDTPNSYG/QGTPLTPRLGTPFSQDSSY
[		ĺ				SSRQPTPSYLFSQDPAVTFKARRHESKFTDAY
						NRRHEHHYVHNSPAVTAVAGATAAFRGSSD
	i					LPFGTVGGTGGSSGPPFKAQPQDSATFAHTPP
1148	2498	A	9302	1026		PAQATPAPGFR
1170	2476	^	9302	1020	6	IASIQNADTMPGVGLLVSHFSTLVSRQRCPNY
						ADPONLTDVSIFLLLEVSGDPELQPVLAGLFL SMCLVTVLGNLLIILAISPDSHLHTPMYFFFSN
	ĺ		1 1		i	LSLPDV\GFTSTTVPK\MIVDI\QSRSRVISYAG
						CLTQKSLFAIFGGTEE\NMLLSVMAYDRFVAI
						CHPLYHSAIMNPCFCAFLVLLSFFFLSLLDSOL
			1 1			HSWIVLQFTIIKNVEISNFVCDPSQLLKFACSD
						SIINSIFIYFHKDPERQLVLAGLFLSMCLVTVL
				,		GNLIILLDVSPDSHLPTPMYFFLSNLSLPDIGFT STTVPKMIVDIQSHGRVIFYAGCLTQMSLFAIF
					l	GGMEERHAPECDGL
1149	2499	A	9303	1	699	MASQEKDIFIGWGTIHLFRKPQRSFFGKLLRE
ĺ						FRLVAADRSMGRYMLFGVINLICTGFLLMWC
						SSINSIALIVSYTYLTIFDLFSLMTCLISYWVTL
			1 1			RKPSPVYSFGFERLEVLAVFASTVLAQLGALF
					į	ILKESAERFLEQPEIHTGRLLVGTFVALCFNLF
						TMLSIRNKPFAYVSEAASTSWLQEHVADLSR SLCGIIPGLSSIFLPRMNPFVLIDLAGAFALCIT
			1 1			YMLIEI
1150	2500	A	9308	797	693	DRSTSVTRAGVQWCSLGSLQPRTPGLLRSSCL
						SLP
1151	2501	A	9309	205	406	VAIKELPVLWKWSKPTR\TAKEPPQTQQRAG
					· 1	SKTAAPPCQWSRMASEGPNIPCPGARHSDKQ
1152	2502	A	9314	913	504	FLICTI
	2002	n.	7314	713	304	KPSPLITPPAVVLPPSAVLNLVNTFSSFPQVEV
	1		1 1	1	ŀ	QGPLCGPRKGRLAVTIPFFGLS/LPKYMDHRR PPPHR\EIFFVFLAETGFHRASQAGPDLPTS/S/I
					Į	PPTSA/FPKCWEYRSEPQCLPGCLSFSGILLDL
	i			_	1	GTNVSLRAA
1153	2503	A	9315	392	1	HPHRPRPGFRSPARSSRPCPVLTSLLPPFPSPSP
						PADDLVKAGRDRKDPOVR/ERRLRPNPGRLG
l	1			,		GPR\PRPARARS/CHOPRLTRVCPRSPPPEARA
						PAPAAPARGRGAPKRNRPRTDTRAPRGSSAR
						PGNS

000 10	Longer	3.6-1	LOPO	David Co. 1	N-1'-4-1	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	0000	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ľ			peptide	_	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
1154	2504	A	9321	331	433	MPCI/QAQYGTPAPSPGPRDHSASDPLTPEFIK
		<u></u>	<u> </u>			PT
1155	2505	Α	9324	180	275	MEEPQSDPSVEPPLSQETFSDLWKLLSENNVL
1156	2506	A	9326	383	619	MISPSRTEGDPLPLPP/EGEGQEVRGFGGGPAK
	į	ļ	ŀ		}	EAAQRHCRASVSILRMRRPGQGSSRPARVPL
		<u> </u>	<u> </u>			RGPDSHRLREPPPSPP
1157	2507	A	9327	152	292	YERRGRSQGGGSHPAGAQPGGRAIGAGWQS
	0.500	ļ	0000	<b>_</b>	420	KEPLWEGLQRSGSPLPG
1158	2508	A	9328	1	430	QELKQGPNPLAPSPSAPSTSAGLGDCNHRVD
	1	1			•	LSKTFSVSSALAMLQERRCLYVVLTDSRCFL VCMCFLTFIQALMVSGYLSSVITTIERRYSLKS
ŀ		Ì		1		SESGLLVSCFDIGNLVVVVFVSYFRGRRRRP/
	1	]	l		ļ	RVAAVGGLLDLEGGEMI
1159	2509	A	9334	108	383	KGNQVNGNGNQLKRKHESMCPVSLTQNTVR
1135	2309	^	7554	100	303	LMEAGLPQKQAERADELFEAGLVIYVKLDER
						VLNAL\YSSVGLQWFKESDLSHLRLLEISFR
1160	2510	A	9338	2	430	FVGRPRGLSDRLEDLFLAGFRVGERLRTAAM
	1			-	1	KRYVRILLLGEGAEHVADPVPGGRGVPRGEA
	ļ	ł		*	1	DHTDQELREEIHKANVERVVHDVSQEATIEKI
1	ļ	ł	}		ł	RTKWIPLV/RWGDHA/EGPVGIKSYLPSGRSM
			1			EAELPIMSQLTEIETCVEC
1161	2511	A	9341	1	390	NSRVDDFVAPGLSEAGKLLGLEFPERQRLAA
l .				i	1	AVG/CSPMSGVISMSAPFFLGKIIDAIYTNPTV
1				]	ł	DYSDNLTRLCLGLSGVFLCGAAANAIRVYLM
						QTSRQRVVKRLRTSLFSSILGQEVAFSDKAGT
	L	<u> </u>				GELI
1162	2512	A	9343	84	837	QGRFRAFCWQRDFLQPPGMRLSALLALASKV
		1	1			TLPPHYRYGMSPPGSVADKRKNPPWIRRRPV VVEPISDEDWYLFCGDTVEILEGKDAGKQGK
		1	Į.		1	VVQVIRQRNWVVVGGLNTHYRYIGKTMDYR
ŀ	:					GTMIPSEAPLLHRQVKLVDPMDRKPTEIEWR
		1				FTEAGERVRVSTRSGRIIPKPEFPRADGIVPET
	İ	1	1 .			WIDGPKDTSVEDALERTYVPCLKTLQEEVME
İ	1	1	1	1	1	AMGIKETR\NTRRSIGIEPGAEQLLPNFCPSLE
						G
1163	2513	A	9346	967	616	DSLALSPRIECSGAISAHCNLTPPGFTPFSCLS
1			1	1		LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ
	1		1	i ·	1	AGLKLLISSDPPTSA/FPKCWDYRRD\SSAPAT
<u> </u>			<u></u>			FSSYQRNNPDLILNDTIMPNIK
1164	2514	A	9347	3	1099	SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI
ĺ	1	1 .		Ì	ĺ	HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL
	1 .			1	1	FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV
1		1				VAGASVGAGVWARNPRYRTEGEACVEFKA
}	1			1	1	MLIAVGIHLLLLMFEVLVCDRVERGTHFWLL
l	1				1	VFMPLFFVSPVSVAACVWGFRHDRSLELEILC
ł	1	1			1	SVNILQFIFIALKLDRIIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEORRTH
l ·					ł	VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS
1	!	İ		ĺ	1	YVSIFVPLWLSLLTLMATTFRRKGGNHWWF
	.1				1	AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA
•					1	LPLQNKDRGSWPASRGSPRLL
1165	2515	A	9362	547	991	DVSIGPPLLRRPCSGREOTRSLSFPSDPESSFSP
		1		1	1	VPEGVRLADGPGHCKGRVEVKHQNQWYTV
1	1					CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC
	1					TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP
1	1	1		1	1	LGEDTLFHVEYTSVHGRERLSAKD
1166	2516	A	9363	201	387	PPILRWTPPSGKNFFFFFFFESEFY/SSPRVECS
						GAISAHLAHCNLCLPGSSDSPASAFQVAS
1167	2517	A	9368	707	1087	AVLTPCLSPCSPSRIPRP\SRPYPGRRSLSHTPP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	L Amino cold common (A. AlL- C. C. C.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ŀ	Ì	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
}	ļ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ľ		1 '	1	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	!	!	!	ļ		PRPLILYAPAP\RPAGTAFIPHSHPPPPDLLRPT
İ		1	1 .	İ	ĺ	ATPA/TPCPSLPPPPRPLHPTQPSTALLPDPPPW
1168	2518	<del> </del>	0275		<del> </del>	PLPFPPPSS/RPPRPDCSTSYSPTFPPPT
1100	2318	Α	9375	511	15	MMLSEETSAVRPQKQTRFNGAKLVWMLKGS
ľ	Ì	l	1		ľ	PITVTSAVIIVLMLLMM/IFSPWLATHDPNAID
	]	l			ļ	LTARLLPPSAAHWFGTDEVGRDLFSRVLVGS
			ŀ			QQSILAGLVVVATTGMIGSPLECLFGELGGRA   DAIFMRVMDIMRS/IPSLVLTMBKTAALGPSL
		ĺ				FNAMQASSEH
1169	2519	A	9377	42	410	GNGRVAPRDPGAVASAEPGLTTHDSGVNPN
1		ı.,	33,,	72	1 710	NSARRMEAMASGSNWLSGVNVVLVMAYWS
		1	1			LVFVLLFIFAKRQIMRFAMKSLRGPHGPVGH
			1			NAPKDLKEEIDILLSRVHNIKYEP\HLLADDDA
1170	2520	Α	9378	302	1303	GVSGFSASVLRQRRMEDELEPSLRPRTQIQGR
ł	l	!				ILLLTICAAGIGGTFOFGYNLSIINAPTLHIOEF
						TNETWQARTGEPLPDHLVLLMWSLIVSLYPL
ļ						GGLFGALLAGPLAITLGRKKSLL\VNNIFVVS
İ						AAILFGFSRKAGSFEMIMLGRLASWGVNAGV
İ		ł				SMNIQP\MLPGGESAPKELRGAVAMSSAIFTA
						LGIVMGQVVGLSTTAATGLRGL\AGELEELEE
						ERAACQGCRARRPWELFQHRALRRQVTSLV
						VLGSAMELCGNDSVYAYASSVFRKAGVPEA
-			1			KIQYAIIGTGSCELLTAVVSVSLEGALPPPAL
1171	2521	A	9381	2	412	WGGTPRSFALNQFILQKKKK
	2321	1.	2301	2	412	RGPASAQEDERARTAPLERVRARGRMTTSSA LFPSLLPCSWSTSNKYLAEFRAGKMSLKGTTE
						TPDKRKGLAY/IQQTDDSLIHFCWKDRTSGNV
		Ì	į .			EDDLIIFPDDCEFKRLPQCPNGRVYVLKFKAG
		1				SKRLFFWMQEP
1172	2522	A	9384	20	355	GWNGRSTEASPAAEAPHVPHKET\KAAMGTQ
]		}				CTHGGKVRPDPHDMLTTVVHKIKLFVLCHSL
						LQLCAIMISDYLKSSIYTVEKRLGLFRPTSGLL
						ASFNEVGNTALIVLESY
1173	2523	Α	9393	430	87	LCQCIVPGQQKETFSLNPSSATVRFYL*LSLQ
			1 1			QRKEDQ*IIL*YHLNKDCLHIFMSAITLYMKI*
1		ļ				KIFVLFDFNIMFETPFYII*FIFLFSQNLKRIRQV
1174	2524		0000			IRPPISFSKINNGP
11/4	2524	Α	9397	77	374	ERLEIGRLGGERGSGPASCLRVIDVSGMWDQ
				j		RLVKLALLQLLRAFYGIKVKGVRVHRDCGTF
						ESSSTLIRVS*FGVPCNALAHFGVTHF*YILDF
1175	2525	A -	9399	66	397	LGML HESSPADDDVMDTBGSTVTDADBYNKSGGT
****	رعديد	^	2323	vv	331	HESSRADRDKMDTRGSTYTDADPVNKSGGT
[						AKMNKWSKGKVRDKLNNLVLFDTATYDKL CKEVPNYKLITLAVVSERLKIPGSLARAALHE
						LLSRGLI*LVIOHIAOVIY
1176	2526	A	9408	2	299	LDLTHVLSLSISLTVTILGTTFGMVIPLLDVVY
			'	_		GERGYAQNGDF*DAQLDDYSFSCYSHAOVN
( )						GAPNSLTRAYDDP*VKISGLECQKVGALVEV
						KCLNL
1177	2527	A	9416	2	402	CNFLRSSRIRVHSTPAASTMPPKVDPNEIKVV
İ					}	YLRCTGGEVRATSALAPKIGPLGLSSIKVGVD
			i l			FV*ATGDWNVLIISVILTIRILLSHIFVVPPFFCF
						DHLIAFWDLQSLIFLHVIFSLFITLLLFCFFSIF
1178	2528	A	9419	142	426	TPLFDLWPRVVLSWLETVLTSLRTRRAASGPP
						ACRIMPTTVDDVLEHGGEVHFLQKQMLYLL
1170	0.55		اا			ALI*DTFAPIYVGIVFLGFTPDHRCRSPGVAEL
1179	2529	Α	9420	1450	1655	LSSAGTKMNLN*KNYWPGASAHACNPSTLG
	1				1	GQSRCITRSGDRDHPG*HGETPSVLKIQKISRA
						WWRAP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	[	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		Į.	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ļ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	i		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	j	ŀ		peptide	}	/=possible nucleotide deletion, \-possible
				sequence	j	nucleotide insertion
1180	2530	Α	9422	176	375	HRPQTTRPDWKPRT*PQGK*GRLSSEISPASPP
			ľ		ļ	SRFSRSTKPVPPKADPPARQKI.TGVI.HAPLLK
		<u> </u>		<u> </u>		L
1181	2531	A	9436	2	274	PIAASLRMYNLQPYTEENLICTAFATMVETVP
		l	)	ļ		IARTILDRLTGIPHGYCFVE*ADWATADKCVH
	<u> </u>		<u> </u>			IYNGKPLPGATPLLSLQLHQLAHLGS
1182	2532	A	9442	3	240	VDKCSSKSIVLSEYCPHCMCSLSTDPKPFGQL SMILK*MGAGDEKISAMGKARVDHRELYLGL
				1		
		Ļ <u>.</u>	-		3	LYPTEDYKLTFRARH LKDFOPWALHDWPLFCCCTFLLFLVLECFTR
1183	2533	Α	9444	384	3	KGCSGWAPWLSLQCQHFGRPRWADHLRSGV
	]	1		1		RDOPGQYSKTTFLPKIQKLAGHSGAHL*S*LL
		1				ERMRWKNRLNPGGRSCSEPRWHHCIPGWAT
					1	ERG
1184	0524	<del> </del>	9462	391	655	LSGFKSLMPKIPLQYIYVRVRTTWSFCLPLDG
1104	2534	A	7402	331	055	RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV
		1				IHTCNPSTLGGRAGWIV*AQEFET
1185	2535	A	9467	215	566	RCPMWQGQASRMDPAKAKDREASTCCSLA
1103	2333	^	7407	213	300	WWWGWECWVRALKLSSGPAGPLACWVAK
			1	] .		KKSLSLSGPVYPSEKGAGLYVF*DRVSLCHPG
	}					WSAVVQFWLTAASNSCFSLLSSWDYRCA
1186	2536	A	9468	275	452	HIPQLHTKTHYVPTRMVNKI*QIDNSKPWQR
	5555	1	7.55	7.7		GG*TGILTHCW*ESKLVQPLWKIVWHYQ
1187	2537	A	9469	388	3	EVAPGPSQILPRRVTDGGDRPQFSLPGPRLPQ
		]				SSRGAEPCLSNCIHSPAPRKQRMGDSDQ*STP
			1	İ		NPASPHPEAPQEPWDSASGSVGSFSLGRGAK
				1		ASS*VPGKGRGPRQGSELLAETILELFLALAN
	ł	1	}	1	ł	S
1188	2538	A	9471	124	397	TMDKKNRHGNSLDMASEIHMTGPMCLIENTT
	[	.]		ł		GRLMANPEALKILSAITQPMVEEAIAGLYRAC
			L			•FYLTNNLAGMKKGLCLGSTEQAHTIGI
1189	2539	A	9480	584	769	GHVQSQHFGRPRRADHLRSGDRDHPG*HDET
		}		1	İ	PSLLKIQKISWAWWRAPVVPATWEAEAEEW
1100	L	<u> </u>	0.00		!	R VTVGLTLLLRGAPRFTAG*PPSGGGPPLAPLL
1190	2540	A	9483	463	86	
				1	:	PRQHCTLQTHRHLHPEAPVKV*KT*RLFPGLR GASSCRRRCNPVLAARKAGSPRSHSTRENC
	1				İ	RRSRCPDTAHRRRRRGRRRNPSCVRSPRWR
1101	1 2541	<del>                                     </del>	9489		411	LADALCLSAAATGAVRPGARAQPSTRRRLSP
1191	2541	A	7407	1	***	SVRVCCRAAAASNLLYSSCLQRHSERASEEG
		1 .	1	1		ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI
		1	1			MAAFVLLSYEORPLKRPRLGPPDVYPPDPKQ
						KEEELTAVNVK
1192	2542	$\frac{1}{A}$	9497	389	161	VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI*
1134	2542	1^	7471	1 307	101	CEEDERKMAREFLAEFMSTYVMMNIHMIVE
		1		1		KDTYSDHEEINTS
1193	2543	+	9509	186	1	IAKSQ*KRWQRSGAMETLKHGWWECKLVQF
1173	2343	^	1 7509	1.00	1	FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM
1194	2544	A	9512	58	433	PLORSKCLTLRCLRAKPWAWSQSPRACSSAL
****	20.77	1"	"""	1	""	LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA
		ì		1	1	SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI
i	1				1	RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ
1			+	595	1223	GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP
1195	2545	A	9515			
1195	2545	A	9515	3,5		AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC
1195	2545	A	9515			AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP
1195	2545	A	9515			PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP
1195	2545	A	9515			PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPHNL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP
1195	2545	A	9515			PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPHNL*

0EQ 10	DEA TO	1 3 2	1 000	Durali a	10.	
SEQ ID NO: of	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	j	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	Į.	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Scrine,
		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	١,	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	1	/=possible nucleotide deletion, \=possible
1,102	10515	1		sequence		nucleotide insertion
1196	2546	Α	9518	229	468	RSPTATPAPHAMOPGAPFARGGRPLPLLGAM
1	1		1	1		AERVAPGWDLHTPYLPRTNSRRTPHL**EPHA
1100		ļ	<u> </u>			GYIGALFPMSGGWPGGQ
1197	2547	A	9521	289	448	IAWLSGLFFPSNQANLCFLCYKLTADSRYRG
1						HAMRHLTGNTSMAIRFL*ADSRFQVQRARYE
						APNWKYKYGY*IPVDMLC
1198	2548	A	9524	204	1	KNKKTTKCLSIVTLNISGPNQ*NKRHRVAEWI
	1	l			1	VKQEPNICHL*ETHFPFRDTYRLKEREQKKRK
			<u> </u>			SSYS
1199	2549	Α	9546	1785	1943	GGRFKESKLTNAGWQRNSFFIGPPKSIPWAA
		]				V*QRGDGKNPGVTHLNRPVGTX
1200	2550	Α	9548	186	1	VNAEKEF*KIQHYFMTKSQNKLHIEHTYLKPI
	<u></u>	<u></u>	L		l	KAIYDKWTSDIMLNLQKL*AFFLRVIVRQI
1201	2551	A	9549	591	2	SSVVEFPRGPRSSLPPLDSTFPCGSSPNWTGGC
		1			i	GSCPSGE*LVSPGSEQRKKYSNSNVIMHETSQ
		ļ			1	YHVQHLATFIMDKSEAITSVDDAIRKLVQLSS
1	ļ	}	1		j	KEKIWTQEMLLQVNDQSLRLLDIESQEELEDF
						PLPTVQRSQTVLNQLRYPSVLLLVCQDSEQSK
1		İ				PDVHFFHCDEVEAELVHEYMESALTDCRLGK
		l	1 :		}	AMRP
1202	2552	A	9552	428	1	KYGNEGHWSRQCPNPGKPIRPCPLCRGPHWK
		İ		-		LDCERPPQGPLPSLPELAKTSYSDLTGLATED
		1				*WGPGMDAPATTIASSKTRVTLMVAGRPVFF
		l	1			LI*YRATYSALPNFSGPTQSSQVSVVGIDGQV
						SKPRATPPLFCSLHTF
1203	2553	Α	9568	517	738	RRKFERKQKQ*RYREGKQYRQRDKMKEWG
l		1	1			EKEKRREKGEREERKMRHRERKGESGQRD
		l	1			TMENWRVERLTEKER
1204	2554	Α	9573	83	415	EDKRLRLVDGDSRCAGRV*IYHDGFWGTICD
j						DGWDLSDAHVVCQKLGCGVAFNATVSAHFG
1		ļ				EGSGPIWLDDLNCTGTESHLWQCPSRGWGQ
ļ		İ				HDCRHKEDAGVICSEFTALR
1205	2555	Α	9577	64	424	ARGSCPTRPRTANGRMGETKDAPQMLVTFK
{						DVAVTFFREEWRQLVLVHRTLYR*GMLETC
	-				,	GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE
						VSHSPCAGDMRELFTREATLTPHPYNNGA
1206	2556	Α	9584	38	476	TLGAVLFSEVSKESSTSHSGGQLGRQNRHPKL
					***	SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV
						NPQPLSTPSWQIETKYSTKVLTGNWMEERRK
1				ŀ	i	GLPYKHLITHHQEPPHRYLISTYDDHYNRHG
1						YNPGLPPLRTWNGQKLLWL
1207	2557	A	9586	2	412	LRSSPAALLRALCITTVTGTALALRSRVATTN
'''		• •	7500	-	.41%	
		l. I	ľ	1	ł	PDGCRNVLRPKYYRLCDKAESWGIALETVPT
			]		l	GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP
				į		THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS
1208	2558	Α	9597	122	3	
	2000	^	1071	122	J	IKNYWPGMVAHACNPSPLGGRGRWIA*AQK
1209	2559	A	9611	148	450	FADAWADAW
	2007	^	2011	140	558	KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK
			- 1	[	1	GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ
			ŀ	ľ	ŀ	RIRDHDLLDKRKTVTALKAGEDRAILLGLAM
			}	ł		MVCSIMM*FLLGITLLRSYMQSVWTRESQCT
1210	2560	Ā	0610	304	<u></u>	LLNASITETFNC
1410	2300	W.	9618	384	2	SLHDMLMLAEQQQKQKWAVNTQNTAWSNA
		ŀ	- 1	- 1	j	DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI
			1	]	J	KVQVKNNDLGLQATINNEANWIAHQDDFNW
				Í		LLAELNTCQRQETADS***WSPKNSHVGKDS
1211	2561	<del></del>	0600			GELSAK
1411	2561	Α	9620	316	610	QKHPGGGQLGRSPQEDSRFHNKASSGVSRVR

CEO III	CEO ID	N/fet	Lego	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	וויטט	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	[ = Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	l udice	(	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
delice		1	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		i	Ì	peptide	sequence	/=possible nucleotide deletion, \=possible
		J		sequence	]	nucleotide insertion
		├	<del></del> -	Soquenoo		LGRAWWLTPVIPTLWEAKAGGSPE*D*AGRG
•		1				GSRL*SQHFGRPRRVDHLRSAVQDQPGQHGE
		Ì	1		j .	TPSLLKIQKIN*VWGRRL*SSYSEAEAGESL
1212	2562	A	9623	297	344	QFPVDQDYQKIEKITQLFQAQNLSLCLAMTR
	2502	l	, , ,		1	TREL*KGGGKGRHE*AVVPFLKKGGYGVKAP
						AILNTSNCT*CF*ETKMLSDDPKACVFEVSSA
		l				DL*NTSFGVIR
1213	2563	A	9624	2	356	AELSLASTACGRNTSGDSLPDYDRAPISSPLA
	2505	l · · ·	102.	ļ <sup>—</sup>		TSGTILSAISCLWDLPTPVLRVGLSCQPSMSSQ
	}					IPRMYSTDVEAAVNSLEDLYLQAYYAYLCVG
		l				LYFHRDDMALEGVSRFL*ELAE
1214	2564	A	9634	776	912	SLSRWVRAKL*VPYNOENCLNPRGGGCSEPR
	2001	1	1			SHYCTPAWATEKDS
1215	2565	A	9636	220	426	KPGNFAVSSEY*DITSGQLKTAVRG*IEMTST
12.5	2005	1	1000		1.20.	EENFGEKLHDIGFGNGFLDKT*KAQATKAKI
'		i				DK
1216	2566	A	9637	391	76	CFLEDGCTQAS*AEEAAVSPSMAEEEQGSTSC
12.0		'-			1	RERRSIRFKMKNHSPDDTIKENVTISNIRTRKI
		1	}	1		NHLPETERNLLEHGLMYIRLNAAFCSLVAHS
		1				LFGFILKAT
1217	2567	A	9655	2008	2432	LHCKMGALETQTHPCSQNMLRSLQKCCCKV
			1			EEHHLQPVQVLQTLLHSATAGTGCRRPARPP
	į	İ	1			PAPPTPTPWRSRQSGKQSERAS*LKGRGRYGL
	1	1		1	ļ	GALGGRGGRALGGSRWPPPLPGETLFSGCKH
	ļ	1	ļ		į	RRRRGSDAAPGEEAGT
1218	2568	A	9658	3	405	HASARALLSPNLSPNNKMAISGGPVLGFFILA
	1	1		i		VLMSAQEPWAIKEEHVIIQAEFYLNPDQSGEF
İ	ļ	Į.	1.		1	MLDFEGEDTFHGDMAKKETVWRLE*LARLD
			į	·		NFEAQRALANIAADQAALEIMDMGSDYTLIP
		1				NVPPKVTVL
1219	2569	A	9662	3	284	PDWTEKRKMQDTGSILPLHWFGFGYAALVA
		1	i			YGGIIGYVKAGSVPSLAAGLLFGSLSGLGAYQ
		ł	1		l	LSQDPRNVWVFLATSGTLAGIMGMRFYHSG
		L	1			KL
1220	2570	A	9669	200	699	LLLTGYIQTLQNQQLSGNQQEMQAVDNLTSA
ł		1	ł	i	}	PGNTSLCTRDYKITQVLFPLLYTVLFFVGLITN
ŀ		1	1			GLAMRIFFQIRSKSNFIIPLKNTVISDLLMILTF
	1	1	1	1	İ	PFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYI
1	ı	1	1	1		SISPLGLITIDRYQKTTRPFKTSNPKNLLGAKIL
	<u> </u>	<u> </u>	<u> </u>	<del> </del>	1	K
1221	2571	A	9676	164	562	KERDSSTFSAAMTTMQGMEQAMPGAGPGVP
1	· ·		1	1	1	QLGNMAVIHSHLWKGLQEKFLKGEPKVLGV
		1	1			VQILTALMSLSMGITMMCMASNTYGSNPISV
Ì		1 .	1	1	1	YIGYTIWGSVMFIISGSLSIAAGIRTTKGLVRG
		<u> </u>		<u> </u>		SLGMNITSS
1222	2572	A	9688	43	412	VAKMVKCCSAIGCASRCLPNSKLKGLTFHVF
1	1	1	1	1	1	PTDENIKRKWVLAMKRLDVNAAGIWEPKKG
Į.		1	1	1		DVLCSRHFKKTDFDRSAPNIKLKPGVIPSIFDS
100-	0.555	<del> </del>	1000	<del> </del>	<del> </del>	PYHLQGKREKLHCRKNFTLKTVPATNYNH
1223	2573	A	9696	308	564	RTSMGILYSEPICQAAYQNDFGQVWRWVKE
		]	j		]	DSSYANVQDGFNGDTPLICACRRGHVRIVSFL
L	L	<del> </del>	<del></del>	<del></del>	1.00	LKKECLCOPOKPERENLLALCCE
1224	2574	A	9700	3	632	DAWASGGELGSLFDHHVQRAVCDTRAKYRE
	-	1	1			GRRPRAVKVYTINLESQYLLIQGVPAVGVMK
[			1	1		ELVERFAL YGAIEQYNALDEYPAEDFTEVYLI
			1	1.	1	KFMNLQSARTAKRKMDEQSFFGGLLHVCYA
				ſ	1	PEFETVEETRKKLQMRKAYVVKTTENKDHY
1	ı	1		1	ſ	VTKKKLVTEHKDTEDFRQDFHSEMSGFCKA ALNTSAGNSNPYLPYSCELPLCYFSSK
ł						

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	L Amino said seemen (A. Alleit C. C.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	Į .	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1	ļ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	i	peptide		/=possible nucleotide deletion, \=possible
			<u> </u>	sequence	L	nucleotide insertion
1225	2575	A	9710	1	163	RSGCVLRMTEWETGAPAVAETPDIKLFGKWS
1006	1000	<u> </u>	<u> </u>			TDDVHINDISLQDYIAGVRLILL
1226	2576	Α	9713	82	492	QGLPSFLPAFGPSGSWLGPAPTLGSSCNTVDT
•		ĺ	1			ICHGYSEIRPLFYLSFCDLLLGLCWLTETLLYG
		1	1	Ì	}	ASVANKDIICYNLQAVGQIFYISSFLYTVNYI
				ļ	1	WYLYTELRMKHTQSGQSTSPLVIDYTCRVCQ
1227	2577	A	9720	3	416	MAFVFSSLI
1441	2311	^	3/20	3	410	GKWKRTQVPLLGEECADMDLARKEFLRGNG LAAGKMNISIDLDTNYAELVLNVGRVTLGEN
			1			NRKKMKDCQLRKQQNENVSRAVCALLNSGG
	· ·	i	ł		ł	GVIKAEVENKGYSYKKDGIGLDLENSFSNML
						PFVPNFLDFMQNGNYF
1228	2578	A	9723	278	411	EASSSNTVASNVADKTDPHSMNSRVFIGNLN
		1	7.20		711	TLVLQKSDVEAVF
1229	2579	A	9725	121	902	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDY
				1	1	GGSGGPYSKQYAGYDYSQQGRFVPPDMMQP
	1	l				QQPYTGQIYQPTQAYTPASPQPFYGNNFEDEP
				1	,	PLLEELGINFDHIWQKTLTVLHPLKVADGSIM
		1				NETDLAGPMVFCLAFGATLLLAGKIQFGYVY
						GISAIGCLGMFCLLNLMSMTGVSFGCVASVL
						GYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
			}			WCSFSASKIFISALAMEGQQLLVAYPCALLYG
				·		VFALISVF
1230	2580	Α	9739	11	247	TFVLNMNTPKEEFQDWPIVRIAAHLPDLIVYG
						HFSPERPFMDYFDGVLMFVDISGKCKRDVCL
1231	2581	A	9744	37	1100	MWMSNRLAWEFTCRA
1231	2301	A	9/44	3/	1100	TPLFDFWPGFVLSWLQPLSASLRARRAASGPP
			j		,	ACRIMPTTVDDVLEHGGEFHFFQKQMFFLLA
				,		LLSATFAPIYVGIVFLGFTPDHRCRSPGVAELS LRCGWSPAEELNYTVPGPGPAGEASPRQCRR
	1		İ			YEVDWNQSTFDCVDPLASLDTNRSRLPLGPC
						RDGWVYETPGSSIVTEFNLVCANSWMLDLFQ
						SSVNVGFFIGSMSIGYIADRFGRKLCLLTTVLI
	1					NAAAGVLMAISPTYTWMLIFRLIOGLVSKAG
			, i			WLIGYILITEFVGRRYRRTVGIFYOVAYTVGL
						LVLAGVAYALPHWRWLQFTVALPNFFFLLY
	1 1	'				YWCIPESPRWLISQNKNAEAMRIIKHIAKKNG
	5.70					KSLPASL
1232	2582	A	9753	164	517	PGPGMQGPPPITPTSWSLPPWRAYVAAAVLC
						YINLLNYMNWFIIAGVLLDIQEVFQISDNHAG
					l	LLQTVFVSCLLLSAPVFGYLGDRHSRKATMS
1233	2583	Ā	9757	25	410	FGILLWSGAGLSSSFISPRYSWLF
4433	2003	A.	7131	25	419	LPAPWTERVRKSEGLVGTCLGDPMASPRTVT
						IVALSVALGLFFVFMGTIKLTPRLSKDAYSEM
:						KRAYKSYVRALPLLKKMGINSILLRKSIGALE
				[	(	VACGIVMTLVPGRPKDVANFFLLLLVLAVLF
1234	2584	A	9765	71	456	PLEI DWGESI HEI DVAVI CDI SEGRENORIOD
,		**	7,03	'	750	RLELDWGFSLHFLPVAYLCPLSSGFEMNVQP CSRCGYGVYPAEKISCIDQIWHKACFHCEVC
			J	j		KMMLSVNNFVSHQKKPYCHAHNPKNNTFTS
					[	VYHTPLNLNVRTFPEAISGIHDQEDGEQCKSV
i						FHWD
1235	2585	A	9767	52	559	IRSGAMSVDKAELCGSLLTWLOTFHVPSPCA
,			-	1		SPQDLSSGLAVAYVLNQIDPSWFNEAWLQGI
			ŀ			SEDPGPNWKLKVTSGLLIRGQTGEEMTRDGP
				l	ŀ	
		- 1	1			AKHMSWVMGKKKDKCLVINHLFIHSSMEVSP
	[	ľ		1		ARHMSWVMGRKRDRCLVINHLFIHSSMEYSP CARPGHSARNNTDKNLPHTAIILVTSNTYTTI
1236						

CTO II	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1.00	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q-Glutamine, R-Arginine, S-Serine,
		1	l .	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
·		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	•	/=possible nucleotide deletion, \=possible
			<u> </u>	sequence		nucleotide insertion
						LERKQLNLEIYDPCSQTQKAKFSLTSELHWA
		<u> </u>				DGFVIVYDISDRSSFAFAKALI
1237	2587	A	9793	266	515	NILAIIYFPFPRLFLLRDSQSNPKAFALTLCHH
						QKIKNFQILPVSIDALTPPLVVCFLVSFLTHFS RYKPTRPVCITQFQGCS
1238	2588	A	9802	537	967	ELGAGRSDREAMEAAVKEEISVEDEAVDKNI
1238	2588	A	9802	237	907	FRDCNKIAFYRRQKQWLSKKSTYRALLDSVT
		ļ			1	TDEDSTRFQIINEASKVPLLAEIYGIEGNIFRLK
]		1				INEETPLKPRFEVPDVLTSKPSTVRLISCSGDT
İ						GSLILADGKGDLKC
1239	2589	A	9805	105	540	VPGDPAMVRAGAVGAHLPASGLDIFGDLKK
1	1	1	1			MNKROLYYOVLNFAMIVSSALMIWKGLIVLT
ļ		1			1	GSESPIVVVLSGSMEPAFHRGDLLFLTNFRED
		j	1	]	]	PIRAGEIVVFKVEGRDIPIVHRVIKVHEKDNG
Ì				1		DIKFLTKGDNNEGDDRGSYK
1240	2590	A	9819	3	305	TDGRDPLPCAARRRGGGGECCGAGWVAEWS
		ļ		1		PQPLDPAMLLWMQGFVLEAVACQDNDDYLR
		ļ		1		YGILFEDLDCNGDGVVDIIELQEGLRNWSSAF
		<u> </u>			1000	DPNSEEHG
1241	2591	Α	9834	841	1209	SPARGKSNRTDVMITAPKNKKMTENLAAPEA
	i	1				LDSSTHSSSTATQSRAKMNTPAPTPSTVPAIPR GGSGGPPPCAPHDRVSSVLQCDTQAMDHKTE
	] '	}			}	SSHSVVEFLFKRTKTPSPFHPAVRENRN
1242	2592	A	9843	3	589	TISCGPATEPPASLLSSASSDDFCKEKTEDRYS
1242	2372	^	7043	1	1 303	LGSSLDSGMRTPLCRICFQGPEQGELLSPCRC
		1	1		1	DGSVKCTHOPCLIKWISERGCWSCELCYYKY
1			1			HVIAISTKNPLQWQAISLTVIEKVQVAAAILGS
1	[	1	1			LFLIASISWLIWSTFSPSARWQRQDLLFQICYG
	ļ					MYGFMDVMIVAVDSEDMVQAAKEVGKRWS
			<u> </u>			DIPP
1243	2593	Α	9846	198	411	WRISHHAGKMPVMKGLLAPQNTFLDTIATRF
	1					DGTHSNFILANAQVAKGFPIVYCSDGFCELAG
		<u> </u>				FARTEVMQ
1244	2594	Α	9848	116	650	PICGFLYLCSAMASESSPLLAYRLLGEEGVAL
	ł	l	1	1		PANGAGGPGGASARKLSTFLGVVVPTVLSMF SIVVFLRIGFVVGHAGLLQALAMLLVAYFILA
		l				LTVLSVCAIATNGAVQGGGAYCILQHRWTG
						VWPVLPAREVMISRTLGPEVGGSIGLMFYLA
		ļ	J		1	NVCGCAVSLLGLVESVLDVFGA
1245	2595	A	9849	573	1620	KSKCRFPEGLSEGFGPMRKEALSSGSVQEAE
		1	1	1		AMLDEPQEQAEGSLTVYVISEHSSLLPQDMM
J	J			}	]	SYIGPKRTAVVRGIMHREAFNIIGRRIVQVAQ
		1		Į.		AMSLTEDVLAAALADHLPEDKWSAEKRRPL
	1	1			ļ	KSSLGYEITFSLLNPDPKSHDVYWDIEGAVRR
						YVQPFLNALGAAGNFSVDSQILYYAMLGVNP
				1		RFDSASSSYYLDMHSLPHVINPVESRLGSSAA
1		1	1	i	1	SLYPVLNFLLYVPELAHSPLYIQDKDGAPVAT
		1				NAFHSPRWGGIMVYNVDSKTYNASVLPVRV
1				1		EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL
1	1			]	1	LSGPTSEGLMTWELDRLLWARSVENLATATT
1245	2500	<del> </del>	10000	1114	464	TLTSLA
1246	2596	A	9850	114	404	PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS ARSLGRRPRIAMVTVGNYCEAEGPVGPAWM
			1			ODGLSPCFFFTLVPSTRMALGTLALVLALPCK
	1	1	1			RRERPAGADSLSWGAGPRISSYV
1247	2597	A	9851	2	327	FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF
	2371	1.	7031	~	1	HOFPTDTIQRSKWIRAVNRVDPRSKKIWIPGP
	1					GAILCSKHFQESDFESYGIRRKLKKGAVPSVS
1		1	1		1	LYKVFKYSSRCTS
	1		L	L	<u> </u>	LIEALE 199VC19

C0170 70	I ara in	1.4	Tara	15 0	18	
SEQ ID NO: of	SEQ ID NO: of			Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	1	USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	.	09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Scrine.
		1	7.4	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	-		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			peptide	saquenoo	/=possible nucleotide deletion, \=possible
		1	1 .	sequence		nucleotide insertion
1248	2598	A	9853	58	444	RVDDFVYSKGGKDAGGADVSLACRRQSIPEE
i	ł	i			1	FRGITVVELIKKEGSTLGLTISGGTDKDGKPR
İ		1				VSNLRPGGLAARSDLLNIGDYIRSVNGIHLTR
		-	l	·		LRHDEIITLLKNVGERVVLEVEYELPPPGGCP
L	1	1		!	1	WT
1249	2599	A	9856	2	1265	LPPPRPSRHRRGRAGTRASAAAAAGPTVSAV
1	1	1		j		RAPVRGQDSGAGTPQGRLAGRGAHLSRVGA
1				-	1	SGSGVAAGPAARIIAPRRRCADAGEAVGASC
					1	GRCAVALLSGVCTLVSTHVCVGSGCPGAAGT
		1		İ		PMGAGDAGASAESAVTTAPQEPPARPLQAGS
} .	1	l	1	1	1	GAGPAPGRAMRSTTLLALLALVLLYLVSGAL
1		1			İ	VFRALEQPHEQQAQRELGEVREKFLRAHPCV
	1		İ			SDQELGLLIKEVADALGGGADPETNSTSNSSH
	] .	1 .		!		SAWDLGSAFFFSGTIITTIGGGGDWHVGGGK
1	1	1	1	1		ELPHGGRCRETEGSQVAPRLPASPLCPGYGN
1	1		1.			VALRTDAGRLFCIFYALVGIPLFGILLAGVGD
1		1	1	j	1	RLGSSLRHGIGHIEAIFLKWHVPPELVRVLSA
	1	1		ļ		MLFLLIGCLLFVLTPTFVFCYMEDWSKLEAIY
1250	2600	A	0072			FVIVTLTTVGFGDYVA
1230	2000	Ι^	9873	2	652	FVVPSPCGGIPGRAPNGASRPTMGNSASRNDF
1		1	1		ł	EWVYTDQPHTQRRKEILAKYPAIKALMRPDP
		1		,		RLKWAVLVLVLVQMLACWLVRGLAWRWLL
1 .		Ì				FWAYAFGGCVNHSLTLAIHDISHNAAFGTGR
1		ł				AARNRWLAVFANLPEGVPYAASFKKYHVDH
}		1				HRYLGGDGLDVDVPTRLEGWFFCTPARKLL
1		1				WLVLQPFFYSLRPLCVHPKAVTRMEVLNTLV OLA
1251	2601	A	9875	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSR
		1		130	1205	LESYRPDTDLSREDTGCNLQHISDRENIDDLN
						MEFNPSDHPRASTIFLSKSQTDVREKRKSLFIN
ì		1				HHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTI
		1	1 1			KCVALAIYYHIKNRDPDGRMLLDIFDENLHPL
						SKSEVPPDYDKHNPEQKQIYRFVRTLFSAAQL
		ļ				TAECAIVTLVYLERLLTYAEIDICPANWKRIV
1		j	1 1			LGAILLASKVWDDQAVWNVDYCQILKDITVE
						DMNELERQFLELLQFNINVPSSVYAKYYFDL
						RSLAEANNLSFPLEPLSRERAHKLEAISRLCED
1000						KYKDLRRSARKRSASADNLTLPRWSPAIIS
1252	2602	A	9879	6	376	KRPDSRPPAQYRAGPTRPRTRGCELLYWKAT
						KAVGIKMGSLSTANVEFCLDVFKELNSNNIG
				İ		DNIFFSSLSLLYALSMVLLGARGETEEOLEKV
1050	0.00	ļ	1000			WNSSEVCSEPRSLSCSRSGSAKLILSLYQ
1253	2603	A	9880	180	388	KEQAELLYGLYCQCDLTLSSHPSSVPAMSSC
			1			NFTHATFVLIGIPGLEKAHFWVGFPLLSMYVA
1254	2604	L				AMFGNC
1234	2604	A	9881	19	494	VISFQIITDTIMDSSTAHSPVFLVFPPEITASEYE
						STELSATTFSTQSPLQKLFARKMKILGTIOILF
						GIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWG
1 1				ļ	ļ	SVLFINSGAFLIAVKRKTTETLIILSRIMNFLSA
1255	2602	<u>,                                     </u>	1000	70		LGAIAGIILLTFEFHPRSKLHL
1233	2605	A	9896	72	386	RPGREQRDCFQAPPLGLGGRQTDMMHHPLT
			1		İ	GATCVGLP:NVGMCPQLSGALTFMYLQQGNQ
1 1				- 1	į	EATVAPDTMAQPYASAQFAPPQNGIPGEYTA
1250	2000		1			PHPHPAPEYTGQTT
1256	2606	Α	9902	95	399	SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG
	1			•	1	DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK
ļ				i	Į.	PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH
1250	2605				<u> </u>	KEELE
1257	2607	A	9905	374	459	EHLKSTPNRLGVVAHTCNPSTLGGRGGW

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide	}	in USSN	nucleotide location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence		09/496	correspondi	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
delice			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	!	ļ	residue of	sequence.	Y=Tyrosine. X=Unknown, *=Stop codon,
1			ļ	peptide	Sequence.	/=possible nucleotide deletion, \=possible
1.	ł		}	sequence		nucleotide insertion
1258	2608	A	9911	364	1974	AGPGVPAVGGRWASGPGLGGRTLCSGPPDH
			//	•••	1	QRRGPSCGASGDPQCVGSPHPQRARPLLARP
	1					GARLLPGHLPSPRPPRLPTGQPPAAAFRGPVR
Í	1			ĺ	Į.	POGGGHIHPLPTPGGRPCFAVSEGSGSALLLS
1	1		1		}	YLGECGSSSYVTGAACISPVLRCREWFEAGLP
		İ	İ	İ	Í	WPYERGFLLHQKIALSRYATALEDTVDTSRL
	j				}	FRSRSLREFEEALFCHTKSFPISWDAYWDRND
	(	İ		(	ĺ	PLRDVDEAAVPVLCICSADDPVCGPPDITTLTT
				1		ELFHSNPYFFLLLSRHGGHCGFLRQEPLPAWS
{				1		HEVILESFRALTEFFRTEERIKGLSRHRASFLG
ì	ļ			1	1	GRRRGGALQRREVSSSSNLEEIFNWKRSYTRL
[						MAAAAGAAAAPGSREPQDRPECGAGHPGPR
						YYRHPERWLLRPEAFLGPLRTRAPSAEDSQR
	1					ERPAARSGPEMRVRYPVVAAVLAPYLALSQD
	l			1		PMVKSSASGQGASGSYNHVREEMLIKAGGA
1		]		1		MSRRVVRQSKFRHVFGQAAKADQAYEDIRV
Ì		l	1	i		SKVTWDSSFCAVNPKFLAJIVEAGGGGAFIVL
10.70		<u> </u>	1			PLAK
1259	2609	A	9919	693	935	GCFKFIGESTCCWIFPSSVTTQCVVAKAPRAA
						TLSKAERLRSQPGPEQGGSSYRPRTPTAAAIL
1000	0610	-	0001	455	1000	PPRPGRSHRKRKLVSTK
1260	2610	A	9921	455	1082	QRSCLCSAIEKDGGDVKALYRRSQALEKLGR LDQAVLDLQRCVSLEPKNKVFQEALRNIGGQ
1	ļ	l				IQEKVRYMSSTDAKVEQMFQILLDPEEKGTE
	1	l			1	KKQKASQNLVVLAREDAGAEKIFRSNGVQLL
		1				QRLLDMGETDLMLAALRTLVGICSEHQSRTV
	)	]	1	j	]	ATLSILGTRRVVSILGVESQAVSLAACHLLQV
	ł	1				MFDALKEGVKKGFRGKEGAIIV
1261	2611	A	9928	1	438	GFRGAEAPGAAQAPKKKKPRPTEGGPGAGSG
1201	1	••	***	1		RGKDPYRGPTLLHQPKPPKDEFLSSLESYEIAF
	l	l		1		PTRVDHNGALLAFSPPPPQRQRRGTGATAES
			1			RLFYKEASPSTHFLLNLTRSSRLLAGHVSVEY
	}	1		Į.		WTREGLAWQRADRPHCLYA
1262	2612	A	9931	168	435	AAEMGRAGAAAVIPGLALLWAVGLGGPPPA
1	ļ	ł	ļ	1		PPRLPFCLQELQGRHALHTFSLERTCSYQDFL
		L.			i	WADEGRLLHVGAQDLATWHTLSPLGLW
1263	2613	A	9938	247	488	RMSATSVDQRPKGQGNKVSVQNGSIHQKDG
	1			1	I '	CNDDDFEPYLRSPDNQSNSYPPMSDPYMPGY
L			<u></u>	L	<u> </u>	YAPSIGFPYSLGEAAWSQL
1264	2614	A	9941	61	277	ESIGLTALGPRRRPWEHRWSDPITLKMKGWG
		1		1		WLALLLGALLGTAWARRSQDLHCGACKAVR
		<u> </u>				RRVRQFNIYDY
1265	2615	A	9956	2	522	FVASEVSKMPVPASWPHPPGPFLLLTLLLGLT
	1	1	1	ļ		EVAGEELQMIQPEKLLLVTVGKTATLHCTV
	[	{			1	TSLLPVGPVLWFRGVGPGRELIYNQKEGHFP
		1		i		RVTTVSDLTKRNNMDFSIRISSITPADVGTYY
I	1		1	1		CVKFRKGSPDHVEFKSGAGTELSVRGEYSVG
10.22	1	<del> </del>	1,000=	L	200	FLSQVWWWLSSHPFMN
1266	2616	A	10002	243	387	PKNNACHLLFTAVCQPRCKHGECIGPNKCKC
100=	1001-	<del>  .                                     </del>	1 10001	120-	607	HPGYAGKTCNQGRKTV
1267	2617	A	10004	36	707	LPAPASTWSVARETMASSSVPPATVSAATAG
1	1	l	1	1		PGPGFGFASKTKKKHFVQQKVKVFRAADPLV
	1		1			GVFLWGVAHSINELSQVPPPVMLLPDDFKAS
1		ł	1			SKIKVNNHLFHRENLPSHFKFKEYCPQVFRNL RDRFGIDDQDYLVSLTRNPPSESEGSDGRFLIS
	1	1				YDRTLVIKEVSSEDIADMHSNLSNYHOVRPLS
.]	1	ĺ	1	1		SPILSLSSLLTYSSAIVSNRCQLGRKLIGRENP
1268	2618	A	10005	2	209	GEGYELFVPSNGVPAVCHMVGRRPHRAVLSP
1400	2018	1^	10003	4	209	SQDELEHSLGESAAQGAAGVVLWVSWENTR
		<u> </u>	J	L	<u> </u>	ATTENDED TO A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STANDARD A STAN

SEQ ID	SEQ ID	T 3 (-A	Toro	15 10	1	
NO: of	NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	hod	ID NO:	beginning nucleotide	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	1	in	location	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence		USSN 09/496		to last amino	I=Isoleucine, K=Lysine, L=Leucine,
uence	dence	[	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline,
uasco		1	314	amino acid	of peptide	Q=Glutamine, R=Arginine, S=Serine,
	1	i		residue of	sequence	T=Threonine, V=Valine, W=Tryptophan,
1				peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
1			1	sequence	1	
	<del> </del>	<del> </del>	<del> </del>	sequence		nucleotide insertion TKVSLGLA
1269	2619	A	10010	1 245	1 (00	
1207	2019	Α.	10010	245	688	FGMLKNKGHSSKKDNLAVNAVALQDHILHD
				[		LQLRNLSVADHSKTQVQKKENKSLKRDTKAI
1			1	İ	ĺ	IDTGLKKTTQCPKLEDSEKEYVLDPKPPPLTL
1			İ	1	1	AQKLGLIGPPPPPLSSDEWEKVKQRSLLQGDS
1270	2620	A	10011	2	200	VQPCPICKEEFELRPQVFSIRG
1270	2020	1 ^	10011	] 4	588	RVDDFVRPLPPGLMSRSRASIHRGSIPAMSYA
					1	PFRDVRGPSTHRTQYVHSPYDRPGWNPRFCII
		İ	ļ			SGNQLLMLDEDEIHPLLIRDRRSESSRNKLLR
	1		ļ		j	RTVSVPVEGRPHGEHEYHLGRSRRKSVPGGK
			1		1	QYSMEGAPAAPFRPSQGFLSRRLKSSIKRTKS
	l	l	1			QPKLDRTSSFRQILPRFRSADHDRYRGWSMW
1271	2621	<b> </b>	10010	200		DEIDV
12/1	2021	A	10013	209	363	LPAPPNLSPRLSFGFQFPGGNDNYLTITGPSHP
1272	2622		10014			FLSGAEVSQSCRRRGGRA
12/2	2022	A	10014	7	388	SAVTISWKWRSVMGIQTSPALLASLGAGLVT
1	1	1	1.			LLGLAVGSYLVRRSRRPQVTLLDPNEKDLLR
	į	l				LIDKTLSARSPCKHIYLSTRIDGSLSIRPYTPVT
1273	2623		10014			SDEDQGYVDIDIKVYLKGVHPTFPEGGKMSH
12/3	2023	A	10016	1	1339	MAARTLGRGVGRLLGSLRGLSGQPARPPCGV
						SAPRRAASGPSGSAPAVAAAAAQPGSYPALS
						AQAAREPAAFWGPLARDTLVWDTPYHTVW
1						DCDFSTGKIGWFLGGQLNVSVNCLDQHVRKS
1						PESVALIWERDEPGTEVRITYRELLETTCRLA
1	[		1 1			NTLKRHGVHRGDRVAIYMPVSPLAVAAMLA
						CARIGAVHTVIFAGFSAESLAGRINDAKCKVV
1						ITFNQGLRGGRVVELKKIVDEAVKHCPTVQH
	i i		1 1			VLVAHRTDNKVHMGDLDVPLEQEMAKEDP
						VCAPESMGSEDMLFMLYTSGSTGMPKGIVHT
	1					QAGYLLYAALTHKLVFDHQPGDIFGCVADIG
						WITGHSYVVYGPLCNGATSVLFESTPVYPNA
			1			GRYWETVERLKINQFYGAPTAVRLLLKYGD
	[		ĺĺĺ			AWVKKYDRSSLRTLGSVGEPINCEAWEWLH
1274	2624	A	10017	1	200	RVVGDSRCTLVDTWWQT
12/7	2024	Λ	10017	1	3750	FRPQGTPRSPASHVLTMSAPDEGRRDPPKPKG
	1 1		1 1			KTLGSFFGSLPGFSSARNLVANAHSSARARPA
Ì			i			ADPTGAPAAEAAQPQAQVAAHPEQTAPWTE
						KELQPSEKMVSGAKDLVCSKMSRAKDAVSS
			[ [			GVASVVDVAKGVVQGGLDTTRSALTGTKEV
						VSSGVTGAMDMAKGAVQGGLDTSKAVLTG
						TKDTVSTGLTGAVNVAKGTVQAGVDTTKTV
[	i i		i	l		LTGTKDTVTTGVMGAVNLAKGTVQTGVETS
				j		KAVLTGTKDAVSTGLTGAVNVARGSIQTGV
						DTSKTVLTGTKDTVCSGVTGAMNVAKGTIQT
						GVDTSKTVLTGTKDTVCSGVTGAMNVAKGT
				}		IQTGVDTSKTVLTGTKDTVCSGVTGAMNVA
						KGTIQTGVDTTKTVLTGTKNTVCSGVTGAVN
						LAKEAIQGGLDTTKSMVMGTKDTMSTGLTG
1						AANVAKGAMQTGLNTTQNIATGTKDTVCSG
		1				VTGAMNLARGTIQTGVDTTKIVLTGTKDTVC
		ŀ		ļ	j	SGVTGAANVAKGAVQGGLDTTKSVLTGTKD
	ľ			.		AVSTGLTGAVNVAKGTVQTGVDTTKTVLTG
				ı		TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV
				ļ		VIGTKDTMSTGLTGAANVAKGAVQTGVDTA
		ĺ		Í	İ	KTVLTGTKDTVT1GLVGAVNVAKGTVQTGM
	ĺ	1		İ		DTTKTVLTGTKDTIYSGVTSAVNVAKGAVQT
		i		1		GLKTTQNIATGTKNTFGSGVTSAVNVAKGAA
	1	- 1	1	- 1	1	QTGVDTAKTVLTGTKDTVTTGLMGAVNVAK
ــــــــــــــــــــــــــــــــــــــ						GTVQTSVDTTKTVLTGTKDTVCSGVTGAAN

WO 01/57188 PCT/US01/03800

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl- cotide	peptide seq-	}	in USSN	nucleotide location	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		J	}.	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	)	]	]	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ			peptide		/=possible nucleotide deletion, \=possible
			ļ	sequence		nucleotide insertion
	1	1		i	ĺ	VAKGAIQGGLDTTKSVLTGTKDAVSTGLTGA VKLAKGTVQTGMDTTKTVLTGTKDAVCSGV
ĺ		1	[			TGAANVAKGAVQMGVDTAKTVLTGTKDTV
			Ì		·	CSGVTGAANVAKGAVOTGLKTTONIATGTK
į	1	ì	1	•	ł	NTLGSGVTGAAKVAKGAVQGGLDTTKSVLT
ļ	1	ļ	ł		ł	GTKDAVSTGLTGAVNLAKGTVQTGVDTSKT
}			1	1	1	VLTGTKDTVCSGVTGAVNVAKGTVQTGVDT
		1	ļ	}	]	AKTVLSGAKDAVTTGVTGAVNVAKGTVQTG
		j	}	j	1	VDASKAVLMGTKDTVFSGVTGAMSMAKGA
	]	1			ł	VQGGLDTTKTVLTGTKDAVSAGLMGSGNVA
		ĺ	1		,	TGATHTGLSTFQNWLPSTPATSWGGLTSSRT
-	İ		1	4	Í	TDNGGEQTALSPQEAPFSGISTPPDVLSVGPEP
	1	l	l		ł	AWEAAATTKGLATDVATFTQGAAPGREDTG
			ł	Į	1	LLATTHGPEEAPRLAMLQNELEGLGDIFHPM NAEEQAQLAASQPGPKVLSAEQGSYFVRLGD
						LGPSFRORAFEHAVSHLOHGQFQARDTLAQL
	j	j	}	<b>J</b>	}	ODCFRL
1275	2625	A	10025	124	415	TILARKKEKTCPCKKEIGRNSRSGMYSRKAM
				l		YKRKYSAANTKVEKKKKEKVLAPVTKPVGG
					1	DKNGGTRVVKLPTMPRYYPTEDVPRKLLSHG
		Ĺ				KKPFS
1276	2626	A	10030	3	507	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMS
		l		l		ASRPQSPTTPWCLPRRYMKHKRDDGPEKQED
ļ		ł	ļ	]	l	EAVDVTPVMTCVFVVMCCSMLVLLYYFYDL
		1		ł	1	LVYVVIGIFCLASATGLYSCLAPCVRRLPFGK CRIPNNSLPYFHKRPQARMLLLALFCVAVSV
	•	ŀ		į	Į .	VWGVFRNEDQ
1277	2627	A	10035	51	869	YSRPTVPLPATMASSEVARHLLFOSHMATKT
		]				TCMSSQGSDDEQIKRENIRSLTMSGHVGFESL
						PDQLVNRSIQQGFCFNILCVGETGIGKSTLIDT
				1		LFNTNFEDYESSHFCPNVKLKAQTYELQESN
		l	1	ſ	1	VQLKLTIVNTVGFGDQINKEERQLGRSQSTEN
1		1			ĺ	PQKYRSEQHPVEPKKCTSFWKGALGKWAGIE
			1		1	SSGQSAQQPYLPINSPPHRLADVADVHLFSSV LSGAFGCYHLDVTVNEFKKQQNRDEQEGYS
	l	l	ŀ		ł	KGDQEQGSWKHGADPLRGGEM
1278	2628	A	10036	3	457	RAFDVRRKKSLRPCCPRDFHAGCLTVSGPST
/ 0	~~~~	١.,	13030	١	'-'	VMGAVGESLSVQCRYEEKYKTFNKYWCRQP
1	]	1		1	}	CLPIWHEMVETGGSEGVVRSDQVIITDHPODL
1		]		j	)	TFTVTLENLTADDAGKYRCGIATILQEDGLSG
<u>L</u>	<u> </u> _	<b>!</b>		L		FLPDPFFQVQVLVSSASSTENSVKTP
1279	2629	A	10039	214	435	NDSLVPMSSWRSCARAPSSESAWRRSAATRR
İ	1	1	1	ł ·	l	SRKCLRTKRKRWSSGKGTQMQSTLSETPRRA
100-		<del></del>	1.55.5	L	l	QMPCMWWYPFWG
1280	2630	A	10043	2	344	RATWHNAGKEREAVQLMAGAEKRVKASHS
1	1	1	ļ			FLRGLFGGNTRIEEACEMYTRAANMFKMAK
}				1	}	NWSAAGNAFCQAAKLHMQLQSKHDSATSFV DAGNAYKKADPQGKTARHVACYLCV
1281	2631	- A	10080	620	818	VIYKLDSSLFSYFIYFFIFETESHFLPLMKWTG
1201	2001	^	10000	525	""	PIMAHCSLKILASRNSADSAFLSAGDTSLSHST
1282	2632	A	10084	3	1640	SASIIIRGDKRASGEVGIAPSSRHILIGEPSAKY
		1	1.550	1	[	NGTAIISLVRGPGILGEVTVFWRIFPPSVGEFA
	1	1		1	1	ETSGKLTMRDEQSAVIVVIQALNDDIPEEKSF
ł		l	}	1	ł	YEFQLTAVSEGGVLSESSSTANITVVASDSPY
ł	1	1	}	[	l	GRFAFSHEQLRVSEAQRVNITIIRSSGDFGHVR
1		1		1	ļ	LWYKTMSGTAEAGLDFVPAAGELLFEAGEM
J		1	}	Į	]	RKSLHVEILDDDYPEGPEEFSLTITKVELQGR
	J	1		]		GYDFTIQENGLQIDQPPEIGNISIVRIIIMKNDN
L	<u> </u>	L	L	l	L	AEGIIEFDPKYTAFEVEEDVGLIMIPVVRLHGT

SEO ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
}		Ì	Į	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ĺ	peptide	1	/=possible nucleotide deletion, \=possible
		ļ		sequence		nucleotide insertion
i '	l I	l	ľ	] [		YGYVTADFISOSSSASPGGVDYILHGSTVTFQ
			1		· ·	HGQNLSFINISIIDDNESEFEEPIEILLTGATGG
1						AVLGRHLVSRIIIAKSDSPFGVIRFLNQSKISIA
l		l				NPNSTMILSLVLERTGGLLGEIQVNWETVGPN
l			1		}	SQEALLPQNRDIADPVSGLFYFGEGEGGVRTII
						LTIYPHEEIEVEETFIIKLHLVKGEAKLDSRAK
1		ł				DVTLTIQEFGDPNGVVQFAPETLSKKTYSEPL ALEGPLLITFFVRRVKGTFGEIM
1283	2633	A	10088	316	516	MGSKTLPAPVPIHPSLQLTNYSFLQAVNGLPT
1203	2033	^	10000	310	310	VPSDHLPNLYGFSALHAVHLHQWTLGYPAM
1		1				HLXRS
1284	2634	A	10091	2	569	FVSPSRAMASALIYVSKFKSFVILVVTPLLLLP
	20,54	l <b>'</b> '	10071	~	307	LVILMPAKFVRCAYVIILMAIYWCTEVIPLAV
		ł				TSLMPVLLFPLFQILDSRQVCVQYMKDTNML
		ŀ				FLGGLIVAYAVERWNLHKRIALRTLLWVGA
		ĺ	[		i .	KPARLMLGFMGVTALLSMWISNTATTAMMV
						PIVEAILQQMEATSAATEAGLELVDKGKAKE
						LP
1285	2635	A	10092	290	728	KOSTRPDVMTLYPLHWOEEMSGESVVSSAVP
1						AAATRTTSFKGTSPSSKYVKLNVGGALYYTT
1		1				MOTLTKODTMLKAMFSGRMEVLTDSEGWIL
						IDRCGKHFGTILNYLRDGAVPLPESRREIEELL
						AEAKYYLVQGLVEECQAALQV
1286	2636	A	10100	1	574	RPRGRGAWAGPGGDYSGVRRQORRTRISGS
						QRGSDAAGTMGCCTGRCSLICLCALQLVSAL
						ERQIFDFLGFQWAPILGNFLHIIVVILGLFGTIQ
						YRPRYIMVYTVWTALWVTWNVFIICFYLEVG
l						GLSKDTDLMTFNISVHRSWWREHGPGCVRR
1						VLPPSAHGMMDDYTYVSVTGCIVDFQYLEVI
						HSA
1287	2637	A	10103	252	376	RSRMGDKPIWEQIGSSFIQHYYQLFDNDRTQL
1000	0600	-,	4040	<u> </u>		GAIYVSFQL
1288	2638	A	10107	ı	478	MEEBDESRGKTEESGEDRGDGPPDRDPTLSPS
, ,						AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL
						RWRRCRSPRSEPRSQESGGTDTATVLDMATD
						SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM
						LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG
1289	2639	A	10113	237	438	KT LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT
1207	2033	Λ.	10112	L\$1	430	
						DLREIGHGSFGAAYFARDVRTNEVVAIKKMS
1290	2640	A	10114	367	856	YSG RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG
****	~~~	r.	10114	301	630	TEATRPTAMSKSLKKKSHWTSKVHESVIGRN
						PEGQLGFELKGGAENGOFPYLGEVKPGKVAY
						ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI
			İ			KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR
						GAGQ
1291	2641	Ā	10116	128	591	RTIRETERRSALSCSVLKSEPLPGLQPQASQQR
:	20.1	•	10110	.20	571	RRRLPGRRQVQVQEGGGSGLRAWVLAMASV
						LGSGRGSGGLSSQLKCKSKRRRRRRSKRKDK
						VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE
						VKENRNVGNLAARPPPSGDRARGGATR
1292	2642	A	10121	1	749	QRRFRAGLWGGHGLTDGLRRNGGCGCSAR
		١٠٠		•	. 17	VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG
						SWESWCCCCLIPADRPWDRGQIIWQLEMADT
						RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM
						LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW
						DAWSSLGDMTKEEAMIAYVEEMKKIIETMP
						MTEKVEELLRVIGPFYEIVEDKKSGRSSDITSD

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nucleotide sequence USSN location corresponding periodic sequence unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee unnee	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Sequence			hod				
1949			1				
1293	eotide	seq-	1				
mino acid residue of peptide requence purplies expuence per putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence putide sequence pu	seq-	uence	1	09/496	correspondi	to last amino	
residue of peptide sequence   y=Tyrosine, x=Unknown, ==Siop codon, peptide nucleotide deletion, y=possible nucleotide deletion, y=possible nucleotide file nucleotide filesettion   LONVLTSTPNAKTVNGKAESDSGAESEEEE   AC	uence		1	914		acid residue	
Peptide   Sequence	į	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Peptide   Sequence		1		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ł	ł	ļ	peptide	·	/=possible nucleotide deletion. \=possible
10124   2   989			İ		,	1	
1293			<del> </del>	<del> </del>	1040000		
1933	]						
	1203	2643	<u> </u>	10124		080	
CGRGIRDSARMCSTCACVEYYGKALECI.V.GVKIMCHIGKMKYKRNKIMERERICI.OSGILV CTDVMARGIDIPEVNWVLQYDPPSNASAPUR (CGRTARIGHGGSAL VFLIMERISTNFILAIN QKCPI QEMKPQRYTADILIPKLKSMALADRA VPEKGMKAFVSYVQAYAKHECNLIPRI.KDI. DFASI.ARGFALIRMFKMPELRIKQGPTDFVPV DVNTIDTIPFRDKIREKQRQKILEQQREKTEN LORGKETKIKNAWAKOKAKKK LORGKAKKY LORGKET LEGRREFIKINAWAKOKAKKK LORGKET LEGRREFIKINAWAKOKAKKK LORGKET LEGRREFIKINAWAKOKAKKK LORGKET LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIPUTALI LIP	1273	2043	^h	10124	2	707	
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CTDVMARGIDIEVNWVLQYDPFSNABAY     CGRTARIGHGGSAI VFILEMESSYNFILAIN     QKCPLQEMEPQRNTADILIPKLKSMALAND     VFKGMKARVSVQAYAKHELGIRIKNID     VFKGMKARVSVQAYAKHELGIRIKNID     VFKGMKARVSVQAYAKHELGIRIKNID     VTMYKDCIESTIGD YFLLOAEGFWGIILESLA     LGIVVTILLILAFFLMRKIQDCSQMVLPTQ     LLFLISVLGIFGLAFAFIELNQQTAPWAYEL     GVLFALCPSCLLAHASNLVKLVGGVSFSWT     TLCIAIGCSLQIILATEVYTLMTRIGMMFVN     MTCQLNVPFVULLVYVLEMITYGGVSFSWT     TLCIAIGCSLQIILATEVYTLMTRIGMMFVN     MTCQLNVPFVULLVYVLEMITYGGVSFSWT     TLCIAIGCSLQIILATEVYTLMTRIGMMFVN     MTCQLNVPFVULLVYVLEMITYGGVSFSWT     LLYIVPELCIL YRSCRQECPLQGNACPVLTVN     HSQVPNQELSRDKWEVLINSDFLSHSQA     HSQVPNQELSRDKWEVLINSDFLSHSQA     HSQVPNQELSRDKWEVLINSDFLSHSQA     HSQVPNQELSRDKWEVLINSDFLSHSQA     HSQVPNQELSRDKWEVLINSDFLSHSQA     1295   2645   A   10135   3   551     EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE     MIQDVLSALPNPDDYFLLRMLQARSPDLQKS     EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE     MIQDVLSALPNPDDYFLRMLQARSPDLQKS     EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE     MIQDVLSALPNPDDYFLRMLQARSPDLQKS     EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE     MIQDVLSALPNPDDYFLRMLQARSPDLQKS     EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE     MIQDVLSALPNPDDYFLRMLQARSPDLQKS     EWSLDFFMGIMSGQVGDLSPSQEKSLAQFRE     MIQDVLSALPNPDDYFLRMLQARSPDLQKS     EWSLDFFMGIMSGQVGDLCGSPCCQSVCCQP     EWSLDFFMGIMSGQVGGDDLCGFSCCE     TCCRTTCCRPSCCVSSCCRPQCQSVCCQP     CSPSSCCQTTCCRTTCVRSCCVSSCCRPQC     CSPSSCCQTTCCRTTCVRSCCVSSCCRPQC     CSPSSCCQTTCCRTTCVRSCCVSSCCRPQC     CSPSSCCQTTCCRTTCVRSCCVSSCCRPQC     QEMYLRFDOTTRSPYRNSRILARHQLVTKI     QEMEAKAGDFWAYCHSOLPSDFP     NIVAYKNDDFLEKDLGBFLCRRLNT     SASQLEMMERAPRAVSLALQLPEDSOP     NIVAYKNDDFLEKDLGBFLCRRLNT     ASSQLEMMERAPRAVSLALQLPEDSOP     NIVAYKNDDFLEKDLGBFLCRRLNT     SASQLEMMERAPRAVSLALQLPEDSOP     NIVAYKNDDFLEKDLGBFLCRRLNT     SASQLEMMERAPRAVSLALQLPEDSOP     SASQLEMMERAPRAVSLALQLPEDSOP     NIVAYKNDDFLEKDLGBFLCRRLNT     SASQLEMMERAPRAVSLALQLPEDSOP     SASQLEMMERAPRAVSLALQLPEDSOP     NIVAYKNDDFLEKDLGBFLCRRLNT     SASQLEMMERAPQASAGGSPWGRKAQT     RVI_GKPD9GRKRRSSSSDLQCKAQT     RVI_GKPD9GRKRAPSSSDLQCKGFCAQT     RVI_GKPD9GRK	1		1	1	!	ł	
RCGRTARIGHGGSALVELLMERSINTALIN   QKCPLQEMKPQRNTADLIPKLKSMALADRA   VFEKGMKAFVSYVQAYAKHECNLIFRI KDL   DFASILARGFALLRMFKMPELRGKQFPDFVFV   DVNTDTIPFKDKIREKQRQKLLEQQRREKTEN   EGRKRIFINKAWSKOKAKKK   ELGARKTINKAWSKOKAKKK   UTVAYKDCIESTGDYFLLCDAGGPWGIILESLA   LGIVVIILLLLAFLFLMRKIQDCSQWAVLFTQ   LLFLLSVLGIFGLAFAFIELINGQTAPVRYELF   GVLFALCFSCLLAHASRLVKLVRGCVSFSWT   TICLAIGCSLQIHATEVYTINKGMMFVN   MTPCQLNVDFVVLLVYVLFLMALTFFVSKAT   FCCPCENWKOHGRIFITVLSWISTWYWISML   LRONPOFQRQPOWDDPVVCLALVTNAWFL   LJVIVPELCILLYRSCRQEPCJOACPVTAYV   HSPQVENQELSRDKWKVLLNSDFLSHSGA   RFRVVTHNSQWCFLFQDIFFWCHQSGAFG   GRGAFRQGEFGSSWKQV   HSPQVENQELSRDKWKVLLNSDFLSHSGA   STILL   LJVIVPELCILLYRSCRQEPCJOACPVTAYV   HSPQVENQELSRDKWKVLLNSDFLSHSGA   RFRVVTHNSQWCFLFQDIFFWCHQSGAFG   GRGAFRQGEFGSSWKQV   STILL   LJVIVPELCILLYRSCRQEPCJOACPVTAYV   HSPQVENQELSRDKWKVLLNSDFLSHSGA   RFRVVTHNSQWCFLFQDIFFWCHQSGAFG   GRGAFRQGEFGSSWKQV   HSPQVENQELSRDKWKVLLNSDFLSKSGA   HQDVLSALFMFFRCQDLANILAWQPPEVVRL   YANAGICGHDGGSPVWTHVGSQDFKGLLL   SASQBLIRDSFRSCELLIRECELQSOKLGKR   VEKIAFGLEGLGIRDLWKFUQARSFDLQKS   EDMLRHMFFRCQDLANILAWQPPEVVRL   YANAGICGHDGGSPVWTHVGSQDFKGLLL   SASQBLIRDSFRSCELLIRECELQSOKLGKR   VEKIAFGLEGLGIRDLWKFQCQSVCCOPT   CGRPSCCTTCCRTCCCYSCCCGPCC   QPVCCQPTCCRPSCCETTCCHFXCC   QPVCCQPTCCRPSCCETTCCHFXCC   QPVCCQPTCCRPSCCCTTCCHFXCC   QPVCCQPTCCRPSCCCTTCCHFXCC   QPVCCQPTCCRPSCCCTTCCHFXCC   QEMYLRAPDTTRRSSPYRMSRLARRIQLVTK   QEJEAKBACDWLRAAGFPCQVSVCCOPT   ASQLENMEBAPKRYSLALQLPEHGSKLGING   VPVCCQPTCCRPSCCCTTCCHFXCC   QEMYLRAPDTTRRSSPYRMSRLARRIQLVTK   QEJEAKBACDWRGAFGA   QPVCCQPTCCRPSCCTTCTHFXCC   QPVCCQPTCCRPSCCTTCTHFXCC   QPVCCQPTCCRPSCCTTCTHFXCC   QPVCCQPTCCRPSCCTTCCHFXCC   QPVCCQPTCCRPSCCTTCCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRPSCCTTCHFXCC   QPVCCQPTCCRP	1			1	ì		1
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DFASILARGEALLRAMEKMPELRGKQFPDFVPV	1 -	ļ	l		!		
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PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV		Į	1	1	1	į	
LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV		1	]				
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IMEGVQEETDTRDVKRQVERSEICTEEPQKQ	1	İ	1				
	L	L	<u> </u>	1			IMEGVQEETDTRDVKRQVERSEICTEEPQKQ

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, B=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	ŀ			amino acid residue of	of peptide sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide	Seducince	/=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
				55411111		KSTLKNEKHLKKDDSETPHLKSLLKKEVKSS
i	İ	i			İ	KEKPEREKTPSEDKLSVKHKYKGDCMHKTG
l			1			DETELHSSEKGLKVEENIQKQSQQTKLSSDDK
1						TERKSKHRNERKLSVLGKDGKPVSEYIIKTDE
l			1			NVRKENNKKERRLSAEKTKAEHKSRRSSDSK
						IQKDSLGSKQHGITLQRRSESYSEDKCDMDST NMDSNLKPEEVVHKEKRRTKSLLEEKLVLKS
	}					KSKTQGKQVKVVETELQEGATKQATTPKPD
						KEKNTEENDSEKORKSKVEDKPFEETGVEPV
				1		LETASSSAHSTQKDSSHRAKLPLAKEKYKSD
1		1				KDSTSTRLERKLSDGHKSRSLKHSSKDIKKKD
				,		ENKSDDKDGKEVDSSHEKARGNSSLMEKKL
1	,					SRRLCENRRGSLSQEMAKGEEKLAANTLSTP
						SGSSLQRPKKSGDMTLIPEQEPMEIDSEPGVE NVFEVSKTQDNRNNNSHQDIDSENMKQKTS
	i .	1				ATVOKDELRTCTADSKATAPAYKPGRGTGV
	1					NSNSEKHADHRSTLTKKMHIQSAVSKMNPGE
						KEPIHRGTTEVNIDSETVHRMLLSAPSENDRV
						QKNLKNTAAEEHVAQGDATLEHSTNLDSSPS
	ì		Ì			LSSVTVVPLRESYDPDVIPLFDKRTVLEGSTA
	ļ					STSPADHSALPNQSLTVRESEVLKTSDSKEGG EGFTVDTPAKASITSKRHIPEAHQATLLDGKQ
	l	1	<u> </u>			GKVIMPLGSKLTGVIVENENITKEGGLVDMA
		Į.				KKENDLNAEPNLKQTIKATVENGKKDGIAVD
İ						HVVGLNTEKYAETVKLKHKRSPGKVKDISID
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						DVATGPRRAEKTSVATSTEGKDKDVTLSPVK
						AGPATTTSSETRQSEVALPCTSIEADEGLIIGT
						HSRNNPLHVGAEASECTVFAAAEEGGAVVTE GFAESETFLTSTKEGESGECAVAESEDRAADL
	ĺ	ĺ				LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE
						KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG
		ĺ				TEIRAGSISSEEVDGSQGNMMRMGPKKETEG
	İ	ł				TVTCTGAEGRSDNFVICSVTGAGPREERMVT
						GAGVVLGDNDAPPGTSASQEGDGSVNDGTE
						GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS SESEENGESAMDSTVAKEGTNVPLVAAGPCD
	1	]				DEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGH
						ASTCTGLGESEGVLICESAEGDSQIGTVVEH
	1					VEAEAGAAIMNANENNVDSMSGTEKGSKDT
	j					DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE
						GPMTSAASDQSDSQLEKVEDTTISTGLVGGS YDVLVSGEVPECEVAHTSPSEKEDEDIITSVE
	1					NEECDGLMATTASGDITNONSLAGGKNOGK
1	1	1				VLIISTSTTNDYTPQVSAITDVEGGLSDALRTE
						ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS
	1		]		]	RSEEKDECAMISTSIGEEFELPISSATTIKCAES
	[	1				LQPVAAAVEERATGPVLISTADFEGPMPSAPP
1	}		ļ			EAESPLASTSKEEKDECALISTSIAEECEASVS
	[					GVVVESENERAGTVMEEKDGSGIISTSSVEDC EGPVSSAVPOEEGDPSVTPAEEMGDTAMISTS
	j					TSEGCEAVMIGAVLODEDRLTITRVEDLSDA
	ł					AIISTSTAECMPISASIDRHEENQLTADNPEGN
		)				GDLSATEVSKHKVPMPSLIAENNCRCPGPVR
	1	١.				GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGII
	1	•				PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL
	}	1				HLINAEEKNVLLNSLQKEDKSPETGTAGGSST
						ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK DSSVSSIRYLAAVNTGAIKADDMPPVQGTVA
	[	1				EHSFLPAEQQGSEDNLKTSTTKCITGQESKIAP
	ــــــــــــــــــــــــــــــــــــــ	L	L	L	1	

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion SHTMIPPATYSVALLAPKCEQDLTIKNDYSGK WTDQASAEKTGDDNSTRKSFPEEGDIMVTVS SEENVCDIGNEESPLNVLGGLKLKANLKMEA YVPSEEEKNGEILAPPESLCGGKPSGIAELQRE PLLVNESLNVENSGFRTNEEIHSESYNKGEISS
						GRKDNAEAISGHSVEADPKEVEEERHMPKR KRKQHYLSSEDEPDDNPDVLDSRIETAQRQC PETEPHATKEENSRDLEELPKTSSETNSTTSRV MEEKDEYSSSETTGEKPEQNDDDTIKSQE
1302	2652	A	10167	321	842	EPSLFPFLRPSPARPPPRPPAPFPSPELAGPEPH FVFYFFLSYVHPPKELAKYEYMEEQVILTEKG NSTVAGRGTSVRCLSPSPRPLPPLLPLLADLLE DGFGEHPFYHCLVAEVPKEHWTPEGNPSPFP EARETKCYVRSSVGCVEPLTTQAEVTENLDR KNSQQVFKLLKKK
1303	2653	A	10171	206	429	NMILLKKRRLLINSLGEGTINGLLDELLETNV LSQEDTEIVKCENVTVIDKARDLLDSVIRKGA RACEICITYI
1304	2654	A	10184	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSFAQNGF YHEAVVLFTQALKLNPQDHRLFGNRSFCHER LGQPAWALADAQVALTLRPGWPRGLFRLGK ALMGLQRFREAAAVFQETLRGGSQPDAAREL RSCLLHLTLQGQRGGICAPPLSPGALQPLPHA ELAPSGLPSLRCPRSTALRSPGLSPLLH
1305	2655	A	10194	2	394	TDLLGRRFRVDGAAMAACEGRRSGALGSSQ SDFLTPPVGGAPWAVATTVVMYPPPPPPHR DFISVTLSFGESYDNSKSWRRRSCWRKWKQL SRLQRNMILFLLAFLLFCGLLFYINLADHWKG IRNTCT
1306	2656	A	10195		410	IPGSTISLEGPLSKWTNVMKGWQYRWFVLDY NAGLLSYYTSKDKMMRGSRRGCVRLRGAVI GIDDEDDSTFTTTVDQKTFHFQARDADEREK WIHALEETILRHTLQLQVRVFTWFPDSSLVGA FFFWLVSGFFFK
1307	2657	A	10205	85	308	QGLPSTMVKLGCSFSGKPGKDPGDQDGAAM DSVPLISPLDISQLQPPLPDQVVIKTQTEYQLS SPDQQNYTKSR
1308	2658	A	10214	2	453	ECGGIROPGPGPPPALASAPAATMNRVGGSPS AAANYLLCTNCRKVLRKDKRIRVSQPLTRGP SAFIPEKEVVQANTVDERTNFLVEEYSTSGRL DNITQVMSLHTQYLESFLRSQFYMLRMDGPL PLPYRHYIAIMAAARHQCSYLINM
1309	2659	A	10233	45	421	RGWPEQQSTGRPRDVARQPRCQKEEGRRLRP RALESRTFQGSERSRWGPPLESTKENVQCGH RPAFPNSSWLPFHERLQVQNGECPWQVSIQM SRKHLCGGSILHWWWVLTAAHCFRRTLLDM AV
1310	2660	A	10241	243	442	AFQLFNAKCESAFLSKRNPLQRNWTVLYRRK HKKGQSAEIQKKRTRRAFKFQRAITGASLADI MAK
1311	2661	Ā	10261	751	176	LPGADYGGGHLSLRLFHLLLTSAAWVPDESQ VTLNSAICVLSTVLIMEFPDLGKHCSEKTCKQ LDFLPVKCDACKQDFCKDHFPYAAHKCPFAF QKDVHVPVCPLCNTPIPVKKGQIPDVVVGDHI DRDCDSHPGKKKEKIFTYRCSKEGCKKKEML QMVCAQCHGNFCIQHRHPLDHSCRHGSRPTI KAG
1312	2662	A	10270	3	669	STSSDEGSPSASTPMINKTGFKFSAEKPVIEVP SMTILDKKDGEQAKALFEKVRKFRAHVEDSD

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- eotide seq-	peptide seq- uence		in USSN 09/496	nucleotide location correspondi	location corresponding to last amino	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence		f	914	ng to first amino acid	acid residue of peptide	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
				residue of peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
	-			sequence		nucleotide insertion LIYKLYVVOTVIKTAKFIFILCYTANFVNAISF
						EHVCKPKVEHLIGYEVFECTHNMAYMLKKL LISYISIICVYGPICLYTLFWLFRIPLKEYSFEKV REESSFSDIPDVKNDFAFLLHMVDQYDQLYS
1313	2663	A	10287	1221	266	KRFGVFLSEVSENKLREISLNHEWTFEKL GAHRVLSPAQGAQPRLRSAASVEVSMVGOR
						VLLLVAFLLSGVLLSEAAKILTISTLGGSHYLL LDRVSQILQEHGHNVTMLHQSGKFLIPDIKEE
				!		EKSYQVIRWFSPEDHQKRIKKHFDSYIETALD
						GRKESEALVKLMEIFGTQCSYLLSRKDIMDSL KNENYDLVFVEAFDFCSFLIAEKLVKPFVAIL
	ļ					PTTFGSLDFGLPSPLSYVPVFPSLLTDHMDFW
	]	ì				GRVKNFLMFFSFSRSQWDMQSTFDNTIKEHF PEGSRPVLSHLLLKAELWFVNSDCAFDFARPL
1214	6224		10000	-23.6	1000	LPNTVYIGGLMEKPIKPVPQVSEPSAFSLGFT
1314	2664	Α	10288	536	1890	NVQLAKFSSTLVFFFSCDADPSALAKYVLAL VKKDKSEKELKALCIDQLDVFLQKETQIFVEK
						LFDAVNTKSYLPPPEQPSSGSLKVEFFPPQEK
i .	i					DIKKEEITKEEEREKKFSRRLNHSPPQSSSRYR ENRSRDERKKDDRSRKRDYDRNPPRRDSYRD
ļ	j					RYNRRGRSRSYSRSRSWSKERLRERDRD
						RSRTRSRSRTRSRERDLVKPKYDLDRTDPLEN
Ī						NYTPVSSVPSISSGHYPVPTLSSTITVIAPTHHG NNTTESWSEFHEDQVDHNSYVRPPMPKKRC
						RDYDEKGFCMRGDMCPFDHGSDPVVVEDVN
	· .					LPGMQPFPAQPPVVEGPPPPGLPPPPPILTPPPV   NLRPPVPPPGPLPPSLPPVTGPPPPLPPLQPSG
]						MDAPPNSATSSVPTVVTTGIHHQPPPAPPSLFT
						ADTYDTDGYNPEAPSITNTSRPMYRHRVHPR AKLG
1315	2665	A	10293	447	1331	SHPLLSCPEKVSAKLRAAAEAAAEERRTRGA
						GSRGICAGLRSVAPGPEPLKQEEGRREWGSSI GTPSPCGSAQAAAAAAAEEATEKIPALRPALL
						WALLAL WLCCATPAHALQCRDGYEPCVNEG
						MCVTYHNGTGYCKCPEGFLGEYCQHRDPCE
						KNRCQNGGTCVAQAMLGKATCRCASGFTGE DCQYSTSHPCFVSRPCLNGGTCHMLSRDTYE
						CTCQVGFTGRNPKCPGGNLNYQFNGIIVVYS
1			İ			GGSVPPSGTKTSKPAEHNAMGTGSKNFASGT LWVMVSGATSTSTSTL
1316	2666	A	10294	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTG
						YSLVQENGQRKYGGPPPGWDAAPPERGCEIFI GKLPRDLFEDELIPLCEKIGKIYEMRMMMDF
						NGNNRGYAFVTFSNKVEAKNAIKQLNNYEIR
1317	2667	<u> </u>	10201	160	105/	NGRLLGVCASVDNCRLFVGGIPKTKK
131/	2667	Α	10301	158	1956	LLKSCGVLLSGVCIPCEGKGPTVLVIQTAVPQ DRPTKSSMRSAAKPWNPAIRAGGHGPDRVRP
}						LPAASSGMKSSKSSTSLAFESRLSRLKRASSE
						DTLNKPGSTAASGVVRLKKTATAGAISELTES RLRSGTGAFTTTKRTGIPAPREFSVTVSRERSV
}						PRGPSNPRKSVSSPTSSNTPTPTKHLRTPSTKP
						KQENEGGEKAALESQVRELLAEAKAKDSEIN
1						RLRSELKKYKEKRTLNAEGTDALGPNVDGTS VSPGDTEPMIRALEEKNKNFQKELSDLEEENR
						VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ
}						ESSFGSPTGNQLSSDIDEYKKNIHGNALRTSG SSSSDVTKASLSPDASDFEHITAETPSRPLSSTS
						NPFKSSKCSTAGSSPNSVSELSLASLTEKIQKM
L	L					EENHHSTABELQATLQELSDQQQMVQELTAE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	}	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
delice	l	l	1 /17	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}	ł	ł			Y-Touring W-Yutmann to Cton and an
ļ	}	i	ļ.	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1	l ·	ł	peptide	1.	/=possible nucleotide deletion, \=possible
	i.	ł		sequence		nucleotide insertion
						NEKLVDEKTILETSFHQHRERAEQLSQENEKL
ł	1	1	ł	}	1	MNLLQERVKNEEPTTQEGKIIELEQKCTGILE
İ	1	1	1			QGRFEREKLLNIQQQLTCSLRKVEEENQGAL
ł	Į	ļ	İ		1	EMIKRLKEENEKLNEFLELERHNNNMMAKTL
ĺ	l	ł	1	·	[	
	<del> </del>	ļ. <u></u>	<b>1</b>			EECRVTLEGLKMENGSLKSHLQG
1318	2668	A	10303	333	879	GECFIMAAVVQQNDLVFEFASNVMEDERQL
1		1	1		1	GDPAIFPAVIVEHVPGADILNSYAGLACVEEP
ì	1		İ			NDMITESSLDVAEEEIIDDDDDDDTLTVEASCH
}	}		Į.	1	ļ	DGDETIETIEAAEALLNMDSPGPMLDEKRINN
		İ	1		İ	NIFSSPEDDMVVAPVTHVSVTLDGIPEVMETQ
	l		Į.	i		
1010	-	ļ.,	1	1		QVQEKYADSPGASSPEQPKRKKK
1319	2669	A	10322	169	654	MEVRMSGSVAVTRAIAVPGLLLLLIIATALSL
(	1	1	1	1	[	LIGAKSLPASVVLEAFSGTCQSADCTIVLDAR
]	į			1		LPRTLAGLLAGGALGLAGALMQTLTRNPLAD
[ '	1	1	ł	1	·	PGLLGVNAGASFAIVLGAALFGYSSAOEOLA
l		1	1		]	MAFAGALVASLIVAFTGSQGGGQLSPVRLTL
]	}	]	j		j	AGVXL
1320	2670	A	10323	441	2	
1320	2070	ΙΑ.	10323	441	4	KMNQVAVVIGGGQTLGAFLCHGLAAEGYRV
ł	ł	ł	ľ	1	l ' '	AVVDIQSDKAANVAQEINAEYGESMAYGFG
	· [				ļ	ADATSEQSVLALSRGVDEIFGRVDLLVYSAGI
1	1					AKAAFISDFQLGDFDRSLQVNLVGYFLCARE
1	İ	1	ļ			FSRLMIRDGIQGRIIQINSKSDE
1321	2671	A	10332	1	453	RHRTAGPGSTISSRTDSASAPAARAMPCEYTY
		1		_	1	AKLTSDCSRPSLQWYTRAQSKMRRPRLLLKD
	ļ	1	)			ILKCTLLVFGVRILYILKLNYTTEECDMKNMH
l	1		1		ļ	
Ì	j	i	Į.		1	YVDPDHVKRAQKYAQQVLQKESPPKFAKTS
		<u> </u>			<u></u>	MALLFEHRYSVDLLPFVQKAPTDSEA
1322	2672	A	10333	25 .	423	EPSNGPVVYSALGNEDDEILLLGKDIIGTFAAS
i	1	1	ł	!		ERKMRAHQVLTFLLLFVITSGASENASTSRGC
ĺ	1	ĺ	<b>S</b>	ĺ		GLDLLPQNVYLCDLDAIWGIVVEAVAGAGA
<u> </u>		i	l	1		LITLLLMLILLGRLPFIKEKEKKSPAVLHFLFL
ļ	1	}	į.		}	LGTLG
1323	2673	A	10334	52	426	SSLGNEDDEILSLAKDITGMFVASHRKMRAH
1323	2073	Ι^	10334	32	420	•
	1	İ	ł		l	QVLTFLLLFVITSVASENASTSRGCGLDLLPQ
i	1	ł	1			YVSLCDLDAIWGIVVEAAAGAGALITLLLMLI
			<u></u>	i		LLVRLPFFKEKEKKSPVGLHFLFLLGTLGP
1324	2674	A	10336	1	932	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEE
ļ	1	1,		İ		NSVTHHEVKCQGKPLAGIYRKREEKRNAGN
İ		ľ	l ·		1	AVRSAMKSEEQKIKDARKGPLVPFPNQKSEA
ļ		]	ľ	ļ	}	
		I	1	l	1	AEPPKTPPSSCDSTNAAIAKQALKKPIKGKQA
1		I	1	l		PRKKAQGKTQQNRKLTDFYPVRRSSRKSKAE
(	.	i	1	l	İ	LQSEERKRIDELIESGKEEGMKIDLIDGKGRG
i	1	l	1	1		VIATKQFSRGDFVVEYHGDLIEITDAKKREAL
ļ		l	1			YAQDPSTGCYMYYFQYLSKTYCVDATRETN
1		1	1	l		RLGRLINHSKCGNCOTKLHDIDGVPHLILIAS
ĺ		[	[	Ī		RDIAAGEELLYDYGDRSKASIEAHPWLKH
1325	2675	A	10338	3	870	PGSTISCSELKGTQCRATAGSRGRRPPMTCWL
1525	2073	1 ^	10220	١	370	1
	1	1	İ	1		RGVTATFGRPAEWPGYLSHLCGRSAAMDLG
l		1			[	PMRKSYRGDREAFEETHLTSLDPVKQFAAWF
1	1	ł	ŀ	{	l	EEAVQCPDIGEANAMCLATCTRDGKPSARML
		1	1	ĺ		LLKGFGKDGFRFFTNFESRKGKELDSNPFASL
		I		1		VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS
		l	ļ	1		RPKSSOIGAVVSHOSSVIPDREYLRKKNEELE
	1	1		1		QLYQDQEVPKPKSWGGYVLYPQVMEFWQG
	i	1	1		ļ	
		1	ļ	}		QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE
100-	<u> </u>	<b>I</b>	L	ļ		DWLYERLAP
1326	2676	Α	10344	2	984	ARAAAHCGICRLVRWWRKRRSVMGIQTSPV
ł	1	ł	{	1	ļ	LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT
İ	1	1				LLDPNEKYLLRLLDKTTVSHNTKRFRFALPTA
		1	<b></b> .	·	L_,	L. Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO; of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
10000		l	l	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
1 1		Ì	l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ļ	peptide	Sequence	/=possible nucleotide deletion, \=possible
}		ì	Ì			nucleotide insertion
		ļ	<u> </u>	sequence		
!!!		ł	!	!	•	HHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSD
1 1						EDQGYVDLVIKVYLKGVHPKFPEGGKMSQY
				ļ		LDSLKVGDVVEFRGPSGLLTYTGKGHFNIQP
1 1		1		Ì	•	NKKSPPEPRVAKKLOMIAGGTGITPMLQLIRA
1			1		Į	ILKVPEDPTQCFLLFANQTEKDIILREDLEELQ
1		ŀ	ŀ			ARYPNRFKLWFTLDHPPKDWAYSKGFVTAD
1						MIREHLPAPGDDVLVLLCGPPPMVQLACHPN
1		1				LDKLGYSQKMRFTY
1327	2677	A	10345	1	968	LQSAGEGYTHVLILLESPARPVAAVTQVQRR
				-		RYHRLSDMSMLAERRRKQKWAVDPQNTAW
1						SNDDSKFGQRMLEKMGWSKGKGLGAQEQG
1 1		,				ATDHIKVQVKNNHLGLGATINNEDNWIAHQ
1 1						1
1						DDFNQLLAELNTCHGQETTDSSDKKEKKSFS
1						LEEKSKISKNRVHYMKFTKGKDLSSRSKTDL
1						DCIFGKRQSKKTPEGDASPSTPEENETTTTSAF
1 1						TIQEYFAKRMAALKNKPQVPVPGSDISETQVE
1						RKRGKKRNKEATGKDVESYLQPKAKRHTEG
1						KPERAEAQERVAKKKSAPAEEQLRGPCWDQ
						SSKASAQDAGDHVQPA
1328	2678	Α	10346	173	439	GSAAMKVKIKCWNGVATWLWVANDENCGI
1 1				,		CRMAFNGCCPDCKVPGDDCPLVWGQCSHCF
1						HMHCILKWLHAQQVQQHCPMCRQEWKFKE
1329	2679	A	10351	3	964	OMEPGNDTOISEFLLLGFSOEPGLOPFLFGLFL
					74.	SMYLVTVLGNLLIILATISDSHLHTPMYFFLSN
1 1						LSFADICVTSTTIPKMLMNIQTQNKVITYIACL
1 1						MQMYFFILFAGFENFLLSVMAYDRFVAICHP
1 1						, -
1 1						LHYMVIMNPHLCGLLVLASWTMSALYSLLQI
1 1						LMVVRLSFCTALEIPHFFCELNQVIQLACSDSF
1 1			ļ			LNHMVIYFTVALLGGGPLTGILYSYSKIISSIH
1						AISSAQGKYKAFSTCASHLSVVSLFYGAILGV
1						YLSSAATRNSHSSATASVMYTVVTPMLNPFI
<del></del>						YSLRNKDIKRALGIHLLWGTMKGQFFKKCP
1330	2680	Α	10352	34	2573	IPFLKSCCCCCLFDFPPPPLDQVQEEECEVERV
1 1						TEHGTPKPFRKFDSVAFGESQSEDEQFENDLE
1 1						TDPPNWQQLVSREVLLGLKPCEIKRQEVINEL
1 1						FYTERAHVRTLKVLDQVFYQRVSREGILSPSE
1						LRKIFSNLEDILQLHIGLNEQMKAVRKRNETS
1 1						VIDQIGEDLLTWFSGPGEEKLKHAAATFCSNQ
1 1						PFALEMIKSRQKKDSRFQTFVQDAESNPLCRR
				İ		LQLKDIIPTQMQRLTKYPLLLDNIATYTEWPT
1		l				EREKVKKAADHCRQILNYVNQAVKEAENKQ
						RLEDYORRLDTSSLKLSEYPNVEELRNLDLTK
j l						RKMIHEGPLVWKVNRDKTIDLYTLLLEDILV
[						LLQKQDDRLVLRCHSKILASTADSKHTFSPVI
	-					1 2. 7
1	Ì					KLSTVLVRQVATDNKALFVISMSDNGAQIYE
						LVAQTVSEKTVWQDLICRMAASVKEQSTKPI
1	j		,			PLPQSTPGEGDNDEEDPSKLKEEQHGISVTGL
1 1	ļ					QSPDRDLGLESTLISSKPQSHSLSTSGKSEVRD
	ţ					LFVAERQFAKEQHTDGTLKEVGEDYQIAIPDS
]						HLPVSEERWALDALRNLGLLKQLLVQQLGLT
				í		EKSVQEDWQHFPRYRTASQGPQTDSVIQNSE
1 1						NIKAYHSGEGHMPFRTGTGDIATCYSPRTSTE
, 1	1					SFAPRDSVGLAPQDSQASNILVMDHMIMTPE
				l	l	OTTE TOO COME OF OUT OF THE PROPERTY OF THE
						MPTMEPEGGLDDSGEHFFDAREAHSDENPSE
						MPTMEPEGGLDDSGEHFFDAREAHSDENPSE GDGAVNKEEKDVNLRISGNYLILDGYDPVQE
						MPTMEPEGGLDDSGEHFFDAREAHSDENPSE GDGAVNKEEKDVNLRISGNYLILDGYDPVQE SSTDEEVASSLTLQPMTGIPAVESTHQQQHSP
						MPTMEPEGGLDDSGEHFFDAREAHSDENPSE GDGAVNKEEKDVNLRISGNYLILDGYDPVQE SSTDEEVASSLTLQPMTGIPAVESTHQQQHSP QNTHSDGAISPFTPEFLVQQRWGAMEYSCFEI
						MPTMEPEGGLDDSGEHFFDAREAHSDENPSE GDGAVNKEEKDVNLRISGNYLILDGYDPVQE SSTDEEVASSLTLQPMTGIPAVESTHQQQHSP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end a nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1331	2681	A	10353	1	2100	AVEFAEGALTMAPWPELGDAQPNPDKYLEG AAGQQPTAPDKSKETNKTDNTEAPVTKIELLP SYSTATLIDEPTEVDDPWNLPTLQDSGIKWSE RDTKGKILCFFQGIGRLILLGFLYFFVCSLDIL SSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIG VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIP IIMGANIGTSITNTIVALMQVGDRSEFRRAFA GATVHDFFNWLSVLVLLPVEVATHYLEIITQL IVESFHFKNGEDAPDLLKVITKPFTKLIVQLDK KVISQIAMNDEKAKNKSLVKIWCKTFTNKTQ INVTVPSTANCTSPSLCWTDGIQNWTMKNVT YKENIAKCQHIFVNFHLPDLAVGTILLILSLLV LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP FPFAWLTGYLAILVGAGMTFIVQSSSVFTSAL TPLIGIGVITIERAYPLTLGSNIGTTTTAILAAL ASPGNALRSSLQIALCHFFFNISGILLWYPIPFT RLPIRMAKGLGNISAKYRWFAVFYLIFFFLIP LTVFGLSLAGWRVLVGVGVPVVFIIILVLCLR LLQSRCPRVLPKKLQNWNFLPLWMRSLKPW DAVVSKFTGCFQMRCCCCCRVCCRACCLLC GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET
1332	2682	A	10354	30	1377	FDNITISREAQGEVPASDSKTECTAL  SQQGSQPHRQGPPSLLTAPHSLDLPALPPGPR GSQGKLRRVLVPMSVKPSWGPGPSEGVTAVP TSDLGEIHNWTELLDLFNHTLSECHVELSQST KRVVLFALYLAMFVVGLVENLLVICVNWRG SGRAGLMNLYILNMAIADLGIVLSLPVWMLE VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF LVCLSVDRYVTLTSASPSWQRYQHRVRRAM CAGIWVLSAIIPLPEVVHIQLVEGPEPMCLFM APFETYSTWALAVALSTTILGFLLPFPLITVFN VLTACRLRQPGQPKSRRHCLLLCAYVAVFV MCWLPYHVTLLLITLHGTHISLHCHLVHLLY FFYDVIDCFSMLHCVINPILYNFLSPHFRGRLL NAVVHYLPKDQTKAGTCASSSSCSTQHSIIIT KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP TOPLTPS
1333	2683	A	10358	2	884	AAGAGADGREPASERASRAEPPAVAMGOND LMGTAEDFADQFLRVTKQYLPHVARLCLIST FLEDGIRMWFQWSEQRDYIDTTWNCGYLLA SSFVFLNLLGQLTGCVLVLSRNFVQYACFGLF GIIALQTIAYSILWDLKFLMRNLALGGGLLLL LAESRSEGKSMFAGVPTMRESSPKQYMQLGG RVLLVLMFMTLLHFDASFFSIVQNIVGTALMI LVAIGFKTKLAALTLVVWLFAINVYFNAFWT IPVYKPMHDFLKYDFFQTMSVIGGLLLVVAL GPGGVSMDEKKKEW
1334	2684	A	10367	59	1562	QAWSLQVALSPFFFPASPSNSFAAAVPQLLFP ELPLPHVPGQESAKRRSARRFLIMSELTKELM ELVWGTKSSPGLSDTIFCRWTQGFVFSESEGS ALEQFEGGPCAVIAPVQAFLLKKLLFSSEKSS WRDCSQEEQKELLCHTLCDILESACCDHSGS YCLVSWLRGKTTEETASISGSPAESSCQVEHS SALAVEELGFERFHALIQKRSFRSLPELKDAV LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN EIEDASEPLIDPVYGHGSQSLINLLTGHAVSN VWDGDRECSGMKLLGIHEQAAVGFLTLMEA LRYCKVGSYLKISKIPYLDCLASETHLTVFFA KDMALVAPEAPSEQARRVFQTYDPEDNGFIP DSLLEDVMKALDLVSDPEYINLMKNKLDPEG

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nuci-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	į	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1		}	i '	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	j		peptide	ļ	/=possible nucleotide deletion, \=possible
		ļ		sequence		nucleotide insertion
	1					LGIILLGPFLQEFFPDQGSSGPESFTVYHYNGL
ĺ	İ	1				KQSNYNEKVMYVEGTAVVMGFEDPMLQTD
		<u> </u>	L			DTPIKRCLQTKWPYIELLWTTDRSPSLN
1335	2685	A	10375	82	2929	TRTKRRLGREKAMASPPRGWGCGELLLPFML
						LGTLCEPGSGQIRYSMPEELDKGSFVGNIAKD
		1				LGLEPQELAERGVRIVSRGRTQLFALNPRSGS
1						LVTAGRIDREELCAQSPLCVVNFNILVENKM
1						KIYGVEVEIIDINDNFPRFRDEELKVKVNENA
						AAGTRLVLPFARDADVGVNSLRSYQLSSNLH
1						FSLDVVSGTDGQKYPELVLEQPLDREKETVH
1						DLLLTALDGGDPVLSGTTHIRVTVLDANDNA
	<u> </u>			!		PLFTPSEYSVSVPENIPVGTRLLMLTATDPDE
1						GINGKLTYSFRNEEEKISETFQLDSNLGEISTL
1	(			,		QSLDYEESRFYLMEVVAQDGGALVASAKVV
1						VTVQDVNDNAPEVILTSLTSSISEDCLPGTVIA
	ļ					LFSVHDGDSGENGEIACSIPRNLPFKLEKSVD
1						NYYHLLTTRDLDREETSDYNITLTVMDHGTP
						PLSTESHIPLKVADVNDNPPNFPQASYSTSVT
Ì						ENNPRGVSIFSVTAHDPDSGDNARVTYSLAE
ĺ					,	DTFQGAPLSSYVSINSDTGVLYALRSFDYEQL
İ		١.				RDLQLWVTASDSGNPPLSSNVSLSLFVLDQN
						DNTPEILYPALPTDGSTGVELAPRSAEPGYLV
1			l i			TKVVAVDKDSGQNAWLSYRLLKASEPGLFA
]						VGLHTGEVRTARALLDRDALKQSLVVAVED
						HGQPPLSATFTVTVAVADRIPDILADLGSIKTP
1						IDPEDLDLTLYLVVAVAAVSCVFLAFVIVLLV
1						LRLRRWHKSRLLQAEGSRLAGVPASHFVGV
1						DGVRAFLQTYSHEVSLTADSRKSHLIFPQPNY
						ADTLLSEESCEKSEPLLMSDKVDANKEERRV   QQAPPNTDWRFSQAQRPGTSGSQNGDDTGT
]						WPNNQFDTEMLQAMILASASEAADGSSTLGG
						GAGTMGLSARYGPQFTLQHVLQGELGSDYR
						QNVYIPGSNATLTNAAGKRDGKAPAGGNGN
						KKKSGKKEKK
1336	2686	A	10379	1	557	RPRRRQPSFSCRVLVLEDPPCFRFTNSMNOEK
	5555		100,7	1	331	LAKLQAQVRIGGKGTARRKKKVVHRTATAD
						DKKLQSSLKKLAVNNIAGIEEVNMIKDDGTVI
			ļ			HFNNPKVQASLSANTFAITGHAEAKPITEMLP
		i				GILSQLGADSLTSLRKLAEQFPRQVLDSKAPK
		- 1	i	1		PEDIDEEDDDVPDLVENFDEASKNEAN
1337	2687	A	10380	1	1263	IPGSTISWSPAAARGLSVCRCCRLHPASAMDL
			1			FGDLPEPERSPRPAAGKEAQKGPLLFDDLPPA
			1	Į		SSTDSGSGGPLLFDDLPPASSGDSGSLATSISQ
				l		MVKTEGKGAKRKTSEEEKNGSEELVEKKVC
		İ	1	ľ	ĺ	KASSVIFGLKGYVAERKGEREEMQDAHVILN
			ŀ		1	DITEECRPPSSLITRVSYFAVFDGHGGIRASKF
1		1		• .	l	AAQNLHQNLIRKFPKGDVISVEKTVKRCLLD
}		1	ì			TFKHTDEEFLKQASSQKPAWKDGSTATCVLA
.	,	1	j	J	J	VDNILYIANLGDSRAILCRYNEESQKHAALSL
1			1	ļ		SKEHNPTQYEERMRIQKAGGNVRDGRVLGV
		Į	ſ	Ì	ł	LEVSRSIGDGQYKRCGVTSVPDIRRCQLTPND
1 1	1	1	. !	}	1	RFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ
1 1	l	ł	ł	i	Į	TREGKSAADARYEAACNRLANKAVQRGSAD
						NVTVMVVRIGH
1338	2688	À	10385	3	589	GPSQSMAAGELEGGKPLSGLLNALAQDTFHG
]	1	- 1	[	1		YPGITEELLRSQLYPEVPPEEFRPFLAKMRGIL
		- 1	ſ	ĺ	ĺ	KSIASADMDFNQLEAFLTAQTKKQGGITSDQ
						AAVISKFWKSHKTKIRESLMNQSRWNSGLRG
	ļ		ŀ	l	Į.	LSWRVDGKSQSRHSAQIHTPVAIIELELGKYG
				]		QESEFLCLEFDEVKVNQILKTLSEVEESISTLIS

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion OPN
1339	2689	A	10386	50	390	LGAMAKHHPDLIFCRKQAGVAIGRLÆEKCDG KCVICDSYVRPCTLVRICDECNYGSYQGRCVI CGGPGVSDAYYCKECTIQEKDRDGCPKIVNL GSSKTDLFYERKKYGFKKR
1340	2690	A	10388	113	3472	SQLRKGASATHSSPSRTDCIAQMMDIYVCLK RPSWMVDNKRMRTASNFQWLLSTFILLYLM NQVNSQKKGAPHDLKCVTNNLQVWNCSWK APSGTGRGTDYEVCIENRSRSCYQLEKTSIKIP ALSHGDYEITINSLHDFGSSTSKFTLNEQNVSL IPDTPEILNLSADFSTSTLYLKWNDRGSVFPHR SNVIWEIKVLRKESMELVKLVTHNTTLNGKD TLHHWSWASDMPLECAIHFVEIRCYIDNLHFS GLEEWSDWSPVKNISWIPDSQTKVFPQDKVIL VGSDITFCCVSQEKVLSALIGHTNCPLIHLDGE NVAIKIRNISVSASSGTNVVFTTEDNIFGTVIF AGYPPDTPQQLNCETHDLKEICSWNPGRVTA LVGPRATSYTLVESFSGKYVRLKRAEAPTNES YQLLFQMLPNQEIYNFTLNAHNPLGRSQSTIL VNITEKVYPHTPTSFKVKDINSTAVKLSWHLP GNFAKINFLCEIEIKKSNSVQEQRNVTIKGVE NSSYLVALDKLNPYTLYTFRIRCSTETTWKW SKWSNKKQHLTTEASPSKGPDTWREWSSDG KNLIIYWKPLPINEANGKILSYNVSCSSDEETQ SLSEIPDPQHKAEIRLDKNDYIISVVAKNSVGS SPPSKIASMEIPNDDLKIEQVVGMGKGILLTW HYDPNMTCDYVIKWCNSSRSEPCLMDWRKV PSNSTETVIESDEFRPGIRYNFFLYGCRNQGY QLLRSMIGYIEELAPIVAPNFTVEDTSADSILV KWEDIPVEELRGFLRGYLFYFGKGERDTSKM RVLESGRSDIKVKNITDISQKTLRIADLQGKTS YHLVLRAYTDGGVGPEKSMYVVTKENSVGL IIAILIPVAVAVIVGVVTSILCYRKREWIKETFY PDIPNPENCKALQFQKSVCEGSSALKTLEMNP CTPNNVEVLETRSAFPKIEDTEIVSPVAERPEN RSDAKPENHVVESYCPPIIEEEIPNPAADETGG TAQVIYIDVQSMYQPQAKPEBEQENDPVGGA GYKPQMHLPINSTVEDIAAEEDLDKTAGYRP QANVNTWNLVSPDSPRSIDSNSEIVSFGSPCSI NSRQFLIPPKDEDSPKSNOGGWSFTNFFQNKP ND
1341	2691	A	10392	1	5057	MLPPKHLSATKPKKSWAPNLYELDSDLTKEP DVIIGEGPTDSEFFHQRFRNLIYVEFVGPRKTL IKLRNLCLDWLQPETRTKEEIIELLVLEQYLTII PEKLKPWVRAKKPENCEKLVTLLENYKEMY QPEGESLHGVLVVSAGLRCPLGLSASTLLTW SGLDNSLSWAAVGMSCVLWDIELHHDFLGV ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRESSPPH SVIISFSGDRDWDRRGRSRDTEPRDRWSITTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRYHFDTDGK GSIHDQKGCPRKKPFECGSEMRKAMSVSSLS SLSSPSFTESQPIDFGAMPYVCDECGRSFSVIS EFVEHQIMHTRENLYEYGESFIHSVAVSEVQK

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OPO TO	L OPG 10	) A C-4	CEC	Dendicted	Deadigted and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Mct	SEQ	Predicted	Predicted end	
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	ł	in	nucleotide .	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	O-Glutamine, R-Arginine, S-Scrine,
		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l	1	peptide	Soquotico	/=possible nucleotide deletion, \=possible
}		ł				
<u> </u>		<u> </u>	ļ <u>.</u>	sequence		nucleotide insertion
		ļ				SQVGGKRFECKDCGETFNKSAALAEHRKIHA
[		1	1	· ·	1	RGYLVECKNQECEEAFMPSPTFSELQKIYGK
	1	l	1			DKFYECRVCKETFLHSSALIEHQKIHFGDDKD
ĺ	1	1	{	(	1	NEREHERERERERGETFRPSPALNEFQKMYG
	1	l	1	İ		KEKMYECKVCGETFLHSSSLKEHOKIHTRGN
ł		l	1			PFENKGKVCEETFIPGQSLKRRQKTYNKEKLC
Î		1	1	,	1	DFTDGRDAFMQSSELSEHQKIHSRKNLFEGR
		l		i		GYEKSVIHSGPFTESQKSHTITRPLESDEDEKA
Į.		1				
i '	1	1	1	ĺ	ł	FTISSNPYENQKIPTKENVYEAKSYERSVIHSL
1			1	i	1	ASVEAQKSHSVAGPSKPKVMAESTIQSFDAIN
1	1	1	1		ĺ	HQRVRAGGNTSEGREYSRSVIHSLVASKPPRS
	1	1	Ì	!		HNGNELVESNEKGESSIYISDLNDKRQKIPAR
		1	1	1		ENPCEGGSKNRNYEDSVIQSVFRAKPQKSVP
1		1	1	I		GEGSGEFKKDGEFSVPSSNVREYQKARAKKK
1	1	1		ĺ	1	YIEHRSNETSVIHSLPFGEQTFRPRGMLYECQ
l		1.		Ì		ECGECFAHSSDLTEHQKIHDREKPSGSRNYE
1			1	1		WSVIRSLAPTDPQTSYAQEQYAKEQARNKCK
1	l .	Į.	1	ļ		DFRQFFATSEDLNTNQKIYDQEKSHGEESQGE
	1		1	i		NTDGEETHSEETHGQETIEDPVIQGSDMEDPQ
		j	1			
i		ļ				KDDPDDKIYECEDCGLGFVDLTDLTDHQKVH
	)	ļ	)	i	1	SRKCLVDSREYTHSVIHTHSISEYQRDYTGEQ
		ŀ				LYECPKCGESFIHSSFLFEHQRIHEQDQLYSM
i		j			]	KGCDDGFIALLPMKPRRNRAAERNPALAGSA
İ		1				IRCLLCGQGFIHSSALNEHMRLHREDDLLEQS
	l	l			· ·	QMAEEAIIPGLALTEFQRSQTEERLFECAVCG
1		ŀ				ESFVNPAELADHVTVHKNEPYEYGSSYTHTS
1		1				FLTEPLKGAIPFYECKDCGKSFIHSTVLTKHKE
		Į.		1		LHLEEEEDEAAAAAAAAQEVEANVHVPQ
1	1	ŀ	l			VVLRIQGLNVEAAEPEVEAAEPEVEAAEPEV
1		1	١,			EAAEPNGEAEGPDGEAAEPIGEAGQPNGEAE
i		1		1		
						QPNGDADEPDGAGIEDPEERAEEPEGKAEEPE
ł		ľ			1	GDADEPDGVGIEDPEEGEDQEIQVEEPYYDC
		[	1		<u> </u>	HECTETFTSSTAFSEHLKTHASMIFEPANAFG
l		1	i	l	l	ECSGYIERASTSTGGANQADEKYFKCDVCGQ
		İ			·	LFNDHLSLARHQNTHTG
1342	2692	Α	10393	2	1350	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSA
l		1	1			ASRRSPAARPPVPAPPALPRGRPGTEGSTSLS
1		ì	1 .		1	APAVLVVAVAVVVVVVSAVAWAMANYIHV
		l	1			PPGSPEVPKLNVTVQDQEEHRCREGALSLLQ
l	1	İ	1	1	1	HLRPHWDPQEVTLQLFTDGITNKLIGCYVGN
l		1	1	ļ	1	TO CONTRACTOR AND DEPARTMENT AND DEPARTMENT OF THE
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		1		I		QAHGCAPQLYCTFNNGLCYEFIQGEALDPKH
1		1	1	1	ļ	VCNPAIFRLIARQLAKIHAIHAHNGWIPKSNL
!		1	i	1	]	WLKMGKYFSLIPTGFADEDINKRFLSDIPSSQI
l		1		1	1	LQEEMTWMKEILSNLGSPVVLCHNDLLCKNII
		1	1		ł	YNEKQGDVQFIDYEYSGYNYLAYDIGNHFNE
1		1	1	[	1	FAGVSDVDYSLYPDRELQSQWLRAYLEAYK
	1		1		l	EFKGFGTEVTEKEVEILFIQVNQFALASHFFW
1		1	1	l	Í	GLWALIQAKYSTIEFDFLGYAIVRFNQYFKM
1		1			l	KPEVTALKVPE
1343	2693	A	10394	102	839	PEAQTSAVLAREKGHLPTMRHEAPMQMASA
1242	2073	] ^	10394	102	037	
		1		1	1	QDARYGQKDSSDQNFDYMFKLLIIGNSSVGK
1		1	t		1	TSFLFRYADDSFTSAFVSTVGIDFKVKTVFKN
ĺ		I	Ì	I	1	EKRIKLQIWDTAGQERYRTITTAYYRGAMGFI
}		l	1	1	1	LMYDITNEESFNAVQDWSTQIKTYSWDNAQ
		1	1		ŀ	VILVGNKCDMEDERVISTERGQHLGEQLGFE
1	-	1	1	}	J.	FFETSAKDNINVKOTFERLVDIICDKMSESLET
	1	ì	1		Į.	DPAITAAKQNTRLKETPPPPQPNCAC
1344	2694	A	10395	2	4136	DRPPWNSRVDDFVTNLIHLSSKGHISPAKDTS
	2077	1"	10393	1	1130	LQQRTPAEMSPVLHFYVRPSGHEGAASGHTR
L		ــــــــــــــــــــــــــــــــــــــ	J		L	PAKELL UTWING ATTEL LAND DOLLTOWNOUTLY

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RKLQGKLPELQGVETELCYNVNWTAEALPSA EETKKLMWLFGCPLLLDDVARESWLLPGSN DLLLEVGPRLNFSTPTSTINIVSVCRATGLGPV DRVETTRYRLSFAHPPSAEVEAIALATLHDR MTEQHFPHPIQSFSPESMPEPLNGPINILGEGR LALEKANQELGLALDSWDLDFYTKRFQELQR NPSTVEAFDLAQSNSEHSRHWFFKGQLHVDG QKLVHSLFESIMSTQESSNPNNVLKFCDNSSA IQGKEVRFLRPEDPTRPSRFQQQQGLRHVVFT AETHNFPTGVCPFSGATTGTGGRIRDVQCTG RGAHVVAGTAGYCFGNLHIPGYNLPWEDLSF QYPGNFARPLEVAIGASNGASDYGNKFGEPV LAGFARSLGLQLPDGQRREWIKPIMFSGGIGS MEADHISKEAPEPGMEVVKVGGPVYRIGVGG GAASSVQVQGDNTSDLDFGAVQRGDPEMEQ KMNRVIRACVEAPKGNPICSLHDQGAGGNG NVLKELSDPAGAIIYTSRFQLGDPTLNALEIW GAEYQESNALLLRSPNRDFLTHVSARERCPA CFVGTITGDRRIVLVDDRECPVRRNGQGDAP PTPPPTPVDLELEWVLGKMPRKEFFLQRKPP MLQPLALPPGLSVHQALERVLRLPAVASKRY LTNKVDRSVGGLVAQQQCVGPLQTPLADVA VVALSHEELIGAATALGEQPVKSLLDPKVAA RLAVAEALINLVFALVTDLRDVKCSGNWM WAAKLPGEGAALADACEAMVAVMAALGVA VDGGKDSLSMAARVGTETVRAPGSLVISAYA VCPDITATVTTPDLKHPEGRGHLLYVALSPGQ HRLGGTALAQCFSQLGEHPPDLDLPENLVRA FSITQGLLKDRLLCSGHDVSDGGLVTCLLEM AFAGNCGLQVDVPVPRVDVLSVLFAEEPGLV LEVQEPDLAQVLKRYRDAGLHCLELGHTGE AGPHAMVRVSVNGAVVLEEPVGELRALWEE TSFQLDRLQAEPRCVAEEERGLRERMGPSYC LPTTPPKASVPREPGGPSPRVALLREEGSNGDR EMADAFHLAGFEVWDVTMQDLCSGAIGLDT FRGVAFVGGFSYADVLGSAKGWAAAVTFHP RAGAELRRFRKRPDTFSLGVCNGCQLLALLG WVGGDPNEDAAEMGPDSQPARPGLLLRHNL SGRYESRWASVRVOPGPALMRRMEGAVLP VWSAHGEGYVAFSSPELQAQIEARGLAPLHW ADDDGNPTEQYPLNPNGSPGGVAGICSCDGR HLAVMPHPERAVRPWQWAWRPPPFDTLTTS
1345	2695	A		65	642	PWLQLFINARNWTLEGSC  GVRGFWAGTMASRAGPRAAGTDGSDFQHRE RVAMHYQMSVTLKYEIKKLIYVHLVIWLLLV AKMSVGHLRLLSHDQVAMPYQWEYPYLLSI LPSLLGLLSFPRNNISYLVLSMISMGLFSIAPLI YGSMEMFPAAQQLYRHGKAYRFLFGFSAVSI MYLVLVLAVQVHAWQLYYSKKLLDSWFTST QEKKHK
1346					718	DDFVRCGPQSAAMGASARLLRAVIMGAPGS GKGTVSSRITTHFELKHLSSGDLLRDNMLRGT EIGVLAKAFIDQGKLIPDDVMTRLALHELKNL TQYSWLLDGFPRTLPQAEALDRAYQIDTVINL NVPFEVIKQRLTARWIHPASGRVYNIEFNPK TVGIDDLTGEPLIQREDDKPETVIKRLKAYED QTKPVLEYYQKKGVLETFSGTETNKIWPYVY AFLQTKVPQRSQKASVTP
1347	2697	A	10402	153	1969	KHRQENNALDMAPEIHMTGPMCLIENTNGEL VANPEALKILSAITQPVVVVAIVGLYRTGKSY

SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	J	]	j	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	[	į	peptide		/=possible nucleotide deletion, \=possible
l	Ì	1		sequence		nucleotide insertion
		<del></del>	<del> </del>	- Coquanto		LMNKLAGKNKGFSLGSTVKSHTKGIWMWCV
İ	i	i	i	İ	İ	PHPKKPEHTLVLLDTEGLGDVKKGDNQNDS
ľ	i	Ì	ľ		1	WIFTLAVLLSSTLVYNSMGTINQQAMDQLYY
		1	1	i	i	VTELTHRIRSKSSPDENENEDSADFVSFPPDFV
}	ł	ł			!	WTLRDFSLDLEADGOPLTPDEYLEYSLKLTQ
i		1		Į	İ	GTSQKDKNFNLPRLCIRKFFPKKKCFVFDLPI
	l	!	ł	ŀ	1	HRRKLAQLEKLQDEELDPEFVQQVADFCSYI
		1	į		i	FSNSKTKTLSGGIKVNGPRLESLVLTYINAISR
ì		1				GDLPCMENAVLALAQIENSAAVQKAIAHYD
į	1	]			!	QQMGQKVQLPAETLQELLDLHRVSEREATEV
	)	ļ	]	ļ	ļ	YMKNSFKDVDHLFQKKLAAQLDKKRDDFCK
1				ľ ·		ONOEASSDRCSALLOVIFSPLEEEVKAGIYSK
		ļ				PGGYCLFIQKLQDLEKKYYEBPRKGIQAEEIL
I	[	1	l			OTYLKSKESVTDAILQTDQILTEKEKEIEVEC
						VKAESAQASAKMVEEMQIKYQQMMEEKEKS
		İ				YQEHVKQLTEKMERERAQLLEEQEKTLTSKL
	1	l	l	!		QEQARVLKERCQGESTQLQNEIQKLQKTLKK
			l			KTKRYMSHKLKI
1348	2698	A	10404	5	892	TOLPAPLSGVLSRLQLGSGAPLLTWVQETAG
1340	2076	1	10104	١	672	VAGGAPRRTTPVTMWRLLARASAPLLRVPLS
į .			l			DSWALLPASAGVKTLLPVPSFEDVSIPEKPKL
1		l				RFIERAPLVPKVRREPKNLSDIRGPSTEATEFT
	Ì		l			EGNFAILALGGGYLHWGHFEMMRLTINRSM
1	l	İ			i	DPKNMFAIWRVPAPFKPITRKSVGHRMGGGK
1	İ	l				GAIDHYVTPVKAGRLVVEMGGRCEFEEVQG
	1				ł	FLDQVAHKLPFAAKAVSRGTLEKMRKDQEE
1	l	i	i		1	RERNNONPWTFERIATANMLGIRKVLSPYDL
1		l	i		[	THKGKYWGKFYMPKRV
1349	2699	A	10409	59	1184	LRRNCSALGGLFQTTISDMKGSYPVWEDFINK
1.577	1	١	1.07.07		-10.	AGKLQSQLRTTVVAAAAFLDAFQKVADMAT
	İ		l	1	!	NTRGGTREIGSALTRMCMRHRSIEAKLROFSS
	1	1	l	ĺ	İ	ALIDCLINPLQEQMEEWKKVANQLDKDHAK
	1			]		EYKKARQEIKKKSSDTLKLQKKAKKGRGDIQ
İ	1	}	l		i	POLDSALQDVNDKYLLLEETEKQAVRKALIE
				1		ERGRECTEISMLRPVIEEEISMLGEITHLQTISE
ļ				ĺ		DLKSLTMDPHKLPSSSEQVILDLKGSDYSWS
.	l			1	Ì	YOTPPSSPSTTMSRKSSVCSSLNSVNSSDSRSS
	1	[	1	{	[	GSHSHSPSSHYRYRSSNLAQQAPVRLSSVSSH
				ļ	ļ	DSGFISQDAFQSKSPSPMPPEAPNQRRKEKRE
1	l	l	l	ł	1	PDPNGGGPTTASGPPAAAEBAQRPRSM
1350	2700	A	10410	511	958	AGRGGPGKPVSWSSGPGSPGQTQRRSWVKST
1330	2,00	^	10410	1 "	730	RGHSSLLPPSODFVAGLSVILRGTVDDRLNW
1				!	1	AFNLYDLNKDGCITKEEMLDIMKSIYDMMG
	ļ	1 .	1	1	1	P
				•	1	KYTYPALREEAPREHVESFFQKMDRNKDGV VTIEEFIESCQKDENIMRSMQLFDNVI

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1350.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-1350, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).
- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1351-2700, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-1350.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

Pages  $\,340\,\mathrm{to}\,1963\,$  of this application contain amino acid sequence listings. They can be obtained at the address given below.

Les pages 340 to 1963 de cette demande contiennent des listages des séquences d'acides aminés. Elles peuvent être obtenues à l'adresse indiquée ci-dessous.

World Intellectual Property Organization 34, chemin des Colombettes CH-1211 Genève 20

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.